

Table 9: GBS genes shared with pneumococcus

ORFxxxxx Annotation

ORF01580 polysaccharide biosynthesis protein, putative
ORF01612 conserved hypothetical protein
ORF01613 glycosyl transferase, group 1 family protein
ORF01617 conserved hypothetical protein
ORF01618 conserved hypothetical protein
ORF01621 glycosyl transferase, putative
ORF01622 glycosyl transferase, group 2 family protein
ORF01623 glycosyl transferase, family 8, degenerate
ORF01624 IS1381, transposase OrfB
ORF01625 IS1381, transposase OrfA
ORF01626 glycosyl transferase family 8
ORF01627 glycosyl transferase, family 8
ORF01628 conserved hypothetical protein
ORF01630 cell wall surface anchor family protein
ORF01635 protease, putative
ORF01643 aminopeptidase PepS (pepS)
ORF01702 peptidase, M20/M25/M40 family
ORF01731 IS1381, transposase OrfA
ORF01732 IS1381, transposase OrfB
ORF01740 tellurite resistance protein TehB (tehB)
ORF01747 methylated-DNA--protein-cysteine S-methyltransferase (ogt)
ORF01749 acetyltransferase, GNAT family
ORF01763 AcuB family protein
ORF01764 branched-chain amino acid ABC transporter, ATP-binding protein (livF)
ORF01765 branched-chain amino acid ABC transporter, ATP-binding protein (livG)
ORF01766 branched-chain amino acid ABC transporter, permease protein
ORF01767 branched-chain amino acid ABC transporter, permease protein (livH)
ORF01769 branched-chain amino acid ABC transporter, amino acid-binding protein
ORF01775 aminotransferase, class I
ORF01779 potassium uptake protein, Trk family
ORF01780 cation uptake protein, Trk family
ORF01824 cobalt transport family protein
ORF01826 conserved hypothetical protein
ORF01832 peptidase, M20/M25/M40 family
ORF01845 conserved hypothetical protein
ORF01848 transcriptional regulator, MerR family
ORF01853 isochorismatase family protein
ORF01859 membrane protein
ORF01875 oxidoreductase, aldo/keto reductase family
ORF01880 phospho-2-dehydro-3-deoxyheptonate aldolase
ORF01981 rRNA (guanine-N1-)-methyltransferase, putative
ORF02083 prophage LambdaSa2, DNA replication protein DnaC, putative
ORF02101 Na ⁺ /H ⁺ exchanger family protein
ORF02107 membrane protein, putative
ORF02139 UDP-glucose 4-epimerase (galE)
ORF02143 lacX protein
ORF02162 conserved hypothetical protein
ORF02186 hemolysin precursor, putative
ORF02192 transcriptional regulator, MerR family
ORF02195 MutT/nudix family protein
ORF02228 IS1381, transposase OrfB
ORF02229 IS1381, transposase OrfA
ORF02233 conserved hypothetical protein
ORF02234 conserved hypothetical protein
ORF02276 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (metE)

Table 9: GBS genes shared with pneumococcus**ORFxxxxx Annotation**

ORF02278 branched-chain amino acid transport protein AzlC, putative
ORF02288 glycosyl transferase, family 8
ORF02289 glycosyl transferase, family 8
ORF02341 ribosomal protein L32 (rpmF)
ORF02343 conserved hypothetical protein
ORF02358 sensor histidine kinase
ORF02369 conserved hypothetical protein
ORF02384 LysM domain protein
ORF02428 hypoxanthine-guanine phosphoribosyltransferase (hpt)
ORF03011 ribosomal protein L33
ORF03014 ribosomal protein L33

Table 10: GBS genes shared with GAS

ORFxxxxx Annotation

ORF00064 ribosomal protein S14, putative
ORF00095 D-alanyl-D-alanine carboxypeptidase family protein
ORF00096 N-acetylmuramoyl-L-alanine amidase, family 4 protein
ORF00110 conserved hypothetical protein
ORF00112 DNA repair protein RadA (radA)
ORF00124 permease, putative
ORF00148 glycosyl transferase, group 4 family protein
ORF00154 penicillin-binding protein 4, putative
ORF00157 oligopeptide ABC transporter, permease protein
ORF00206 oligopeptide ABC transporter, oligopeptide-binding protein
ORF00207 oligopeptide ABC transporter, permease protein
ORF00208 oligopeptide ABC transporter, permease protein
ORF00209 peptide ABC transporter, ATP-binding protein
ORF00210 peptide ABC transporter, ATP-binding protein
ORF00216 IS1548, transposase
ORF00226 conserved hypothetical protein
ORF00232 conserved hypothetical protein
ORF00239 site-specific recombinase, phage integrase family
ORF00250 conserved hypothetical protein
ORF00251 conserved hypothetical protein
ORF00289 ABC transporter, ATP-binding protein
ORF00305 NADH oxidase, putative
ORF00317 cell division protein FtsL, putative
ORF00333 conserved hypothetical protein
ORF00383 hydrolase, haloacid dehalogenase-like family
ORF00430 expressed putative lipoprotein
ORF00431 transcriptional repressor CopY
ORF00434 membrane protein, putative
ORF00438 transcriptional regulator, Fur family
ORF00442 membrane protein, putative
ORF00445 bioY family protein
ORF00446 AtsA/ElaC family protein
ORF00468 expressed putative protease
ORF00469 glycosyl transferase, group 2 family protein
ORF00471 nrdI protein (nrdI)
ORF00473 expressed protein of unknown function
ORF00474 conserved hypothetical protein
ORF00507 conserved hypothetical protein
ORF00525 bioY family protein
ORF00528 thiolase
ORF00531 AMP-binding enzyme domain protein
ORF00548 YGGT family protein
ORF00565 exodeoxyribonuclease VII, small subunit (xseB)
ORF00568 arginine repressor ArgR, putative
ORF00572 expressed putative lipase/acylhydrolase
ORF00573 conserved hypothetical protein
ORF00586 iron-sulfur cluster-binding protein, putative
ORF00592 oxidoreductase, short chain dehydrogenase/reductase family
ORF00604 dipeptidase
ORF00611 voltage-gated chloride channel family protein
ORF00619 prophage LambdaSa1, repressor protein, putative
ORF00622 conserved hypothetical protein
ORF00627 prophage LambdaSa1, antirepressor, putative
ORF00634 conserved hypothetical protein
ORF00648 conserved hypothetical protein

Table 10: GBS genes shared with GAS

ORFxxxxx Annotation

ORF00654 conserved hypothetical protein
ORF00655 conserved hypothetical protein
ORF00656 conserved hypothetical protein
ORF00658 conserved hypothetical protein
ORF00659 conserved hypothetical protein
ORF00660 prophage LambdaSa1, structural protein, putative
ORF00662 conserved hypothetical protein
ORF00663 conserved hypothetical protein
ORF00664 conserved hypothetical protein
ORF00665 conserved hypothetical protein
ORF00666 prophage LambdaSa1, structural protein
ORF00668 conserved hypothetical protein
ORF00669 prophage LambdaSa1, pblA protein, internal deletion
ORF00677 prophage LambdaSa1, lysin, putative
ORF00679 conserved hypothetical protein
ORF00695 transposase OrfB, IS3 family, truncation
ORF00697 conserved hypothetical protein
ORF00707 conserved domain protein
ORF00713 acid phosphatase precursor, class B
ORF00720 transposase OrfB, IS3 family FRAMESHIFT
ORF00721 transposase OrfA, IS3 family
ORF00751 cylA protein (cylA)
ORF00755 cylI protein (cylI)
ORF00760 serine protease, subtilase family, putative POINT MUTATION
ORF00781 transcriptional regulator, LysR family
ORF00783 regulatory protein, putative
ORF00785 IS1548, transposase
ORF00786 regulatory protein, putative, truncation
ORF00787 D-lactate dehydrogenase (ldhA)
ORF00801 glycosyl transferase, group 1 family protein
ORF00805 conserved hypothetical protein
ORF00826 phage shock protein C, putative
ORF00833 conserved hypothetical protein
ORF00845 hydrolase, haloacid dehalogenase-like family
ORF00852 conserved hypothetical protein
ORF00853 expressed putative lipoprotein
ORF00857 IS1548, transposase
ORF00890 conserved hypothetical protein
ORF00902 conserved hypothetical protein
ORF00926 membrane protein, putative
ORF00927 membrane protein, putative
ORF00987 conserved hypothetical protein
ORF01009 expressed protein of unknown function
ORF01010 lipoyl-binding domain protein
ORF01011 oxidoreductase, putative
ORF01012 conserved hypothetical protein
ORF01024 expressed putative lipoprotein
ORF01061 signal peptidase I, putative
ORF01064 IS1548, transposase
ORF01084 glyoxylase family protein
ORF01104 SatD
ORF01126 conserved hypothetical protein
ORF01191 conserved hypothetical protein
ORF01192 conserved hypothetical protein
ORF01193 glycine cleavage system H protein, putative

Table 10: GBS genes shared with GAS

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ORF01194 bacterial luciferase family protein
ORF01195 oxidoreductase, FMN-binding
ORF01197 lipoate-protein ligase A family protein
ORF01202 IS861, transposase OrfA
ORF01223 drug resistance transporter, EmrB/QacA family, putative
ORF01224 conserved hypothetical protein
ORF01225 potassium uptake protein, putative
ORF01237 membrane protein, putative
ORF01249 dihydroneopterin aldolase (folB)
ORF01256 polysaccharide deacetylase family protein
ORF01273 transcriptional regulator, GntR family/potassium uptake protein, TrkA family
ORF01280 conserved hypothetical protein
ORF01281 conserved hypothetical protein
ORF01289 lipoprotein, putative
ORF01291 conserved hypothetical protein
ORF01298 conserved hypothetical protein
ORF01318 conserved hypothetical protein
ORF01320 voltage-gated chloride channel family protein, putative
ORF01322 arsenate reductase (arsC)
ORF01340 dTDP-glucose 4,6-dehydratase (rfbB)
ORF01341 dTDP-4-dehydrorhamnose 3,5-epimerase
ORF01342 glucose-1-phosphate thymidyltransferase (rfbA)
ORF01356 hypothetical protein
ORF01368 conserved hypothetical protein
ORF01374 ISSdy1, transposase OrfB
ORF01388 transposase OrfA, IS3 family
ORF01389 transposase OrfB, IS3 family, truncation
ORF01391 ISSdy1, transposase OrfB FRAMESHIFT
ORF01396 transcriptional regulator, Cro/C1 family
ORF01419 repressor protein, putative
ORF01461 amino acid permease
ORF01469 conserved hypothetical protein
ORF01483 sensor histidine kinase
ORF01485 GTP pyrophosphokinase family protein
ORF01490 5'-nucleotidase family protein
ORF01509 2-dehydropantoate 2-reductase, putative
ORF01510 regulatory protein, putative
ORF01522 carbamoyl-phosphate synthase, large subunit, putative
ORF01542 sulfatase
ORF01549 conserved hypothetical protein
ORF01554 iron compound ABC transporter, substrate-binding protein
ORF01557 conserved hypothetical protein
ORF01563 conserved hypothetical protein TIGR01212
ORF01583 glycosyltransferase, group 2 family protein
ORF01584 glycosyltransferase, group 2 family protein
ORF01585 glycosyltransferase, putative
ORF01586 dTDP-4-dehydrorhamnose reductase (rfbD)
ORF01593 conserved hypothetical protein
ORF01599 conserved hypothetical protein
ORF01600 glycerol-3-phosphate transporter, putative
ORF01639 conserved hypothetical protein
ORF01650 nitroreductase family protein
ORF01653 amino acid permease
ORF01665 transcriptional regulator, MutR family
ORF01683 MutT/nudix family protein

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ORF01686	67 kDa Myosin-crossreactive streptococcal antigen
ORF01688	peptide methionine sulfoxide reductase (msrA)
ORF01694	peptide ABC transporter, permease protein
ORF01704	conserved hypothetical protein
ORF01705	IS861, transposase OrfA
ORF01741	membrane protein, putative
ORF01770	conserved hypothetical protein
ORF01772	IS1548, transposase
ORF01790	conserved hypothetical protein
ORF01794	conserved hypothetical protein
ORF01800	amino acid ABC transporter, substrate-binding protein
ORF01810	IS1548, transposase
ORF01827	sodium:dicarboxylate symporter family protein
ORF01877	immunogenic secreted protein, putative
ORF01913	transcriptional regulator, Cro/C1 family
ORF01928	membrane protein, putative
ORF01931	transporter, putative
ORF01932	transcriptional regulator, Crp/Fnr family
ORF01947	transcriptional regulator, merR family
ORF01970	acid phosphatase
ORF02002	amino acid ABC transporter, permease protein
ORF02028	perfringolysin O regulator protein (pfoR)
ORF02029	conserved hypothetical protein
ORF02031	expressed protein of unknown function
ORF02032	expressed protein of unknown function
ORF02035	deoxynucleoside kinase family protein
ORF02042	alkyl hydroperoxide reductase, subunit C (ahpC)
ORF02126	transcriptional regulator, MarR family
ORF02128	N-acetylmuramoyl-L-alanine amidase, family 4 protein
ORF02135	malate oxidoreductase
ORF02136	citrate carrier protein, CCS family
ORF02137	sensor histidine kinase family protein
ORF02138	response regulator
ORF02166	conserved hypothetical protein
ORF02169	PTS system, IIB component
ORF02170	PTS system, IIA component, putative
ORF02202	ABC transporter, ATP-binding protein
ORF02262	ABC transporter, ATP-binding protein
ORF02270	cAMP factor (cfb)
ORF02280	serine protease, subtilase family, putative
ORF02286	major facilitator family protein
ORF02292	preprotein translocase, SecE subunit, putative
ORF02295	Lyme disease proteins of unknown function, putative
ORF02298	Na ⁺ dependent nucleoside transporter
ORF02301	transcriptional regulator, GntR family
ORF02313	virulence factor MviM, putative
ORF02316	membrane protein, putative
ORF02319	conserved hypothetical protein TIGR00250
ORF02328	transporter, putative
ORF02331	cold shock protein, CSD family
ORF02332	DNA mismatch repair protein HexA (hexA)
ORF02335	conserved hypothetical protein
ORF02372	conserved hypothetical protein
ORF02383	expressed putative lipoprotein
ORF02393	transporter, putative

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ORF02398	transcriptional regulator, Crp/Fnr family
ORF02399	conserved hypothetical protein
ORF02401	acetyltransferase, GNAT family
ORF02403	arginine/ornithine antiporter (arcD)
ORF03002	conserved hypothetical protein, truncation

Table 11: GBS genes not shared with GAS or pneumococcus

ORFxxxxx Annotation
ORF00008 protease, putative
ORF00010 acyl carrier protein (acpP)
ORF00016 acetyltransferase, GNAT family
ORF00018 peptidase, M23/M37 family, putative secreted protein
ORF00035 membrane protein, putative
ORF00087 lipoprotein, putative
ORF00088 hypothetical protein
ORF00089 hypothetical protein
ORF00091 conserved hypothetical protein
ORF00117 ribose ABC transporter, periplasmic D-ribose-binding protein (rbsB)
ORF00118 ribose ABC transporter, permease protein (rbsC)
ORF00120 ribose ABC transporter protein RbsD (rbsD)
ORF00121 ribokinase (rbsK)
ORF00123 hypothetical protein
ORF00130 argininosuccinate lyase (argH)
ORF00137 conserved hypothetical protein
ORF00138 hypothetical protein
ORF00166 4-diphosphocytidyl-2C-methyl-D-erythritol kinase (ispE)
ORF00182 conserved domain protein
ORF00186 transcriptional regulator, Cro/C1 family
ORF00187 hypothetical protein
ORF00188 hypothetical protein
ORF00192 hypothetical protein
ORF00193 conserved hypothetical protein
ORF00196 conserved hypothetical protein
ORF00199 hydrolase, haloacid dehalogenase-like family
ORF00200 sensor histidine kinase, putative
ORF00201 response regulator
ORF00203 conserved hypothetical protein
ORF00204 membrane protein, putative
ORF00205 hypothetical protein
ORF00228 lipoprotein, putative
ORF00234 hypothetical protein
ORF00235 hypothetical protein
ORF00238 hypothetical protein
ORF00240 transcriptional regulator, Cro/C1 family
ORF00241 hypothetical protein
ORF00242 conserved hypothetical protein
ORF00243 hypothetical protein
ORF00244 conserved domain protein
ORF00245 conserved hypothetical protein, fusion
ORF00246 replication initiation protein, putative
ORF00247 hypothetical protein
ORF00248 recombination protein
ORF00249 hypothetical protein
ORF00252 conserved hypothetical protein
ORF00253 hypothetical protein
ORF00254 hypothetical protein
ORF00255 hypothetical protein
ORF00256 hypothetical protein
ORF00257 hypothetical protein
ORF00258 hypothetical protein
ORF00259 hypothetical protein
ORF00260 hypothetical protein
ORF00272 expressed putative lipoprotein

Table 11: GBS genes not shared with GAS or pneumococcus

ORFxxxxx Annotation
ORF00273 hypothetical protein
ORF00274 hypothetical protein
ORF00275 hypothetical protein
ORF00276 hypothetical protein
ORF00278 membrane protein, putative
ORF00279 transcriptional regulator, Cro/C1 family
ORF00280 acetyltransferase, GNAT family
ORF00281 acetyltransferase, GNAT family
ORF00283 conserved hypothetical protein
ORF00284 RNA polymerase sigma factor, ECF subfamily
ORF00285 lipoprotein, putative
ORF00287 transcriptional regulator, TetR family
ORF00288 ABC transporter efflux protein, DrrB family, putative
ORF00292 hypothetical protein
ORF00294 expressed protein of unknown function
ORF00298 acyl carrier protein phosphodiesterase, putative
ORF00308 conserved hypothetical protein
ORF00324 conserved hypothetical protein
ORF00332 hypothetical protein
ORF00340 hypothetical protein
ORF00347 conserved hypothetical protein
ORF00384 hypothetical protein
ORF00402 membrane protein, putative
ORF00408 hypothetical protein
ORF00409 membrane protein, putative
ORF00414 conserved hypothetical protein
ORF00416 hypothetical protein
ORF00417 hypothetical protein
ORF00433 copper-transporter protein CopZ
ORF00448 hypothetical protein
ORF00466 conserved hypothetical protein
ORF00467 acetyltransferase, GNAT family
ORF00475 conserved domain protein
ORF00476 hypothetical protein
ORF00478 carboxymuconolactone decarboxylase family protein
ORF00479 conserved hypothetical protein
ORF00486 transcriptional regulator, AraC family
ORF00487 surface protein Rib
ORF00488 transposase, IS256 family, truncation
ORF00489 DNA-damage-inducible protein J, putative
ORF00490 hypothetical protein
ORF00491 lipoprotein, putative
ORF00493 bacteriophage L54a, integrase, truncation
ORF00497 conserved domain protein
ORF00503 oxidoreductase, Gfo/Idh/MocA family
ORF00506 transposase, IS256 family
ORF00510 bacteriocin transport accessory protein, putative
ORF00512 hypothetical protein
ORF00526 biotin synthetase (bioB)
ORF00527 hypothetical protein
ORF00533 type IV prepilin peptidase-related protein
ORF00538 conserved hypothetical protein
ORF00556 hypothetical protein
ORF00563 expressed protein of unknown function
ORF00575 hypothetical protein

Table 11: GBS genes not shared with GAS or pneumococcus

ORFxxxxx Annotation
ORF00584 conserved hypothetical protein
ORF00585 fructose-1,6-bisphosphatase, putative
ORF00590 carboxymethylenebutenolide-related protein
ORF00597 conserved hypothetical protein
ORF00598 inosine-uridine preferring nucleoside hydrolase
ORF00599 hypothetical protein
ORF00600 OsmC/Ohr family protein
ORF00608 adenosine deaminase, putative
ORF00610 chorismate mutase, putative
ORF00615 prophage LambdaSa1, site-specific recombinase, phage integrase family
ORF00617 conserved domain protein
ORF00618 hypothetical protein
ORF00620 hypothetical protein
ORF00621 conserved hypothetical protein
ORF00623 hypothetical protein
ORF00624 hypothetical protein
ORF00626 prophage LambdaSa1, transcriptional regulator, Cro/C1 family
ORF00628 hypothetical protein
ORF00630 hypothetical protein
ORF00632 hypothetical protein
ORF00633 conserved hypothetical protein
ORF00635 hypothetical protein
ORF00636 hypothetical protein
ORF00637 hypothetical protein
ORF00638 conserved hypothetical protein
ORF00639 conserved domain protein
ORF00641 prophage LambdaSa1, reverse transcriptase/maturase family protein
ORF00642 conserved hypothetical protein
ORF00643 conserved hypothetical protein
ORF00644 hypothetical protein
ORF00645 hypothetical protein
ORF00646 conserved hypothetical protein
ORF00647 hypothetical protein
ORF00649 hypothetical protein
ORF00650 hypothetical protein
ORF00652 conserved hypothetical protein
ORF00653 conserved hypothetical protein
ORF00657 conserved hypothetical protein, truncation
ORF00661 conserved hypothetical protein
ORF00667 conserved hypothetical protein
ORF00670 prophage LambdaSa1, minor structural protein, putative
ORF00671 prophage LambdaSa1, N-acetylmuramoyl-L-alanine amidase, family 4
ORF00672 prophage LambdaSa1, minor structural protein, putative
ORF00673 hypothetical protein
ORF00674 hypothetical protein
ORF00675 conserved hypothetical protein
ORF00676 conserved hypothetical protein
ORF00678 conserved hypothetical protein
ORF00681 conserved hypothetical protein
ORF00682 hypothetical protein
ORF00683 prophage LambdaSa1, site-specific recombinase, phage integrase family FRAMESHIFT
ORF00685 conserved hypothetical protein
ORF00689 conserved hypothetical protein, FRAMESHIFT
ORF00698 hypothetical protein
ORF00703 phosphoserine phosphatase SerB (serB)

Table 11: GBS genes not shared with GAS or pneumococcus

ORFxxxxx Annotation
ORF00704 MutT/nudix family protein
ORF00712 hypothetical protein
ORF00718 cell wall surface protein, interruption-N
ORF00723 hypothetical protein
ORF00726 transcriptional regulator, AraC family
ORF00727 expressed cell wall surface anchor family protein
ORF00728 expressed cell wall surface anchor family protein
ORF00735 expressed protein of unknown function
ORF00737 conserved hypothetical protein, degenerate
ORF00738 hypothetical protein
ORF00740 hypothetical protein
ORF00741 hypothetical protein
ORF00742 lipoprotein, putative
ORF00747 cylD protein (cylD)
ORF00749 acyl carrier protein AcpC
ORF00750 cylZ protein FRAMESHIFT
ORF00752 cylB protein (cylB)
ORF00753 cylE protein (cylE)
ORF00754 cylF protein (cylF)
ORF00756 cylJ protein (cylJ)
ORF00757 cylK protein (cylK)
ORF00758 hypothetical protein
ORF00759 putative secreted protein
ORF00761 hypothetical protein
ORF00766 expressed putative secreted protein
ORF00767 hypothetical protein
ORF00768 conserved domain protein
ORF00769 permease, putative
ORF00775 conserved hypothetical protein
ORF00777 DedA family protein, putative
ORF00779 membrane protein, putative
ORF00788 sodium:galactoside symporter family protein, putative
ORF00791 transcriptional regulator, GntR family
ORF00793 Glucuronate isomerase (uxaC)
ORF00794 mannonate dehydratase (uxuA)
ORF00795 D-mannonate oxidoreductase
ORF00796 hydrolase, haloacid dehalogenase-like family
ORF00797 glycosyl hydrolase, family 3
ORF00806 conserved hypothetical protein
ORF00822 ABC transporter, ATP-binding protein
ORF00827 hypothetical protein
ORF00834 conserved hypothetical protein
ORF00838 membrane protein, putative
ORF00839 Mn ²⁺ /Fe ²⁺ transporter, NRAMP family
ORF00848 conserved domain protein
ORF00872 cell wall surface anchor family protein
ORF00874 conserved hypothetical protein
ORF00878 ABC transporter, permease protein
ORF00879 YaeC family protein, putative
ORF00888 hydrolase, haloacid dehalogenase-like family
ORF00891 conserved domain protein
ORF00898 conserved hypothetical protein
ORF00900 permease, GntP family
ORF00903 transcriptional regulator, MarR family
ORF00907 glutathione S-transferase family protein

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ORFxxxxx Annotation
ORF00909 hypothetical protein
ORF00921 membrane protein, putative
ORF00922 glycosyl transferase, family 8
ORF00923 hypothetical protein
ORF00924 conserved hypothetical protein
ORF00939 conserved hypothetical protein
ORF00942 expressed putative secreted protein
ORF00943 hypothetical protein
ORF00944 hypothetical protein
ORF00946 conserved hypothetical protein
ORF00950 hypothetical protein
ORF00951 transcriptional regulator, TenA family
ORF00972 ATP synthase F0, C subunit (atpE)
ORF00980 conserved hypothetical protein
ORF00982 conserved hypothetical protein
ORF01003 conserved hypothetical protein
ORF01004 conserved hypothetical protein
ORF01013 hypothetical protein
ORF01014 hypothetical protein
ORF01015 hypothetical protein
ORF01016 hypothetical protein
ORF01018 hypothetical protein
ORF01019 hypothetical protein
ORF01021 hypothetical protein
ORF01025 HD domain protein
ORF01026 acetyltransferase, GNAT family
ORF01032 chloramphenicol acetyltransferase (cat)
ORF01034 Tn916, transposase
ORF01035 Tn916, excisionase
ORF01037 Tn916, hypothetical protein
ORF01038 Tn916, hypothetical protein
ORF01039 Tn916, transcriptional regulator, putative
ORF01041 Tn916, hypothetical protein
ORF01042 Tn916, NLP/P60 family protein
ORF01044 membrane protein, putative FRAMESHIFT
ORF01048 Tn916, hypothetical protein
ORF01049 Tn916, hypothetical protein
ORF01050 Tn916, hypothetical protein
ORF01051 Tn916, transcriptional regulator, putative
ORF01052 Tn916, FtsK/SpoIIIE family protein
ORF01053 Tn916, hypothetical protein
ORF01054 Tn916, hypothetical protein
ORF01062 hypothetical protein
ORF01086 Na ⁺ /H ⁺ exchanger family protein
ORF01092 acetyltransferase, GNAT family
ORF01096 nisin-resistance protein, putative
ORF01103 conserved hypothetical protein
ORF01124 acetyltransferase, GNAT family
ORF01133 iron-compound ABC transporter, iron-compound-binding protein
ORF01140 conserved hypothetical protein
ORF01142 carbon starvation protein CstA, putative
ORF01143 response regulator
ORF01144 sensor histidine kinase, putative
ORF01145 lipoprotein, putative
ORF01146 conserved hypothetical protein, FRAMESHIFT

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ORFxxxxx Annotation
ORF01148 lipoprotein, putative
ORF01149 hypothetical protein
ORF01150 hypothetical protein
ORF01151 hypothetical protein
ORF01152 lipoprotein, putative
ORF01153 hypothetical protein
ORF01157 conserved hypothetical protein
ORF01158 hypothetical protein
ORF01159 hypothetical protein
ORF01160 expressed protein of unknown function FRAMESHIFT
ORF01161 expressed conserved domain protein
ORF01162 conserved hypothetical protein
ORF01164 FtsK/SpolIIE family protein FRAMESHIFT
ORF01166 hypothetical protein
ORF01167 conserved hypothetical protein
ORF01168 conserved hypothetical protein
ORF01169 hypothetical protein
ORF01172 phage infection protein, putative
ORF01173 conserved hypothetical protein
ORF01174 conserved domain protein
ORF01175 hypothetical protein
ORF01182 membrane protein, putative
ORF01186 cell wall surface anchor family protein, putative
ORF01187 hypothetical protein
ORF01204 hypothetical protein
ORF01215 hypothetical protein
ORF01241 transcriptional regulator, AraC family, putative
ORF01253 rarD protein (rarD)
ORF01257 transporter, BCCT family protein
ORF01258 hypothetical protein
ORF01261 expressed protein of unknown function
ORF01262 conserved hypothetical protein, FRAMESHIFT
ORF01263 hypothetical protein
ORF01265 hypothetical protein
ORF01266 hypothetical protein
ORF01269 conserved hypothetical protein
ORF01272 conserved hypothetical protein
ORF01277 conserved hypothetical protein
ORF01287 conserved hypothetical protein
ORF01288 membrane protein, putative
ORF01299 CMP-N-acetylneuraminic acid synthetase NeuA (neuA)
ORF01300 neuD protein (neuD)
ORF01301 UDP-N-acetylglucosamine-2-epimerase NeuC (neuC)
ORF01302 N-acetyl neuramic acid synthetase NeuB (neuB)
ORF01303 polysaccharide biosynthesis protein CpsL (cpsL)
ORF01304 polysaccharide biosynthesis protein CpsK(V) (cpsK)
ORF01307 glycosyltransferase CpsN(V) (cpsN)
ORF01308 polysaccharide biosynthesis protein CpsM(V) (cpsM)
ORF01309 polysaccharide biosynthesis protein cpsH(V) (cpsH)
ORF01310 glycosyltransferase CpsG(V) (cpsG)
ORF01311 polysaccharide biosynthesis protein CpsF (cpsF)
ORF01312 glycosyltransferase CpsE (cpsE)
ORF01348 conserved domain protein
ORF01349 hypothetical protein
ORF01370 conserved hypothetical protein

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ORFxxxxx Annotation
ORF01371 conserved hypothetical protein
ORF01372 expressed protein of unknown function
ORF01373 ISSdy1, transposase OrfA
ORF01375 conserved hypothetical protein
ORF01379 transposase OrfB, IS3 family, truncation
ORF01382 GBSi1, group II intron, maturase
ORF01384 hypothetical protein
ORF01385 hypothetical protein
ORF01386 conserved hypothetical protein
ORF01387 conserved hypothetical protein, truncation
ORF01390 ISSdy1, transposase OrfA FRAMESHIFT
ORF01392 hypothetical protein
ORF01393 hypothetical protein
ORF01394 site-specific recombinase, phage integrase family
ORF01395 conserved hypothetical protein
ORF01401 transposase, ISL3 family
ORF01404 mercuric resistance operon regulatory protein MerR (merR)
ORF01408 cadmium efflux system accessory protein (CadC)
ORF01409 conserved hypothetical protein
ORF01410 hypothetical protein
ORF01417 hypothetical protein
ORF01418 hypothetical protein
ORF01420 hypothetical protein
ORF01421 ImpB/MucB/SamB family protein
ORF01423 conserved hypothetical protein
ORF01424 conserved hypothetical protein
ORF01425 conserved hypothetical protein
ORF01426 conserved hypothetical protein
ORF01427 hypothetical protein
ORF01428 conserved hypothetical protein
ORF01430 hypothetical protein
ORF01431 hypothetical protein
ORF01432 conserved domain protein
ORF01433 SNF2 family protein
ORF01434 hypothetical protein
ORF01435 calcium-binding protein, putative
ORF01436 agglutinin receptor (ssp-5)
ORF01437 abortive infection protein AbiGI (abiGI)
ORF01438 abortive infection protein AbiGII (abiGII)
ORF01439 conserved hypothetical protein
ORF01440 expressed protein of unknown function
ORF01441 conserved hypothetical protein, degenerate
ORF01442 membrane protein, putative
ORF01443 hypothetical protein
ORF01444 Tn5252, Orf 21 protein, internal deletion
ORF01445 hypothetical protein
ORF01450 conserved hypothetical protein
ORF01452 hypothetical protein
ORF01454 conserved hypothetical protein
ORF01459 hypothetical protein
ORF01460 homocysteine S-methyltransferase MmuM, putative
ORF01463 hypothetical protein
ORF01464 hypothetical protein
ORF01465 hypothetical protein
ORF01466 transcriptional regulator, TetR family

Table 11: GBS genes not shared with GAS or pneumococcus

ORFxxxxx Annotation
ORF01477 glutathione S-transferase family protein, putative
ORF01478 conserved domain protein
ORF01486 hypothetical protein
ORF01488 R5 protein
ORF01489 transcriptional regulator, MarR family, putative
ORF01494 membrane protein, putative
ORF01497 acetyltransferase, GNAT family
ORF01502 hypothetical protein
ORF01503 conserved hypothetical protein
ORF01508 surface antigen-related protein
ORF01535 conserved hypothetical protein
ORF01547 conserved hypothetical protein
ORF01566 expressed cell wall surface anchor family protein
ORF01572 glycosyltransferase, group 1 family protein
ORF01573 glycosyltransferase, group 2 family protein
ORF01575 membrane protein, putative
ORF01576 glycosyltransferase, group 2 family protein
ORF01577 glycosyltransferase, group 2 family protein
ORF01578 nucleotide sugar dehydratase, putative
ORF01581 lipoprotein, putative
ORF01582 conserved hypothetical protein
ORF01596 ammonium transporter family protein
ORF01597 conserved hypothetical protein
ORF01601 hypothetical protein
ORF01608 proton/peptide symporter family protein
ORF01611 hypothetical protein
ORF01615 conserved domain protein
ORF01638 conserved hypothetical protein
ORF01641 conserved hypothetical protein
ORF01645 cell wall surface anchor family protein
ORF01660 membrane protein, putative
ORF01661 ABC transporter, ATP binding protein
ORF01666 hypothetical protein
ORF01667 hypothetical protein
ORF01670 hypothetical protein
ORF01672 protease, putative, POINT MUTATION
ORF01673 hypothetical protein
ORF01674 hypothetical protein
ORF01675 hypothetical protein
ORF01680 tetracenomycin polyketide synthesis O-methyltransferase TcmP, putative
ORF01681 hypothetical protein
ORF01682 hypothetical protein
ORF01684 hypothetical protein
ORF01692 peptide ABC transporter, ATP-binding protein
ORF01695 peptide ABC transporter, permease protein
ORF01696 peptide ABC transporter, peptide-binding protein
ORF01699 transposase, IS30 family, putative
ORF01700 transporter, major facilitator family
ORF01703 transcriptional regulator, LysR family
ORF01715 conserved hypothetical protein
ORF01719 hypothetical protein
ORF01720 conserved hypothetical protein
ORF01721 glyoxalase family protein
ORF01727 conserved hypothetical protein
ORF01729 acetyltransferase, GNAT family

Table 11: GBS genes not shared with GAS or pneumococcus

ORFxxxxx Annotation
ORF01730 glycosyl transferase, group 2 family protein
ORF01733 hypothetical protein
ORF01734 conserved hypothetical protein
ORF01735 hypothetical protein
ORF01736 hypothetical protein
ORF01737 hypothetical protein
ORF01742 hypothetical protein
ORF01743 PTS system component, putative
ORF01744 conserved hypothetical protein
ORF01748 D-isomer specific 2-hydroxyacid dehydrogenase family protein
ORF01753 conserved hypothetical protein
ORF01754 hypothetical protein
ORF01761 transposase, IS30 family, putative, truncation
ORF01778 amino acid permease, putative
ORF01807 hypothetical protein
ORF01836 hypothetical protein
ORF01838 hypothetical protein
ORF01839 dihydroxyacetone kinase family protein
ORF01840 transcriptional regulator, TetR family, putative
ORF01842 hypothetical protein
ORF01843 dihydroxyacetone kinase family protein
ORF01844 dihydroxyacetone kinase family protein
ORF01847 conserved hypothetical protein
ORF01850 hypothetical protein
ORF01863 pyruvate phosphate dikinase (ppdK)
ORF01864 expressed protein of unknown function
ORF01865 CBS domain protein
ORF01866 3-hydroxyacyl-CoA dehydrogenase family protein, putative secreted protein
ORF01892 hypothetical protein
ORF01893 hypothetical protein
ORF01894 conserved hypothetical protein
ORF01895 hypothetical protein
ORF01896 hypothetical protein
ORF01897 hypothetical protein
ORF01898 hypothetical protein
ORF01899 hypothetical protein
ORF01903 conserved hypothetical protein
ORF01904 drug resistance transporter, EmrB/QacA family
ORF01905 hypothetical protein
ORF01922 conserved hypothetical protein
ORF01925 FMN-binding protein
ORF01934 hypothetical protein
ORF01936 polyprenyl synthetase family protein
ORF01939 cytochrome d ubiquinol oxidase, subunit II (cydB)
ORF01940 cytochrome d oxidase, subunit I (cydA)
ORF01941 pyridine nucleotide-disulphide oxidoreductase family protein
ORF01942 prenyltransferase, UbiA family
ORF01943 hypothetical protein
ORF01944 hypothetical protein
ORF01946 cyclopropane-fatty-acyl-phospholipid synthase (cfa)
ORF01951 conserved hypothetical protein
ORF01953 hypothetical protein
ORF01954 conserved hypothetical protein
ORF01984 hypothetical protein
ORF01988 hypothetical protein

Table 11: GBS genes not shared with GAS or pneumococcus

ORFxxxxx Annotation
ORF01989 hypothetical protein
ORF01990 hypothetical protein
ORF01991 hypothetical protein
ORF02000 membrane protein, putative
ORF02001 transposase, IS30 family, putative
ORF02005 hypothetical protein
ORF02006 xylulose-5-phosphate/fructose-6-phosphate phosphoketolase (xfp)
ORF02009 conserved hypothetical protein
ORF02010 carbohydrate kinase, FGGY family
ORF02011 hypothetical protein
ORF02012 PTS system component, putative
ORF02015 glyoxylate reductase, NADH-dependent
ORF02016 hypothetical protein
ORF02025 hypothetical protein
ORF02026 hypothetical protein
ORF02030 glutamate--cysteine ligase-related protein
ORF02036 phosphinothricin N-acetyltransferase (pat)
ORF02039 conserved hypothetical protein
ORF02044 conserved hypothetical protein
ORF02045 conserved hypothetical protein
ORF02046 prophage LambdaSa2, lysin, putative
ORF02047 prophage LambdaSa2, holin, putative
ORF02048 conserved hypothetical protein
ORF02049 hypothetical protein
ORF02050 conserved domain protein
ORF02051 prophage LambdaSa2, PblB, putative
ORF02053 conserved hypothetical protein
ORF02056 conserved hypothetical protein
ORF02057 hypothetical protein
ORF02058 hypothetical protein
ORF02059 conserved hypothetical protein
ORF02060 conserved hypothetical protein
ORF02061 hypothetical protein
ORF02062 hypothetical protein
ORF02063 conserved domain protein
ORF02064 conserved domain protein
ORF02066 prophage LambdaSa2, protease, putative
ORF02067 conserved hypothetical protein
ORF02068 prophage LambdaSa2, terminase large subunit, putative
ORF02069 hypothetical protein
ORF02070 hypothetical protein
ORF02071 prophage LambdaSa2, site-specific recombinase, phage integrase family
ORF02072 conserved hypothetical protein
ORF02073 prophage LambdaSa2, transcriptional regulator, Cro/C1 family
ORF02075 hypothetical protein
ORF02077 hypothetical protein
ORF02078 conserved hypothetical protein
ORF02079 conserved hypothetical protein
ORF02080 conserved hypothetical protein
ORF02081 hypothetical protein
ORF02084 prophage LambdaSa2, bacteriophage replication protein/hypothetical protein, truncation/fusion
ORF02085 hypothetical protein
ORF02087 hypothetical protein
ORF02088 conserved hypothetical protein

Table 11: GBS genes not shared with GAS or pneumococcus

ORFxxxxx Annotation
ORF02089 prophage LambdaSa2, HNH endonuclease family protein
ORF02090 prophage LambdaSa2, antirepressor protein, putative
ORF02091 conserved domain protein
ORF02092 hypothetical protein
ORF02093 hypothetical protein
ORF02094 hypothetical protein
ORF02095 prophage LambdaSa2, repressor protein, putative
ORF02097 hypothetical protein
ORF02098 prophage LambdaSa2, site-specific recombinase, phage integrase family
ORF02100 hypothetical protein
ORF02102 hypothetical protein
ORF02103 microcin immunity protein MccF, putative
ORF02105 oxidoreductase, Gfo/Idh/MocA family
ORF02108 hypothetical protein
ORF02109 Cyclic nucleotide-binding domain protein
ORF02119 hypothetical protein
ORF02124 hypothetical protein
ORF02125 nitroreductase family protein
ORF02134 bacteriocin transport accessory protein, putative
ORF02148 neuraminidase-related protein
ORF02160 2',3'-cyclic-nucleotide 2'-phosphodiesterase (cpdB)
ORF02163 conserved hypothetical protein
ORF02171 membrane protein, putative
ORF02172 hypothetical protein
ORF02173 membrane protein, putative
ORF02175 conserved hypothetical protein, truncation
ORF02181 phosphate transport system regulatory protein PhoU, putative
ORF02187 hypothetical protein
ORF02190 conserved hypothetical protein
ORF02191 hypothetical protein
ORF02194 acetyltransferase, GNAT family
ORF02196 hypothetical protein
ORF02198 acetyltransferase, GNAT family
ORF02201 membrane protein, putative
ORF02203 hypothetical protein
ORF02205 transcriptional regulator, Cro/C1 family
ORF02206 conserved hypothetical protein
ORF02207 conserved hypothetical protein TIGR00730
ORF02208 hypothetical protein
ORF02209 site-specific recombinase, phage integrase family
ORF02210 conserved hypothetical protein
ORF02211 conserved hypothetical protein
ORF02212 hypothetical protein
ORF02213 hypothetical protein
ORF02214 transcriptional regulator, Cro/C1 family
ORF02215 expressed protein of unknown function
ORF02216 site-specific recombinase, phage integrase family
ORF02217 conserved hypothetical protein
ORF02219 hypothetical protein
ORF02221 cell wall anchor protein-related protein
ORF02223 hypothetical protein
ORF02224 hypothetical protein
ORF02225 hypothetical protein
ORF02226 membrane protein, putative
ORF02227 conjugal transfer protein, interruption-C

Table 11: GBS genes not shared with GAS or pneumococcus

ORFxxxxx Annotation
ORF02230 conserved hypothetical protein
ORF02231 conserved hypothetical protein
ORF02232 conserved hypothetical protein
ORF02235 hypothetical protein
ORF02236 conserved hypothetical protein
ORF02237 hypothetical protein
ORF02238 hypothetical protein
ORF02239 hypothetical protein
ORF02240 transcriptional regulator, Cro/C1 family
ORF02241 hypothetical protein
ORF02242 transcriptional regulator, Cro/C1 family
ORF02243 FtsK/SpoIIIE family protein
ORF02244 hypothetical protein
ORF02245 hypothetical protein
ORF02246 cell wall surface anchor family protein
ORF02247 transposase, ISL3 family
ORF02250 mercuric resistance operon regulatory protein MerR (merR)
ORF02251 Mn ²⁺ /Fe ²⁺ transporter, NRAMP family
ORF02252 membrane protein, putative
ORF02253 ABC transporter, ATP-binding protein
ORF02254 conserved hypothetical protein
ORF02255 streptomycin resistance protein
ORF02257 hypothetical protein
ORF02258 hypothetical protein
ORF02259 conserved hypothetical protein
ORF02260 acetyltransferase, GNAT family
ORF02261 membrane protein, putative
ORF02263 hypothetical protein
ORF02264 transcriptional regulator, Cro/C1 family
ORF02265 PAP2 family protein
ORF02266 conserved hypothetical protein FRAMESHIFT
ORF02267 conserved hypothetical protein TIGR00730
ORF02268 protease, putative
ORF02269 rhodanese family protein
ORF02271 hypothetical protein
ORF02274 conserved hypothetical protein
ORF02275 5-methyltetrahydrofolate--homocysteine methyltransferase, putative
ORF02277 conserved hypothetical protein
ORF02279 hypothetical protein
ORF02282 sensor histidine kinase
ORF02283 chromosome assembly-related protein
ORF02287 expressed protein of unknown function
ORF02291 pathogenicity protein, putative
ORF02308 hydrolase, haloacid dehalogenase-like family
ORF02314 conserved hypothetical protein
ORF02317 hypothetical protein
ORF02330 hypothetical protein
ORF02344 site-specific recombinase, phage integrase family
ORF02345 conserved hypothetical protein
ORF02346 conserved hypothetical protein
ORF02347 hypothetical protein
ORF02349 conserved hypothetical protein
ORF02350 hypothetical protein
ORF02351 transcriptional regulator, Cro/C1 family
ORF02352 conserved domain protein

Table 11: GBS genes not shared with GAS or pneumococcus

ORFxxxxx Annotation
ORF02354 hypothetical protein
ORF02356 expressed putative secreted protein
ORF02362 sensor histidine kinase
ORF02363 response regulator
ORF02367 membrane protein, putative
ORF02368 conserved hypothetical protein
ORF02379 membrane protein, putative
ORF02395 transcriptional regulator, Cro/C1 family
ORF02406 membrane protein, putative
ORF02416 diacylglycerol kinase catalytic domain protein, putative
ORF02418 hypothetical protein
ORF02422 hypothetical protein
ORF02425 conserved hypothetical protein
ORF03001 conserved hypothetical protein
ORF03004 conserved hypothetical protein
ORF03005 cylX protein
ORF03006 Tn916, hypothetical protein
ORF03007 Tn916, hypothetical protein
ORF03008 Tn916, hypothetical protein
ORF03009 Tn916, tetM leader peptide
ORF03010 Tn916, hypothetical protein
ORF03012 prophage LambdaSa2, HNH endonuclease family protein
ORF03013 conserved hypothetical protein
ORF03015 conjugal transfer protein, interruption-N

Table 12: GBS ORF's not shared with GAS, pneumococcus or any published genome

ORFxxxxx Annotation

ORF00035	membrane protein, putative
ORF00087	lipoprotein, putative
ORF00088	hypothetical protein
ORF00089	hypothetical protein
ORF00123	hypothetical protein
ORF00138	hypothetical protein
ORF00187	hypothetical protein
ORF00188	hypothetical protein
ORF00192	hypothetical protein
ORF00205	hypothetical protein
ORF00228	lipoprotein, putative
ORF00234	hypothetical protein
ORF00235	hypothetical protein
ORF00238	hypothetical protein
ORF00240	transcriptional regulator, Cro/C1 family
ORF00241	hypothetical protein
ORF00242	conserved hypothetical protein
ORF00243	hypothetical protein
ORF00247	hypothetical protein
ORF00249	hypothetical protein
ORF00253	hypothetical protein
ORF00254	hypothetical protein
ORF00255	hypothetical protein
ORF00256	hypothetical protein
ORF00257	hypothetical protein
ORF00258	hypothetical protein
ORF00259	hypothetical protein
ORF00260	hypothetical protein
ORF00272	expressed putative lipoprotein
ORF00273	hypothetical protein
ORF00274	hypothetical protein
ORF00275	hypothetical protein
ORF00276	hypothetical protein
ORF00278	membrane protein, putative
ORF00285	lipoprotein, putative
ORF00292	hypothetical protein
ORF00294	expressed protein of unknown function
ORF00308	conserved hypothetical protein
ORF00332	hypothetical protein
ORF00340	hypothetical protein
ORF00384	hypothetical protein
ORF00402	membrane protein, putative
ORF00408	hypothetical protein
ORF00416	hypothetical protein
ORF00417	hypothetical protein
ORF00448	hypothetical protein
ORF00476	hypothetical protein
ORF00489	DNA-damage-inducible protein J, putative
ORF00490	hypothetical protein
ORF00491	lipoprotein, putative
ORF00497	conserved domain protein
ORF00510	bacteriocin transport accessory protein, putative
ORF00512	hypothetical protein
ORF00527	hypothetical protein
ORF00556	hypothetical protein

Table 12: GBS ORF's not shared with GAS, pneumococcus or any published genome

ORFxxxxx Annotation

ORF00575 hypothetical protein
ORF00599 hypothetical protein
ORF00618 hypothetical protein
ORF00620 hypothetical protein
ORF00623 hypothetical protein
ORF00626 prophage LambdaSa1, transcriptional regulator, Cro/C1 family
ORF00628 hypothetical protein
ORF00630 hypothetical protein
ORF00632 hypothetical protein
ORF00635 hypothetical protein
ORF00636 hypothetical protein
ORF00637 hypothetical protein
ORF00642 conserved hypothetical protein
ORF00644 hypothetical protein
ORF00645 hypothetical protein
ORF00647 hypothetical protein
ORF00649 hypothetical protein
ORF00650 hypothetical protein
ORF00653 conserved hypothetical protein
ORF00657 conserved hypothetical protein, truncation
ORF00661 conserved hypothetical protein
ORF00673 hypothetical protein
ORF00674 hypothetical protein
ORF00675 conserved hypothetical protein
ORF00676 conserved hypothetical protein
ORF00682 hypothetical protein
ORF00685 conserved hypothetical protein
ORF00698 hypothetical protein
ORF00712 hypothetical protein
ORF00718 cell wall surface protein, interruption-N
ORF00723 hypothetical protein
ORF00735 expressed protein of unknown function
ORF00737 conserved hypothetical protein, degenerate
ORF00738 hypothetical protein
ORF00740 hypothetical protein
ORF00741 hypothetical protein
ORF00747 cylD protein (cylD)
ORF00753 cylE protein (cylE)
ORF00756 cylJ protein (cylJ)
ORF00757 cylK protein (cylK)
ORF00758 hypothetical protein
ORF00759 putative secreted protein
ORF00761 hypothetical protein
ORF00796 hydrolase, haloacid dehalogenase-like family
ORF00806 conserved hypothetical protein
ORF00822 ABC transporter, ATP-binding protein
ORF00827 hypothetical protein
ORF00872 cell wall surface anchor family protein
ORF00909 hypothetical protein
ORF00923 hypothetical protein
ORF00924 conserved hypothetical protein
ORF00942 expressed putative secreted protein
ORF00943 hypothetical protein
ORF00944 hypothetical protein
ORF01013 hypothetical protein

Table 12: GBS ORF's not shared with GAS, pneumococcus or any published genome

ORFxxxxx Annotation
ORF01014 hypothetical protein
ORF01015 hypothetical protein
ORF01016 hypothetical protein
ORF01018 hypothetical protein
ORF01019 hypothetical protein
ORF01021 hypothetical protein
ORF01035 Tn916, excisionase
ORF01062 hypothetical protein
ORF01096 nisin-resistance protein, putative
ORF01145 lipoprotein, putative
ORF01146 conserved hypothetical protein, FRAMESHIFT
ORF01148 lipoprotein, putative
ORF01149 hypothetical protein
ORF01150 hypothetical protein
ORF01151 hypothetical protein
ORF01152 lipoprotein, putative
ORF01153 hypothetical protein
ORF01158 hypothetical protein
ORF01159 hypothetical protein
ORF01161 expressed conserved domain protein
ORF01162 conserved hypothetical protein
ORF01166 hypothetical protein
ORF01168 conserved hypothetical protein
ORF01169 hypothetical protein
ORF01174 conserved domain protein
ORF01175 hypothetical protein
ORF01186 cell wall surface anchor family protein, putative
ORF01187 hypothetical protein
ORF01204 hypothetical protein
ORF01215 hypothetical protein
ORF01258 hypothetical protein
ORF01262 conserved hypothetical protein, FRAMESHIFT
ORF01263 hypothetical protein
ORF01265 hypothetical protein
ORF01266 hypothetical protein
ORF01304 polysaccharide biosynthesis protein CpsK(V) (cpsK)
ORF01308 polysaccharide biosynthesis protein CpsM(V) (cpsM)
ORF01309 polysaccharide biosynthesis protein cpsH(V) (cpsH)
ORF01349 hypothetical protein
ORF01384 hypothetical protein
ORF01385 hypothetical protein
ORF01386 conserved hypothetical protein
ORF01392 hypothetical protein
ORF01395 conserved hypothetical protein
ORF01409 conserved hypothetical protein
ORF01410 hypothetical protein
ORF01417 hypothetical protein
ORF01418 hypothetical protein
ORF01420 hypothetical protein
ORF01423 conserved hypothetical protein
ORF01424 conserved hypothetical protein
ORF01425 conserved hypothetical protein
ORF01426 conserved hypothetical protein
ORF01427 hypothetical protein
ORF01431 hypothetical protein

Table 12: GBS ORF's not shared with GAS, pneumococcus or any published genome**ORFxxxxx Annotation**

ORF01432 conserved domain protein
ORF01434 hypothetical protein
ORF01435 calcium-binding protein, putative
ORF01437 abortive infection protein AbiGI (abiGI)
ORF01438 abortive infection protein AbiGII (abiGII)
ORF01441 conserved hypothetical protein, degenerate
ORF01443 hypothetical protein
ORF01445 hypothetical protein
ORF01452 hypothetical protein
ORF01459 hypothetical protein
ORF01463 hypothetical protein
ORF01464 hypothetical protein
ORF01465 hypothetical protein
ORF01486 hypothetical protein
ORF01488 R5 protein
ORF01575 membrane protein, putative
ORF01581 lipoprotein, putative
ORF01601 hypothetical protein
ORF01611 hypothetical protein
ORF01638 conserved hypothetical protein
ORF01645 cell wall surface anchor family protein
ORF01660 membrane protein, putative
ORF01666 hypothetical protein
ORF01667 hypothetical protein
ORF01670 hypothetical protein
ORF01673 hypothetical protein
ORF01674 hypothetical protein
ORF01675 hypothetical protein
ORF01681 hypothetical protein
ORF01682 hypothetical protein
ORF01684 hypothetical protein
ORF01719 hypothetical protein
ORF01733 hypothetical protein
ORF01735 hypothetical protein
ORF01736 hypothetical protein
ORF01737 hypothetical protein
ORF01742 hypothetical protein
ORF01754 hypothetical protein
ORF01761 transposase, IS30 family, putative, truncation
ORF01807 hypothetical protein
ORF01836 hypothetical protein
ORF01838 hypothetical protein
ORF01842 hypothetical protein
ORF01850 hypothetical protein
ORF01892 hypothetical protein
ORF01893 hypothetical protein
ORF01895 hypothetical protein
ORF01896 hypothetical protein
ORF01897 hypothetical protein
ORF01898 hypothetical protein
ORF01899 hypothetical protein
ORF01905 hypothetical protein
ORF01934 hypothetical protein
ORF01943 hypothetical protein
ORF01944 hypothetical protein

Table 12: GBS ORF's not shared with GAS, pneumococcus or any published genome**ORFxxxxx Annotation**

ORF01953 hypothetical protein
ORF01984 hypothetical protein
ORF01988 hypothetical protein
ORF01989 hypothetical protein
ORF02005 hypothetical protein
ORF02011 hypothetical protein
ORF02016 hypothetical protein
ORF02025 hypothetical protein
ORF02026 hypothetical protein
ORF02045 conserved hypothetical protein
ORF02047 prophage LambdaSa2, holin, putative
ORF02048 conserved hypothetical protein
ORF02049 hypothetical protein
ORF02050 conserved domain protein
ORF02053 conserved hypothetical protein
ORF02057 hypothetical protein
ORF02058 hypothetical protein
ORF02061 hypothetical protein
ORF02062 hypothetical protein
ORF02063 conserved domain protein
ORF02067 conserved hypothetical protein
ORF02069 hypothetical protein
ORF02070 hypothetical protein
ORF02072 conserved hypothetical protein
ORF02073 prophage LambdaSa2, transcriptional regulator, Cro/Ci family
ORF02075 hypothetical protein
ORF02077 hypothetical protein
ORF02078 conserved hypothetical protein
ORF02081 hypothetical protein
ORF02085 hypothetical protein
ORF02087 hypothetical protein
ORF02088 conserved hypothetical protein
ORF02091 conserved domain protein
ORF02092 hypothetical protein
ORF02093 hypothetical protein
ORF02094 hypothetical protein
ORF02097 hypothetical protein
ORF02100 hypothetical protein
ORF02102 hypothetical protein
ORF02108 hypothetical protein
ORF02119 hypothetical protein
ORF02124 hypothetical protein
ORF02171 membrane protein, putative
ORF02172 hypothetical protein
ORF02173 membrane protein, putative
ORF02191 hypothetical protein
ORF02196 hypothetical protein
ORF02203 hypothetical protein
ORF02208 hypothetical protein
ORF02212 hypothetical protein
ORF02213 hypothetical protein
ORF02214 transcriptional regulator, Cro/Ci family
ORF02215 expressed protein of unknown function
ORF02217 conserved hypothetical protein
ORF02219 hypothetical protein

Table 12: GBS ORF's not shared with GAS, pneumococcus or any published genome**ORFxxxxx Annotation**

ORF02221 cell wall anchor protein-related protein
ORF02223 hypothetical protein
ORF02224 hypothetical protein
ORF02225 hypothetical protein
ORF02231 conserved hypothetical protein
ORF02235 hypothetical protein
ORF02236 conserved hypothetical protein
ORF02237 hypothetical protein
ORF02238 hypothetical protein
ORF02239 hypothetical protein
ORF02241 hypothetical protein
ORF02244 hypothetical protein
ORF02245 hypothetical protein
ORF02263 hypothetical protein
ORF02268 protease, putative
ORF02271 hypothetical protein
ORF02279 hypothetical protein
ORF02283 chromosome assembly-related protein
ORF02317 hypothetical protein
ORF02330 hypothetical protein
ORF02344 site-specific recombinase, phage integrase family
ORF02345 conserved hypothetical protein
ORF02347 hypothetical protein
ORF02349 conserved hypothetical protein
ORF02350 hypothetical protein
ORF02351 transcriptional regulator, Cro/Ci family
ORF02354 hypothetical protein
ORF02356 expressed putative secreted protein
ORF02395 transcriptional regulator, Cro/Ci family
ORF02418 hypothetical protein
ORF02422 hypothetical protein
ORF02425 conserved hypothetical protein
ORF03004 conserved hypothetical protein
ORF03005 cylX protein
ORF03006 Tn916, hypothetical protein
ORF03007 Tn916, hypothetical protein
ORF03008 Tn916, hypothetical protein
ORF03009 Tn916, tetM leader peptide
ORF03010 Tn916, hypothetical protein
ORF03015 conjugal transfer protein, interruption-N

Table 13: Comparative Sequences relating to SAG0466 (thiolase)

SEQ ID NO. 1301: SAG0466 FROM THE 2603V/R GBS STRAIN

CTCCTGCCCTGCAATGGCAGTTAGACCCATAGGTTTATTTTATATTTTAATGCCTGCATAAGATGAAGGATATTAATA
 ATTCCTGAGCAGGCATAAGGGGTGTCCGTAAGCTAATGTCCCTCCAAAAATATTGAATTTTCTCTCTCTCAGGATAATA
 ATGATTAAATAGAGCATCAATCGCTGCAAATGGTTCATTCCATTCAATTGCATCATAATCCGATATTTTAGTATGAGTTT
 CTGTTAATAGTTTTCCGTAGCCGTGTGAACCAATCTGGACTAAGCTTGGGATCTCTGCTACTTCTACAATGTGAACA
 ATCCGGAATTCTGTTTTCTGACTCTGAAGCGTTAGAAATGCAGCAGCATCGTGCATTAAACAAACATTTCCAATAGTGAG
 CAAAGGTGAATTTTCCATCAATCTTGTAATTTTGAAGAAATGTTCTTTTAgTTTTCTAACGCCTTGATCTCGCATCC
 CTTCCATTTGGTAAGATTACyTCTTCTAAATAGCCACCTTGTTTAGCTGTTAAGGCGCGTTTATGGCTCAAGAATGCCAAT
 TTATCTAACATTTCTCTTCTAAaCCATATTTTTTGACAGACTCTCTGGGCCCCCTTCTAACATTACAGTTTCAGCATAGA
 GTCAGGAGAAAACTGAGCAACTGTATATTCTCCGTTACGATTATCTCTTTAGCATAACGCTCTCATAGGTTGAAGAGAAC
 TACTTTCAATCCCCCAACAAGAATTTTTTTCATTAATACCGGTACTGATTTTTTAGATAACCAAAAAACAAGGCAGAACTT
 GATGAAGCACACTGCATATCAATCGTTTGTACTGGAATATAGGATTCAATACAGAAAAAGAGTCATCAACGACCAAT
 ATTGCCCCCAGTACCACCTGTGTTCCACAAATAATCTATCAATGTTAGATTCTGATTCTATTTTTTTTATTGTGATTTA
 AAAGGTGTGCTCTTAAAGATTCTGGACGGTAAGTTTAAATTGCTT

SEQ ID NO. 1302: SAG0466 FROM THE M732 GBS TYPE III STRAIN

TCGGTATAAAGGGGAAGCAATTTAAACATTACCGTCCAGAAGCTTTTAGGAGCACACCTCTTAAATCAAATAAAAAAATA
 GAATCAGAATCTAATATTGATAGTATTATTTGTGGGAACACAGTTGGTACTGGGGGCAATATTGGTCGTTTGATGACTCT
 TTTTTCTGATTATGAATCCTATATTCAGTACAAACGATTGATATGCAGTGTGCTTCATCAAGTTCTGCCTTGTTTTTG
 GTTATCTAAAAATCAGTGGCGGTATTAATGAAAAAGTTCTTGTGGGGGATTGAAAGTAGTTCTCTCAACCTATGAGA
 CGTTACGCTAAAAGAAGATAATCGTAACGGAGAATATACCGTTGCTCAGTTTTCTCTGACTCTTATGCTGAACTGTAAT
 GTTAGAAGGGGCACAAAGAGTCTGTCAAAAATATGGTTTTAGAAAGAGAAATGTTAGATAAATTGGCATTCTTGAGCCATA
 AACGCGCCTTAACAGCTAAACAAGGTGGCTATTTAGAAGAGGTAATCTTACCAATGGAAGGGATGCGAGATCAAGGCGTT
 AGAAAACTAAAAGAAGCATTTTTTCAAAAATTACCAAGATTGATGGAAAATTCACCTTTGCTCACTATTGGAAATGTTG
 TTTAATGCACGATGCTGCTGCATTTCTAACGCTTCAGAGTCAGAAAAACAGAATTCGGGATTGTTACATTGTAGAAGTAG
 CAGGAGATCCCAAGCTTAGTCCAGAATTGGTTACACGGCTACGGAAAACTATTAACAGAACTCATACTAAAATATCG
 GATTATGATGCAATTGAATGGAATGAACATTTCGACGAGATTGATGCTTTATTTAATCATTATTATCTGAAGAGAGAGA
 AAAATTCAATATTTTTGGAGGGGCATTAGCTTACGGACACCCCTTATGCTGCTCAGGAATTA

SEQ ID NO. 1303: SAG0466 FROM THE 090 GBS TYPE Ia STRAIN

TTGTGGGAACACAGTTGGTACTGGGGCAATATTGGTCGTTTGATGACTCTTTTTTCTGATTATGAATCCTATATTCAG
 TACAAACGATTGATATGCAGTGTGCTTCATCAAGTTCTGCCTTGTTTTTGGTTATCTAAAAATCAGTGCCGGTATTAAT
 GAAAAAGTTCTTGTGGGGGATTGAAAGTAGTTCTTCAACCTATGAGACGTTACGCTAAAGAAGATAATCGTAACGG
 AGAATATACCGTTGCTCAGTTTTCTCTGACTCTTAKGCTGAACTGTAATGtTAGAAGGGGCACAAAGAGTCTGTCAAA
 AATATGGTTTTAGAAGAGAAATGTAGATAAATTGGCATTCTTGAGCCATAAACGCGCCTTAACAGCTAAACAAGGTGGC
 TATTTAGAAGAGGTAATCTTACCAATGGAAGGGATGCGAGATCAAGGCGTTAGAAAACTAAAAGAAGCATTTTTTCAAAA
 ATTACCAAGATTGATGGTAAATTACCTTTGCTCATTATTGGAATGTTTTGTTAATGCACGATGCTGCTGCATTTCTWA
 CGCTTCAGAGTCAGAAAAACAGAATTCGGGATTGTTACATTGTAGAAGTAGCAGGAGATCCCAAGCTTAGTCCAGAATTG
 GTTCACAGGCTACGGAAAACTATTAACAGAACTCATACTAAAATATCGGATTATGATGCAATTGAATGGAATGAACC
 ATTTGCAGCGATTGATGCTTTATTTAATCATTATTATCTCTGAAGAGAGAGAAAAATTCAATATTTTTGGAGGGGCATTAG
 CTTACGGACACCCCTTATGCTGCTCAGG

SEQ ID NO. 1304: SAG0466 FROM THE COH1 GBS TYPE Ia STRAIN

ATCGGTATAAAGGGGAAGCAATTTAAAATTACCGTCCAGAAGCTTTTAGGAGCACACCTCTTAAATCAAATAAAAAAATA
 GAATCAGAATCTAATATTGATAGTATTATTTGTGGGAACACAGTTGGTACTGGGGGCAATATTGGTCGTTTGATGACTCT
 TTTTTCTGATTATGAATCCTATATTCAGTACAAACGATTGATATGCAGTGTGCTTCATCAAGTTCTGCCTTGTTTTTG
 GGTATCTAAAA

SEQ ID NO. 1305 : SAG0466 FROM THE CJB GBS NONTYPEABLE STRAIN (REVERSE COMPLEMENT)

TTTTCAAAAATTAcCAAGATTGATGGAAAATTCACCTTTGCTCACTATTGGAAATGTTTGTTTAATGCACGATGCTGCTG
 CATTTCTAACGCTTCAGAGTCAGAAAAACAGAATTCGGGATTGTTACATTGTAGAAGTAGCAGGAGATCCCAAGCTTAGT
 CCAGAATTGGTTACACGGCTACGGAAAACTATTAACAGAACTCATACTAAAATATCGGATTATGATGCAATTGAATG
 GAATGAACCATTTGCAGCGATTGATGCTTTATTTAATCATTATTATCTCTGAAGAGAGAGAAAAATTCAATATTTTTGGAG
 GGGCATTAGCTTACGGACACCCCTTAATGCCTGCTCAGGAATTATTAATATCC

SEQ ID NO. 1306: sag0466 FROM THE CJB110 GBS NONTYPEABLE STRAIN

GGTATAAAGGGGAAGCAATTTAAACATTACCGTCCAGAAGCTTTTAGGAGCACACCTCTTAAATCAAATAAAAAAATA
 ACCAGAATCTAACATTGATAGTATTATTTGTGGGAACACAGTTGGTACTGGGGGCAATATTGGTCGTTTGATGACTCTTT
 TTTCTGATTATGAATCCTATATTC

Table 13: Comparative Sequences relating to SAG0466 (thiolase)

SEQ ID NO. 1307: SAG0466 FROM THE 1169NT1 GBS TYPE V STRAIN REVERSE COMPLEMENT
 CAAGATTGATGGAAAAATTCACCTTTGCTCACTATTGGAAATGTTTGTAAATGCACGATGCTGCTGCATTTCTAACGCTT
 CAGAGTCAGAAAAACAGAATTCGGGATTGTTTCACATTGTAGAAGTAGCAGGAGATCCCAAGCTTAGTCCAGAATTGGTTCA
 CACGGCTACGGAAAACTATTAAACAGAACTCATACTAAAATATCGGATTATGATGCAATTGAATGGAATGAACCATTTG
 CAGCGATTGATGCTTTATTTAATCATTATTATCCTGAAGAGAGAGAAAAATTCAATATTTTGGAGGGGCATTAGCTTAC
 GGACACCCCTTATGCCTGCTCAGGAATTATTAATATCCTTCATCTTATGCAGGCATTAAAAATATAAAAAATAAACCTATGGG
 CCTAACTGCCATTGCAGGGGCA

SEQ ID NO. 1308: SAG0466 FROM THE 18RS21 GBS TYPE II STRAIN
 CCTTAACAGTTAAACAAGGTGGCTATTTAGAAGAGGTAATCTTACCAATGGAAGGGATGCGAGATCAAGGCGTTAGAAAA
 CTAAAGAAACATTTTTTCAAAAATTACCAAGATTGATGGAAAAATTCACCTTTGCTCACTATTGGAAATGTTTGTAAAT
 GCACGATGCTGCTGCATTTCTAACGCTTCAGAGTCAGAAAAACAGAATTCCGGATTGTTTCACATTGTAGAAGTAGCAGGAG
 ATCCCAAGCTTAGTCCAGAATTGGTTTCACACGGCTACGGAAAACTATTAAACAGAACTCATACTAAAATATCGGATTAT
 GATGCAATTGAATGGAATGAACCATTTGCAGCGATTGATGCTCTATTTAATCATTTATTATCCTGAAGAGAGAGAAAAATT
 CAATATTTTGGAGGGACATTAGCTTACGGACACCCCTTATGCCTGCTCAGGAATTATTAATATCCTTCATCTTATGCAGG
 CATTAAAAATATAAAAAATAAACCTATGGGTCTAACTGCCATTGCAGGGGCA

SEQ ID NO. 1309: SAG0466 FROM THE 18RS21 GBS TYPE II STRAIN
 TCGGTATAAAAGGGAAGCAATTTAAACATTACCGTCCAGAACTTTTAGGAGCACACCTTTTAAATCAAATAAAAAATA
 GAATCAGAATCTAACATTGATAGTATTATTTGTGGGAACACAGTTGGTACTGGGGGCAATATTGGTTCGTTTGTGACTCT
 TTTTCTGATTATGAATCCTATATTCAGTACAAACGATTGATATGCAGTGTGCTTCATCAAGTTCTGCCTTGTGTTTGTG
 GTTATCTAAAAATCAGTACCGGTATTAATGAAAAAGTTCTTGTGGGGGATTGAAAGTAGTTCTCTCAACCTATGAGA
 CGTTATGCTAAAGAAGATAATCGTAACGAGAGAAATATACAGTTGCTCAGTTTTCTCTGACTCTTATGCTGAAACTGTAAT
 GTTAGAAGGGGCCAGAGAGTCTGTCAAAAATATGGTTTTAGAAGAGAAATGTTAGATAAATTGGCATTCCTTGAGCCATA
 AACCGCCTTAACAGCTAAACA

SEQ ID NO. 1310: SAG0466 FROM THE H36b GBS TYPE Ib STRAIN
 TTTGGGCTACGAACACCTATCGGTATAAAAGGGAAGCAATTTAAACATTACCGTCCAGAACTTTTAGGAGCACACCTTTT
 AAATCAAATAAAAAATAGAAATCAGAATCTAACATTGATAGTATTATTTGTGGGAACACAGTTGGTACTGGGGGCAATA
 TTGGTCGTTTGTGACTCTTTTTCTGATTATGAATCCTATATTCAGTACAAACGATTGATATGCAGTGTGCTTCATCA
 AGTTCTGCCTTGTGTTTTGTTTATCTAAAAATCAGTACCGGTATTAATGAAAAAGTTCTTGTGGGGGATTGAAAGTAG
 TTCTCTTCAACCTATGAGACGTTATGCTAAAGAAGATAATCGTAACGAGAGAAATATACAGTTGCTCAGTTTCTCTGACT
 CTTATGCTGAAACTGTAATGTTAGAAGGGGCC

SEQ ID NO. 1311: SAG0466 FROM THE H36b GBS TYPE Ib STRAIN (REVERSE COMPLEMENT)
 GAAAATTCACCTTTGCTCACTATTGGAAATGTTTGTAAATGCACGATGCTGCTGCATTTCTAACGCTTCAGAGTCAGAA
 AACAGAATTCGGGATTGTTTCACATTGTAGAAGTAGCAGGAGATCCCAAGCTTAGTCCAGAATTGGTTTCACACGGCTACGG
 AAAAATCTAATAACAGAACTCATACTAAAATATCGGATTATGATGCAATTGAATGGAATGAACCATTTGCAGCGATTGAT
 GCTCTATTTAATCATTATTATCCTGAAGAGAGAGAAAAATTCAATATTTTGGAGGGCATTAGCTTACGGACACCCCTTA
 TGCCTGCTCAGGAATTATTAATATCCTTCATCTTATGCAGGCATTAAAAATATAAAAAATAAACCTATGGGTCTAACTGCCA
 TTGCAGGGGCAGGA

SEQ ID NO. 1312: SAG0466 FROM THE M781 GBS TYPE III STRAIN (REVERSE COMPLEMENT)
 CCTTTGCTCACTATTGGAAATGTTTGTAAATGCACGATGCTGCTGCATTTCTAACGCTTCAGAGTCAGAAAAACAGAATT
 CCGGATTGTTTCACATTGTAGAAGTAGCAGGAGATCCCAAGCTTAGTCCAGAATTGGTTTCACACGGCTACGGAAAACTAT
 TAACAGAACTCATACTAAAATATCGGATTATGATGCAATTGAATGGAATGAACCATTTGCAGCGATTGATGCTTTATTT
 AATCATTATTATCCTGAAGAGAGAGAAAAATTCAATATTTTGGAGGGCATTAGCTTACGGACACCCCTTATGCCTGCTC
 AGGAATTATTAAATATCCTTCATCTTATGCAGGCATTAAAAATATAAAAAATAAACCTATGGGTCTAACTGCT

SEQ ID NO. 1313: SAG0466 FROM THE M781 GBS TYPE III STRAIN
 GCAATTTAAACATTACCGTCCAGAACTTTTAGGAGCACACCTCTTAAATCAAATAAAAAATAGAAATCAGAATCTAATA
 TTGATAGTATTATTTGTGGGAACACAGTTGGTACTGGGGGCAATATTGGTTCGTTTGTGACTCTTTTTCTGATTATGAA
 TCCTATATTCAGTACAAACGATTGATATGCAGTGTGCTTCATCAAGTTCTGCCTTGTGTTTTGTTTATCTAAAAATCAG
 TGCCGGTATTAATGAAAAAGTTCTTGTGGGGGATTGAAAGTAGTTCTCTTCAACCTATGAGACGTTACGGACACCCCTTA
 ATAATCGTAACGGAATATACCGTTGCTCAGTTTTCTCTGACTCTTATGCTGAAACTGTAATGTTAGA

SEQ ID NO. 1314: SAG0466 FROM THE A909 GBS TYPE Ia STRAIN (REVERSE COMPLEMENT)
 CCTTTGCTCACTATTGGAAATGTTTGTAAATGCACGATGCTGCTGCATTTCTAACGCTTCAGAGTCAGAAAAACAGAATT
 CCGGATTGTTTCACATTGTAGAAGTAGCAGGAGATCCCAAGCTTAGTCCAGAATTGGTTTCACACGGCTACGGAAAACTAT
 TAACAGAACTCATACTAAAATATCGGATTATGATGCAATTGAATGGAATGAACCATTTGCAGCGATTGATGCTCTATTT
 AATCATTATTATCCTGAAGAGAGAGAAAAATTCAATATTTTGGAGGGACATTAGCTTACGGACACCCCTTATGCCTGCTC
 AGGAATTATTAAATATCCTTCATCTTATGCAGGCATTAAAAATATAAAAAATAAACCTATGGGTCTAACTGCCATTGCAGGGG
 C

Table 13: Comparative Sequences relating to SAG0466 (thiolase)

SEQ ID NO. 1315: SAG0466 FROM THE JM9130013 GBS TYPE VIII STRAIN REVERSE COMPLEMENT

GCTCACTATTGGAAATGTTTGTGTTAATGCACGATGCTGCTGCATTTCTAACGCTTCAGAGTCAGAAAACAGAATTCCGGA
TTGTTACATTGTAGAAGTAGCAGGAGATCCCAAGCTTAGTCCAGAATTGGTTACACGGCTACGGAAAACTATTAACA
GAACTCATACTAAAATATCGGATTATGATGCAATTGAATGGAATGAACCATTTCAGCGATTGATGCTCTATTTAATCA
TTATTATCCTGAAGAGAGAGAAAAATTCAATATTTTGGAGGGGCATTAGCTTACGGACACCCTTATGCCTGCTCAGGAA
TTATTAATATCCTTCATCTTATGCAGGCATTAAATATAAAAAATAACCTATGGGTCTAACTGCCATTGCAGGGGCAGGA

SEQ ID NO. 1316: SAG0466 FROM THE JM9130013 GBS TYPE VIII STRAIN

TTTGGGCTACGAACACCTATCGGTATAAAAGGGAAGCAATTTAAACATTACCGTCCAGAACCTTTAGGAGCACACCTTTT
AAATCAAATAAAAAAATAGAAATCAGAATCTAACATTGATAGTATTATTTGTGGGAACACAGTTGGTACTGGGGGCAATA
TTGGTCGTTTGATGACTCTTTTTCTGATTATGAATCCTATATTCCAGTACAACGATTGATATGCAGTGTGCTTCATCA
AGTTCTGCCTTGTTTTTGGTTATCTAAAAATCAGTACCGGTATTAATGAAAAAGTTCTTGTGGGGGATTGAAAGTAG
TTCTCTTCAACCTATGAGACGTTATGCTAAAGAAGATAATCGTAACGGAGAATATA

SEQ1301	-----CTCCTGCCCCCTGCAATGGCAGTTAGACCCATAGGTTTATTTTATATTTTA
SEQ1302	-----
SEQ1303	-----
SEQ1304	-----
SEQ1305	-----
SEQ1306	-----
SEQ1307	-----
SEQ1308	CCTAACAGTTAAACAAGGTGGCTATTTAGAAGAGGTAATCTTACCAATGGAAGGGATGC
SEQ1309	-----
SEQ1310	-----
SEQ1311	-----
SEQ1312	-----
SEQ1313	-----
SEQ1314	-----
SEQ1315	-----
SEQ1316	-----
SEQ1301	TGCCTGCATAAGATGAAGGATATTAATAATTCCTGAGCAGGCATAAGGGTGTCCGTAAG
SEQ1302	-----TCGGTATAAAA
SEQ1303	-----
SEQ1304	-----ATCGGTATAAAA
SEQ1305	-----TTTTCAAAAATTACCAAGATTGATGG
SEQ1306	-----GGTATAAAA
SEQ1307	-----CAAGATTGATGG
SEQ1308	AGATCAAGGCGTTAGAAAATAAAAGAAACATTTTTTCAAAAATTACCAAGATTGATGG
SEQ1309	-----TCGGTATAAAA
SEQ1310	-----TTTGGGCTACGAACACCTATCGGTATAAAA
SEQ1311	-----G
SEQ1312	-----
SEQ1313	-----
SEQ1314	-----
SEQ1315	-----
SEQ1316	-----TTTGGGCTACGAACACCTATCGGTATAAAA
SEQ1301	TAAATGTCCCTCCAAA-AATATTGAATTTTTCTCTCTC-TTCAGGATAAATGATTAAA
SEQ1302	GGGAAGCAATTTAAACATTACCGTCCAGAACTTTTAGGAGCACACCTCTTAAATCAAAT
SEQ1303	-----
SEQ1304	GGGAAGCAATTTAAA-ATTACCGTCCAGAACTTTTAGGAGCACACCTCTTAAATCAAAT
SEQ1305	AAATTCACCTTTGCTCACTATTGGAAATGTTTGTGTTAATGCACGATGCTGCTGCATTTC
SEQ1306	GGGAAGCAATTTAAACATTACCGTCCAGAACTTTTAGGAGCACACCTCTTAAATCAAAT
SEQ1307	AAATTCACCTTTGCTCACTATTGGAAATGTTTGTGTTAATGCACGATGCTGCTGCATTTC
SEQ1308	AAATTCACCTTTGCTCACTATTGGAAATGTTTGTGTTAATGCACGATGCTGCTGCATTTC
SEQ1309	GGGAAGCAATTTAAACATTACCGTCCAGAACTTTTAGGAGCACACCTTTTAAATCAAAT
SEQ1310	GGGAAGCAATTTAAACATTACCGTCCAGAACTTTTAGGAGCACACCTTTTAAATCAAAT
SEQ1311	AAATTCACCTTTGCTCACTATTGGAAATGTTTGTGTTAATGCACGATGCTGCTGCATTTC
SEQ1312	-----CCTTTGCTCACTATTGGAAATGTTTGTGTTAATGCACGATGCTGCTGCATTTC
SEQ1313	-----GCAATTTAAACATTACCGTCCAGAACTTTTAGGAGCACACCTCTTAAATCAAAT
SEQ1314	-----CCTTTGCTCACTATTGGAAATGTTTGTGTTAATGCACGATGCTGCTGCATTTC
SEQ1315	-----GCTCACTATTGGAAATGTTTGTGTTAATGCACGATGCTGCTGCATTTC

Table 13: Comparative Sequences relating to SAG0466 (thiolase)

SEQ1316	GGGAAGCAATTTAAACATTACCGTCCAGAACTTTTAGGAGCACACCTTTTAAATCAAAT
SEQ1301	AGAGCATCAATCGCTGCAAAATGGTTCATTCC-ATTCAATTGCATCATAATCCGATATTT
SEQ1302	AAAAAATAGAAATCAGAATCTAAT--ATT---GATAGTATTATTGTGGGAACA-CAGT
SEQ1303	-----TTGTGGGAACA-CAGT
SEQ1304	AAAAAATAGAAATCAGAATCTAAT--ATT---GATAGTATTATTGTGGGAACA-CAGT
SEQ1305	AACGCTTCAGAGTCAGAAAACAGA--ATTCCGGATTGTTACATTGTAGAAGTAGCAGG
SEQ1306	AAAAAATATAACCAGAATCTAAC--ATT---GATAGTATTATTGTGGGAACA-CAGT
SEQ1307	AACGCTTCAGAGTCAGAAAACAGA--ATTCCGGATTGTTACATTGTAGAAGTAGCAGG
SEQ1308	AACGCTTCAGAGTCAGAAAACAGA--ATTCCGGATTGTTACATTGTAGAAGTAGCAGG
SEQ1309	AAAAAATAGAAATCAGAATCTAAT--ATT---GATAGTATTATTGTGGGAACA-CAGT
SEQ1310	AAAAAATAGAAATCAGAATCTAAC--ATT---GATAGTATTATTGTGGGAACA-CAGT
SEQ1311	AACGCTTCAGAGTCAGAAAACAGA--ATTCCGGATTGTTACATTGTAGAAGTAGCAGG
SEQ1312	AACGCTTCAGAGTCAGAAAACAGA--ATTCCGGATTGTTACATTGTAGAAGTAGCAGG
SEQ1313	AAAAAATAGAAATCAGAATCTAAT--ATT---GATAGTATTATTGTGGGAACA-CAGT
SEQ1314	AACGCTTCAGAGTCAGAAAACAGA--ATTCCGGATTGTTACATTGTAGAAGTAGCAGG
SEQ1315	AACGCTTCAGAGTCAGAAAACAGA--ATTCCGGATTGTTACATTGTAGAAGTAGCAGG
SEQ1316	AAAAAATAGAAATCAGAATCTAAC--ATT---GATAGTATTATTGTGGGAACA-CAGT
SEQ1301	AGTATGAGTTTCTGTTAATAGTTTTTCCGTAGCCGTGTGAACCAATTCTGGACTAAGCT
SEQ1302	GGTACTGGGGGCAATATTGG-TCGTTTGATGACTCTTTTTTCTGATTATGAATCCTA--
SEQ1303	GGTACTGGGGGCAATATTGG-TCGTTTGATGACTCTTTTTTCTGATTATGAATCCTA--
SEQ1304	GGTACTGGGGGCAATATTGG-TCGTTTGATGACTCTTTTTTCTGATTATGAATCCTA--
SEQ1305	GATCCCAAGCTTAGTCCAGAATTGGTTCACACGGCTACGGAAAACTATTAACAGAAAC
SEQ1306	GGTACTGGGGGCAATATTGG-TCGTTTGATGACTCTTTTTTCTGATTATGAATCCTA--
SEQ1307	GATCCCAAGCTTAGTCCAGAATTGGTTCACACGGCTACGGAAAACTATTAACAGAAAC
SEQ1308	GATCCCAAGCTTAGTCCAGAATTGGTTCACACGGCTACGGAAAACTATTAACAGAAAC
SEQ1309	GGTACTGGGGGCAATATTGG-TCGTTTGATGACTCTTTTTTCTGATTATGAATCCTA--
SEQ1310	GGTACTGGGGGCAATATTGG-TCGTTTGATGACTCTTTTTTCTGATTATGAATCCTA--
SEQ1311	GATCCCAAGCTTAGTCCAGAATTGGTTCACACGGCTACGGAAAACTATTAACAGAAAC
SEQ1312	GATCCCAAGCTTAGTCCAGAATTGGTTCACACGGCTACGGAAAACTATTAACAGAAAC
SEQ1313	GGTACTGGGGGCAATATTGG-TCGTTTGATGACTCTTTTTTCTGATTATGAATCCTA--
SEQ1314	GATCCCAAGCTTAGTCCAGAATTGGTTCACACGGCTACGGAAAACTATTAACAGAAAC
SEQ1315	GATCCCAAGCTTAGTCCAGAATTGGTTCACACGGCTACGGAAAACTATTAACAGAAAC
SEQ1316	GGTACTGGGGGCAATATTGG-TCGTTTGATGACTCTTTTTTCTGATTATGAATCCTA--
SEQ1301	GGGATCTCCTGCTACTTCTACAATGTGAACAATCCGGA-ATTCTGTTTTCTGACTCTGA
SEQ1302	TATTCCAGTACAAACGATTGATATGCAGTGTGCTTCATCAAGT--TCTGCCTTGTTTTT
SEQ1303	TATTCCAGTACAAACGATTGATATGCAGTGTGCTTCATCAAGT--TCTGCCTTGTTTTT
SEQ1304	TATTCCAGTACAAACGATTGATATGCAGTGTGCTTCATCAAGT--TCTGCCTTGTTTTT
SEQ1305	CATACTAAAATATCGGATTATGATGCAATTGAATGGAATGAACCATTTGCAGCGATTGA
SEQ1306	TATTC-----
SEQ1307	CATACTAAAATATCGGATTATGATGCAATTGAATGGAATGAACCATTTGCAGCGATTGA
SEQ1308	CATACTAAAATATCGGATTATGATGCAATTGAATGGAATGAACCATTTGCAGCGATTGA
SEQ1309	TATTCCAGTACAAACGATTGATATGCAGTGTGCTTCATCAAGT--TCTGCCTTGTTTTT
SEQ1310	TATTCCAGTACAAACGATTGATATGCAGTGTGCTTCATCAAGT--TCTGCCTTGTTTTT
SEQ1311	CATACTAAAATATCGGATTATGATGCAATTGAATGGAATGAACCATTTGCAGCGATTGA
SEQ1312	CATACTAAAATATCGGATTATGATGCAATTGAATGGAATGAACCATTTGCAGCGATTGA
SEQ1313	TATTCCAGTACAAACGATTGATATGCAGTGTGCTTCATCAAGT--TCTGCCTTGTTTTT
SEQ1314	CATACTAAAATATCGGATTATGATGCAATTGAATGGAATGAACCATTTGCAGCGATTGA
SEQ1315	CATACTAAAATATCGGATTATGATGCAATTGAATGGAATGAACCATTTGCAGCGATTGA
SEQ1316	TATTCCAGTACAAACGATTGATATGCAGTGTGCTTCATCAAGT--TCTGCCTTGTTTTT

Table 13: Comparative Sequences relating to SAG0466 (thiolase)

SEQ1301	GCGTTAGAAATGCAGCAGCATCGTGCATTAAACAAACATTTTC--CAATAGTGAGCAAAG
SEQ1302	GGT-TATCTAAAAATCAGTG-CCGGTATTAATGAAAAAGTTCTTGTGGGGGGATTGAA
SEQ1303	GGT-TATCTAAAAATCAGTG-CCGGTATTAATGAAAAAGTTCTTGTGGGGGGATTGAA
SEQ1304	GGG-TATCTAAAAA-----
SEQ1305	GCTTTATTTAATCATTATTATCCTGAAGAGAGAGAAAAATTCAATATTTTGGAGGGGC
SEQ1306	-----
SEQ1307	GCTTTATTTAATCATTATTATCCTGAAGAGAGAGAAAAATTCAATATTTTGGAGGGGC
SEQ1308	GCTCTATTTAATCATTATTATCCTGAAGAGAGAGAAAAATTCAATATTTTGGAGGGAC
SEQ1309	GGT-TATCTAAAAATCAGTA-CCGGTATTAATGAAAAAGTTCTTGTGGGGGGATTGAA
SEQ1310	GGT-TATCTAAAAATCAGTA-CCGGTATTAATGAAAAAGTTCTTGTGGGGGGATTGAA
SEQ1311	GCTCTATTTAATCATTATTATCCTGAAGAGAGAGAAAAATTCAATATTTTGGAGGGAC
SEQ1312	GCTTTATTTAATCATTATTATCCTGAAGAGAGAGAAAAATTCAATATTTTGGAGGGGC
SEQ1313	GGT-TATCTAAAAATCAGTG-CCGGTATTAATGAAAAAGTTCTTGTGGGGGGATTGAA
SEQ1314	GCTCTATTTAATCATTATTATCCTGAAGAGAGAGAAAAATTCAATATTTTGGAGGGGC
SEQ1315	GCTCTATTTAATCATTATTATCCTGAAGAGAGAGAAAAATTCAATATTTTGGAGGGGC
SEQ1316	GGT-TATCTAAAAATCAGTA-CCGGTATTAATGAAAAAGTTCTTGTGGGGGGATTGAA
SEQ1301	TGAATTTTCCATCAATCTTGG--TAATTTTGAAGAAATGTTTCTTTAGTTTCTAAC
SEQ1302	GTAAGTTCTCTTCAACCTATGAGACGTTACGCTAAAGAAGATAATCGTAACGGAGAATAT
SEQ1303	GTAAGTTCTCTTCAACCTATGAGACGTTACGCTAAAGAAGATAATCGTAACGGAGAATAT
SEQ1304	-----
SEQ1305	TTAGCTTACGGACACCCTTAA--TGCCTGCTCAGGAATTATTAATATCC-----
SEQ1306	-----
SEQ1307	TTAGCTTACGGACACCCTTA---TGCCTGCTCAGGAATTATTAATATCCTTCATCTTAT
SEQ1308	TTAGCTTACGGACACCCTTA---TGCCTGCTCAGGAATTATTAATATCCTTCATCTTAT
SEQ1309	GTAAGTTCTCTTCAACCTATGAGACGTTATGCTAAAGAAGATAATCGTAACGGAGAATAT
SEQ1310	GTAAGTTCTCTTCAACCTATGAGACGTTATGCTAAAGAAGATAATCGTAACGGAGAATAT
SEQ1311	TTAGCTTACGGACACCCTTA---TGCCTGCTCAGGAATTATTAATATCCTTCATCTTAT
SEQ1312	TTAGCTTACGGACACCCTTA---TGCCTGCTCAGGAATTATTAATATCCTTCATCTTAT
SEQ1313	GTAAGTTCTCTTCAACCTATGAGACGTTACGCTAAAGAAGATAATCGTAACGGAGAATAT
SEQ1314	TTAGCTTACGGACACCCTTA---TGCCTGCTCAGGAATTATTAATATCCTTCATCTTAT
SEQ1315	TTAGCTTACGGACACCCTTA---TGCCTGCTCAGGAATTATTAATATCCTTCATCTTAT
SEQ1316	GTAAGTTCTCTTCAACCTATGAGACGTTATGCTAAAGAAGATAATCGTAACGGAGAATAT
SEQ1301	CCTTGATCTCGCATCCCTTCCATTGGTAAGATTACYTCTTCTAAATAGCCACCTTGTTT
SEQ1302	CCGTTGCTCAGTTTCTCCTGACTCTTATGCTG--AAACTGTAATGTTAGAAGGGGCAC
SEQ1303	CCGTTGCTCAGTTTCTCCTGACTCTTAKGCTG--AAACTGTAATGTTAGAAGGGGCAC
SEQ1304	-----
SEQ1305	-----
SEQ1306	-----
SEQ1307	CAGGCATTAAAAATATAAAAAATAAACCTATGGGC-CTAACTGCCATTGCAGGGGCA----
SEQ1308	CAGGCATTAAAAATATAAAAAATAAACCTATGGGT-CTAACTGCCATTGCAGGGGCAG--
SEQ1309	CAGTTGCTCAGTTTCTCCTGACTCTTATGCTG--AAACTGTAATGTTAGAAGGGGCCC
SEQ1310	CAGTTGCTCAGTTTCTCCTGACTCTTATGCTG--AAACTGTAATGTTAGAAGGGGCCC
SEQ1311	CAGGCATTAAAAATATAAAAAATAAACCTATGGGT-CTAACTGCCATTGCAGGGGCAGGA-
SEQ1312	CAGGCATTAAAAATATAAAAAATAAACCTATGGGTCTAACTGC-----
SEQ1313	CCGTTGCTCAGTTTCTCCTGACTCTTATGCTG--AAACTGTAATGTTAGA-----
SEQ1314	CAGGCATTAAAAATATAAAAAATAAACCTATGGGT-CTAACTGCCATTGCAGGGGC----
SEQ1315	CAGGCATTAAAAATATAAAAAATAAACCTATGGGT-CTAACTGCCATTGCAGGGGCAGGA-
SEQ1316	TABCMARATVSTNCSRATNGTSAGTHAS-----

Table 13: Comparative Sequences relating to SAG0466 (thiolase)

SEQ1301	GCTGTTAAGGCGCGTTTATGGCTCAAGAATGCCAATTTATCTAACATTTCTCTTCTTAAA
SEQ1302	AAGAGTCTGTCAAAAATATGGTTTTAGAAAGAGAAATGTTAGATAAAATTGGCATTCTTGA
SEQ1303	AAGAGTCTGTCAAAAATATGGTTTTAGAAAGAGAAATGTTAGATAAAATTGGCATTCTTGA
SEQ1304	-----
SEQ1305	-----
SEQ1306	-----
SEQ1307	-----
SEQ1308	-----
SEQ1309	GAGAGTCTGTCAAAAATATGGTTTTAGAAAGAGAAATGTTAGATAAAATTGGCATTCTTGA
SEQ1310	-----
SEQ1311	-----
SEQ1312	-----
SEQ1313	-----
SEQ1314	-----
SEQ1315	-----
SEQ1316	-----
SEQ1301	CCATATTTTTGACAGACTCTCTGGGCCCCCTT--CTAACATTACAGTTTCAGCATAAGAG
SEQ1302	CCATAAACGCGCCTTAACAGCTAAACAAGGTGGCTATTTAGAAAGAGGTAATCTTACCAA
SEQ1303	CCATAAACGCGCCTTAACAGCTAAACAAGGTGGCTATTTAGAAAGAGGTAATCTTACCAA
SEQ1304	-----
SEQ1305	-----
SEQ1306	-----
SEQ1307	-----
SEQ1308	-----
SEQ1309	CCATAAACGCGCCTTAACAGCTAAACA-----
SEQ1310	-----
SEQ1311	-----
SEQ1312	-----
SEQ1313	-----
SEQ1314	-----
SEQ1315	-----
SEQ1316	-----
SEQ1301	CAGGAGAAAACCTGAGCAACTGTATATTCTCCGTTACGATTATCTTCTTTAGCATAACGT
SEQ1302	GGAAGGGATGCGAGATCAAGGCGTTAGAAAACATAAAGAAGCATTTTTCAAAAATTAC
SEQ1303	GGAAGGGATGCGAGATCAAGGCGTTAGAAAACATAAAGAAGCATTTTTCAAAAATTAC
SEQ1304	-----
SEQ1305	-----
SEQ1306	-----
SEQ1307	-----
SEQ1308	-----
SEQ1309	-----
SEQ1310	-----
SEQ1311	-----
SEQ1312	-----
SEQ1313	-----
SEQ1314	-----
SEQ1315	-----
SEQ1316	-----

Table 13: Comparative Sequences relating to SAG0466 (thiolase)

SEQ1301	TCATAGGTTGAAGAGAACTACTTTCAATCCCCCAACAAGAACTTTTCATTAATACCG
SEQ1302	AAGATTGATGGAAAATTCACCTTTGCTCACTATTGGAAATGTTTGTTTAATGCACGATG
SEQ1303	AAGATTGATGGRAAATTCACCTTTGCTCACTATTGGAAATGTTTGTTTAATGCACGATG
SEQ1304	-----
SEQ1305	-----
SEQ1306	-----
SEQ1307	-----
SEQ1308	-----
SEQ1309	-----
SEQ1310	-----
SEQ1311	-----
SEQ1312	-----
SEQ1313	-----
SEQ1314	-----
SEQ1315	-----
SEQ1316	-----
SEQ1301	TACTGATTTTGTAGATAACCAAAAAC--AAGGCAGAACTTGATGAAGCACACTGCATAT
SEQ1302	TGCTGCATTTCTAACGCTTCAGAGTCAGAAAACAGAATTCCGGATTGTTACATTGTAG
SEQ1303	TGCTGCATTTCTWACGCTTCAGAGTCAGAAAACAGAATTCCGGATTGTTACATTGTAG
SEQ1304	-----
SEQ1305	-----
SEQ1306	-----
SEQ1307	-----
SEQ1308	-----
SEQ1309	-----
SEQ1310	-----
SEQ1311	-----
SEQ1312	-----
SEQ1313	-----
SEQ1314	-----
SEQ1315	-----
SEQ1316	-----
SEQ1301	AATCGTTTGTACTGGAATATAGGATTCATAATCAGAAAAAAGAGTCATCAAACGACCAA
SEQ1302	AGTAGCAGGAGATCCCAAGCTTAGTCCAGAATTGGTTCACACGGCTACGAAAAACTAT
SEQ1303	AGTAGCAGGAGATCCCAAGCTTAGTCCAGAATTGGTTCACACGGCTACGAAAAACTAT
SEQ1304	-----
SEQ1305	-----
SEQ1306	-----
SEQ1307	-----
SEQ1308	-----
SEQ1309	-----
SEQ1310	-----
SEQ1311	-----
SEQ1312	-----
SEQ1313	-----
SEQ1314	-----
SEQ1315	-----
SEQ1316	-----

Table 13: Comparative Sequences relating to SAG0466 (thiolase)

SEQ1301	ATTGCCCCCAGTACCAACTGTGTTCCCAAAATAATACTATCAATGTTAGATTCTGATT
SEQ1302	AACAGAAACTCATACTAAAAATATCGGATTATGATGCAATTGAATGGAATGAACCATTG
SEQ1303	AACAGAAACTCATACTAAAAATATCGGATTATGATGCAATTGAATGGAATGAACCATTG
SEQ1304	-----
SEQ1305	-----
SEQ1306	-----
SEQ1307	-----
SEQ1308	-----
SEQ1309	-----
SEQ1310	-----
SEQ1311	-----
SEQ1312	-----
SEQ1313	-----
SEQ1314	-----
SEQ1315	-----
SEQ1316	-----
SEQ1301	TATTTTTTTTATTTGATTAAAAGGTGTGCTCCTAAAAGTTCTGGACGGTAAGTTTAAA
SEQ1302	AGCGATTGATGCTTTATTTAATCATTATTATCCTGAAGAGAGAGAAAAATTCAATATTT
SEQ1303	AGCGATTGATGCTTTATTTAATCATTATTATCCTGAAGAGAGAGAAAAATTCAATATTT
SEQ1304	-----
SEQ1305	-----
SEQ1306	-----
SEQ1307	-----
SEQ1308	-----
SEQ1309	-----
SEQ1310	-----
SEQ1311	-----
SEQ1312	-----
SEQ1313	-----
SEQ1314	-----
SEQ1315	-----
SEQ1316	-----
SEQ1301	TGCTT-----
SEQ1302	TGGAGGGGCATTAGCTTACGGACACCCTTATGCCTGCTCAGGAATTA
SEQ1303	TGGAGGGGCATTAGCTTACGGACACCCTTATGCCTGCTCAGG-----
SEQ1304	-----
SEQ1305	-----
SEQ1306	-----
SEQ1307	-----
SEQ1308	-----
SEQ1309	-----
SEQ1310	-----
SEQ1311	-----
SEQ1312	-----
SEQ1313	-----
SEQ1314	-----
SEQ1315	-----
SEQ1316	-----

Table 14: Comparative Sequences relating to SAG0471 (glucokinase)**SEQ ID NO. 1401: SAG0471 FROM THE 18RS21 GBS TYPE II STRAIN**

TTAAATTTGGTATCTTGACGCTTGAGGGAGAAGTACAAGAAAATGGGCAATTGAGACCAATACTTTAGAAAACGGAAGACATATCGTT
TCTGATATCGTTGAATCTCTCAAAACATCGTTTGAGCCTCTATGGATTAAACAAAAGATGACTTTCTCGGTATCGGTATGGGTCTCCAGG
AGCTGTTGATAGAAGTAGTAAAAACAGTAACAGGTGCTTTTAATCTAAATTGGGCTGATACTCAAGAAGTAGGTTTCAAGTTATTGAAAAAG
AAGTTGGAATTCCATTTTATTGATAACGATGCTAATGTTGAGCAGCACTTGGTGAACGCTGGGTAGGTGCTGGTGCCAAATATCCCGAC
GTTGTTTTCGTAACCCCTCGGAACAGGAGTAGGTGGAGGTGTTATCGCAGATGGTAAACCTCATCCATGGTGTGTCAGGAGCAGGTGGAGA
AATTGGGCATATGATTGTTGATCCAGAAAATGGATTTACGTGCACATGTGGTAAACAAAGGCTGCCTTGAGACAGTTGCATCAGCGACAG
GTGTTGTTAGAGTAGCACGCTCAACTCGCAGAACAAATATGAGGGTTCGTCTGCCATTAAAGCAGCGATTGACACCGGTGATACTGTTACA
AGTAAAGATATTTTATAGCAGCAGAAAGATGGGGATAAATTTGCTAATCTGTTGTTGAACGTGTATCACGTTACCTTGGACTGCGCAGC
AGCTAATATTTCAAATATTTTAAACCCCTGATTCTGTGGTTATTGGTGGCGGTGTCTCAGCAGCAGGTGAATTTTACGTAGTCGCGTTG
AGAAATACTTTGTACATTTGCTTTCCCAAGTTAAAAAGTCAACTAAAATTAAGAT

SEQ ID NO. 1402: SAG0471 FROM THE 090 GBS TYPE Ia STRAIN

CGTTTTCTGATATCGTTGAATCTCTCAACATCGTTTGAGCCTCTATGGATTAAACAAAAGATGACTTTCTCGGTATCGGTATGGGTCTC
CAGGAGCTGTTGATAGAACTAGTAAAAACAGTAACAGGTGCTTTTAATCTAAATTGGGCTGATACTCAAGAAGTAGGTTTCAAGTTATTGAA
AAAGAAAGTTGGAAATTCATTTTATTGATAACGATGCTAATGTTGAGCAGCACTTGGTGAACGCTGGGTAGGTGCTGGTGCCAAATATCC
CGATGTTGTTTTCGTAACCCCTCGGAACAGGAGTAGGTGGAGGTGTTATCGCAGATGGTAAACCTCATCCATGGTGTGTCAGGAGCAGGTG
GAGAAATTGGGCATATGATTGTTGATCCAGAKAATGGATTTACGTGCACATGTGGTAAACAAAGGCTGTCTTGAGACAGTTGCATCAGCG
ACAGGTGTTGTTAGAGTAGCACGCTCAACTCGCAGAACAAATATGAGGGTTCGTCTGCCATTAAAGCAGCGATTGACAACGGTGATACTGT
TACAAGTAAAGATATTTTATAGCAGCAGAAAGATGGGGATAAATTTGCTAATCTGTTGTTGAACGTGTATCACGTTACCTTGGACTGG
CAGCAGCTAATATTTCAAATATTTTAAACCCCTGATTCTGTGGTTATTGGTGGCGGTGTCTCAGCAGCAGGTGAATTTTACGTAGTCGCG
GTTGAGAAATACTTTGTACATTTG

SEQ ID NO. 1403: SAG0471 FROM THE COH1 GBS TYPE Ia STRAIN

ACAAGAAAAATGGGCAATTGAGACCAATACTTTAGAAAACGGAAGACATATCGTTTCTGATATCGTTGAATCTCTCAACATCGTTTGA
GCCTCTATGGATTAAACAAAAGATGACTTTCTCGGTATCGGTATGGGTCTCCAGGAGCTGTTGATAGAACTAGTAAAAACAGTAACAGGT
GCTTTTAATCTAAATTGGGCTGATACTCAAGA

SEQ ID NO. 1404: SAG0471 FROM THE CJB110 GBS NONTYPEABLE STRAIN

TTGGTATCTTGACGCTTGAGGAGAAGTACAAGAAAATGGGCAATTGAGACCAATACTTTAGAAAACGGAAGACATATCGTTTCTGATA
TCGTTGAATCTCTCAACATCGTTTGAGCCTCTATGGATTAAACAAAAGATGACTTTCTCGGTATCGGTATGGGTCTCCAGGAGCTGTT
GATAGAACTAGTAAAAAC

SEQ ID NO. 1405: SAG0471 FROM THE CJB110 GBS NONTYPEABLE STRAIN

CACCAGCTAATATTTCAAATATTTTAAACCCCTGATTCTGTGGTTATTGGTGGCGGTGTCTCAGCAGCAGGTGAATTTTACGTAGTCGC
GTTGAGAAATACTTTGTACATTTGCTTTCCCAAGTTAAAAAGTCAACTA

SEQ ID NO. 1406: SAG0471 FROM THE 2603V/R GBS TYPE V STRAIN

GGGCAATTGAGACCAATACTTTAGAAAACGGAAGACATATCGTTTCTGATATCGTTGAATCTCTCAACATCGTTTGAGCCTCTATGGA
TTAAACAAAAGATGACTTTCTCGGTATCGGTATGGGTCTCCAGGAGCTG

SEQ ID NO. 1407: SAG0471 FROM THE H36b GBS TYPE Ib STRAIN

GGCAATTGAGACCAATACTTTAGAAAACGGAAGACATATCGTTTCTGATATCGTTGAATCTCTCAACATCGTTTGAGCCTCTATGGAT
TAACAAAAGATGACTTTCTCGGTATCGGTATGGGTCTCCAGGAGCTGTTGATAGAACTAGTAAAAACAGTAACAGGTGCTTTTAATCTA
AATTGGGCTGATACTCAAGAAGTAGGTTCAAGTTATTGAAAAGAGTTGGAATTTTATGATAACGATGCTAATGTTGTCAGC
ACTTGGTGAACGCTGGGTAGGTGCTGGTGCCAAATATCCCGACGTTGTTTTCGTAACC

SEQ ID NO. 1408: SAG0471 FROM THE H36 GBS TYPE Ib STRAIN (REVERSE COMPLEMENT)

GAGACAGTTGCATCAGCGACAGGTGTTGTTAGAGTAGCAGCTCAACTCGCAGAACAAATATGAGGGTTCGTCTGCCATTAAAGCAGCGAT
TGACAACGGTGATACTGTTACAAGTAAAGATATTTTATAGCAGCAGAAAGATGGGGATAAATTTGCTAATCTGTTGTTGAACGTGTAT
CACGTTACCTTGGACTGGCAGCAGCTAATATTTCAAATATTTTAAACCCCTGATTCTGTGGTTATTGGTGGCGGTGTCTCAGCAGCAGGT
GAATTTTACGTAGTCGCGTTGAGAAATACTTTGTACATTTGCTTTCCCA

SEQ ID NO. 1409: SAG0471 FROM THE M732 GBS TYPE III STRAIN

ACAAGAAAAATGGGCAATTGAGACCAATACTTTAGAAAACGGAAGACATATCGTTTCTGATATCGTTGAATCTCTCAACATCGTTTGAGC
CTCTATGGATTAAACAAAAGATGACTTTCTCGGTATCGGTATGGGTCTCCAGGAGCTGTTGATAGAACTAGTAAAAACAGTAACAGGTGC
TTTTAATCTAAATTGGGCTGATACTCAAGAAGTAGGTTCAAGTTATTGAAAAGAGTTGGAATTTTATGATAACGATGCTAATGTTGTCAGC
ATGTTGACGACCTTGGTGAACGCTGGGTAGGTGCTGGTGCCAAATATCCCGATGTTGTTTTCGTAACCCCTCGGAACAGGAGTAGGTGGA
GGTGTATCGCAGATGGTAACCTCATCCATGGTGTGCAAGAGCAGGTGGAGAAATTGGGCATATGATT

SEQ ID NO. 1410: SAG0471 FROM THE M732 GBS TYPE III STRAIN (REVERSE COMPLEMENT)

CAGCAGCAGGTGAATTTTACGTAGTCGCGTTGAGAAATACTTTGTACATTTGCTTTCCCAAGTTAAAAAGTCAACTAAAATTAAG
ATTGCTGAACCTAGGTAATGAT

SEQ ID NO. 1411: SAG0471 FROM THE M781 GBS TYPE III STRAIN

AGAAGTACAAGAAAATGGGCAATTGAGACCAATACTTTAGAAAACGGAAGACATATCGTTTCTGATATCGTTGAATCTCTCAACATCGTT
TGAGCCTCTATGGATTAAACAAAAGATGACTTTCTCGGTATCGGTATGGGTCTCCAGGAGCTGTTGATAGAACTAGTAAAAACAGTAACA
GGTGCTTTTAATCTAAATTGGGCTGATACTCAAGAAGTAGGTTCCGGTTATTGAAAAGAGTTGGAATTTTATGATAACGATGCTA
TGCTAATGTTGACGACCTTGGTGAACGCTGGGTAGGTGCTGGTGCCAAATATCCCGATGTTGTTTTCGTAACCCCTCGGAACAGGAGTA

Table 14: Comparative Sequences relating to SAG0471 (glucokinase)

SEQ ID NO. 1412: SAG0471 FROM THE M781 GBS TYPE III STRAIN (REVERSE COMPLEMENT)
 GATACTGTTACAAGTAAAGATATTTTATAGCAGCAGAAGATGGGGATAAATTGCTAATTCTGTTGTTGAACGTGTATCAGGTTACCT
 TGGACTGGCAGCAGCTAATATTTCAAATATTTTAAACCCTGATTCTGTGGTTATTGGTGGCGGTGTCTCAGCAGCAGGTGAATTTTAC
 GTAGTCGCGTTGAGAAATACTTTGTACATTGCTTTCCCAAGTTAAAA

SEQ ID NO. 1413: SAG0471 FROM THE 090 GBS TYPE Ia STRAIN
 AAATTTGGTATCTTGACGCTTGAGGGAGAAGTACAAGAAAAATGGGCATTGAGACCATACTTAGAAAAACGGAAGACATATCGTTTCTGA
 TATCGTTGAATCTCTCAAACATCGTTTGGCCCTCTATGGATTAAACAAAGATGACTTTCTCGGTATCGGTATGGGTTCTCCAGGAGCTG
 TTGATAGAACTAGTAAAAAGTAAACAGGTGCTTTAATCTAAATTTGGGCTGATACTCAAGAAAGTAGGTTCAAGTTATTTGAAAAAGAGTT
 GGAATTCATTTTATTGATAACGATGCTAATGTTGCAGCACTTGGTGAACGCTGGGTAGGTGCTGGTGCCAATAATCCCGACGTTGT
 TTTCTGAACCCTCGGAACAGGAGTAGGTGGAGG

SEQ ID NO. 1414: SAG0471 FROM THE 090 GBS TYPE Ia STRAIN (REVERSE COMPLEMENT)
 GTGATACTGTTACAAGTAAAGATATTTTATAGCAGCAGAAGATGGGGATAAATTGCTAATTCTGTTGTTGAACGTGTATCAGGTTAC
 CTTGGACTGGCAGCAGCTAATATTTCAAATATTTTAAACCCTGATTCTGTGGTTATTGGTGGCGGTGTCTCAGCAGCAGGTGAATTTT
 ACGTAGTCGCGTTGAGAAATACTTTATCACATTGCTTTCCCAAGTTAAAAAGTCAACTAAAATTAAGATTG

SEQ ID NO. 1415: SAG0471 FROM THE JM9130013 GBS TYPE VIII STRAIN (REVERSE COMPLEMENT)
 GTTATCGCAGATGGTAACCTCATCCATGGTGTTCAGGAGCAGGTGGAGAAATTTGGGCATATGATTGTTGATCCAGAAAATGGATTAC
 GTGCACATGTGGTAACAAAGGCTGCCTTGAGACAGTTGCATCAGCGACAGGTGTTGTTAGAGTAGCACGTCAACTCGCAGAACAAATAG
 AGGGTTCGTCTGCCATTAAAGCAGCGATTGACCACGGTGATCTGTTACAAGTAAAGATATTTTATAGCAGCAGAAGATGGGGATAAA
 TTTGCTAATTTCTGTTGTTGAACGTGTATCAGGTTACCTTGGACTGGCAGCAGCTAATATTTCAAATATTTTAAACCCTGATTCTGTGGT
 TATTGTTGGCGGTGTCTCAGCAGCAGGTGAATTTTACGTAGTCGCGTTGAGAAATACTTTGTACATTGCTTTCCCAAGTTAAAA
 AGTCAACTAA

SEQ ID NO. 1416: SAG0471 FROM THE JM9130013 GBS TYPE VIII STRAIN (REVERSE COMPLEMENT)
 TGGTATCTTGACGCTTGAGGGAGAAGTACAAGAAAAATGGGCAATTGAGACCATACTTAGAAAAACGGAAGACATATCGTTTCTGATATC
 GTTGAATCTCTCAAACATCGTTTGGCCCTCTATGGATTAAACAAAGATGACTTTCTCGGTATCGGTATGGGTTCTCCAGGAGCTGTTGA
 TAGAACTAGTAAAAAGTACAGGTGCTTTAATCTAAATTTGGGCTGATACTCAAGAAAGTAGGTTCAAGTTATTTGAAAAAGAGCTGGAA
 TTCCATTTTTTATTG

SEQ ID NO. 1417: SAG0471 FROM THE 2603V/R TYPE V GBS STRAIN (REVERSE COMPLEMENT)
 AGCAGCTAATATTTCAAATATTTTAAACCCTGATTCTGTGGTTATTGGTGGCGGTGTCTCAGCAGCAGGTGAATTTTACGTAGTCGCG
 TTGAGAAATACTTTGTACATTGTTTCCCAAGGT

SEQ1401_ -----
 SEQ1402 -----
 SEQ1403 -----
 SEQ1404 -----
 SEQ1405 -----
 SEQ1406 -----
 SEQ1407 -----
 SEQ1408 -----
 SEQ1409 -----
 SEQ1410 -----
 SEQ1411 -----
 SEQ1412 -----
 SEQ1413 -----
 SEQ1414 -----
 SEQ1415 TTATCGCAGATGGTAACCTCATCCATGGTGTTCAGGAGCAGGTGGAGAAATTTGGGCAT
 SEQ1416 -----
 SEQ1417 -----

SEQ1401_ -----
 SEQ1402 -----
 SEQ1403 -----
 SEQ1404 -----
 SEQ1405 -----
 SEQ1406 -----
 SEQ1407 -----
 SEQ1408 -----GAG
 SEQ1409 -----
 SEQ1410 -----
 SEQ1411 -----
 SEQ1412 -----
 SEQ1413 -----
 SEQ1414 -----
 SEQ1415 TGATTGTTGATCCAGAAAATGGATTACGTGCACATGTGGTAACAAAGGCTGCCTTGAG
 SEQ1416 -----
 SEQ1417 -----

Table 14: Comparative Sequences relating to SAG0471 (glucokinase)

SEQ1401	-----
SEQ1402	-----
SEQ1403	-----
SEQ1404	-----
SEQ1405	-----
SEQ1406	-----
SEQ1407	-----
SEQ1408	CAGTTGCATCAGCGACAGGTGTTGTTAGAGTAGCACGTCAACTCGCAGAACAAATATGAG
SEQ1409	-----
SEQ1410	-----
SEQ1411	-----
SEQ1412	-----
SEQ1413	-----
SEQ1414	-----
SEQ1415	CAGTTGCATCAGCGACAGGTGTTGTTAGAGTAGCACGTCAACTCGCAGAACAAATATGAG
SEQ1416	-----
SEQ1417	-----
SEQ1401	-----
SEQ1402	-----
SEQ1403	-----
SEQ1404	-----
SEQ1405	-----
SEQ1406	-----
SEQ1407	-----
SEQ1408	GTTTCGTCTGCCATTAAAGCAGCGATTGACACGGTGATACTGTTACAAGTAAAGATATT
SEQ1409	-----
SEQ1410	-----
SEQ1411	-----
SEQ1412	-----GATACTGTTACAAGTAAAGATATT
SEQ1413	-----
SEQ1414	-----GTGATACTGTTACAAGTAAAGATATT
SEQ1415	GTTTCGTCTGCCATTAAAGCAGCGATTGACACGGTGATACTGTTACAAGTAAAGATATT
SEQ1416	-----
SEQ1417	-----
SEQ1401	-----TTAAATTGGTATCTTGACGCTTGAGGGAGAAGTACAA
SEQ1402	-----
SEQ1403	-----ACAA
SEQ1404	-----TTGGTATCTTGACGCTTGAGG-AGAAGTACAA
SEQ1405	-----
SEQ1406	-----
SEQ1407	-----
SEQ1408	TTATAGCAGCAGAAGATGGGGATAAATTGCTAATTCTGTGTTGAACGTGTATCACGT
SEQ1409	-----ACAA
SEQ1410	-----
SEQ1411	-----AGAAGTACAA
SEQ1412	TTATAGCAGCAGAAGATGGGGATAAATTGCTAATTCTGTGTTGAACGTGTATCACGT
SEQ1413	-----AAATTGGTATCTTGACGCTTGAGGGAGAAGTACAA
SEQ1414	TTATAGCAGCAGAAGATGGGGATAAATTGCTAATTCTGTGTTGAACGTGTATCACGT
SEQ1415	TTATAGCAGCAGAAGATGGGGATAAATTGCTAATTCTGTGTTGAACGTGTATCACGT
SEQ1416	-----TGGTATCTTGACGCTTGAGGGAGAAGTACAA
SEQ1417	-----

Table 14: Comparative Sequences relating to SAG0471 (glucokinase)

SEQ1401	AAAAATGGGCAATTGAGACCAATACTTTAGAAAAACGGAAGACATATCGTTTCTGATATC
SEQ1402	-----CGTTTCTGATATC
SEQ1403	AAAAATGGGCAATTGAGACCAATACTTTAGAAAAACGGAAGACATATCGTTTCTGATATC
SEQ1404	AAAAATGGGCAATTGAGACCAATACTTTAGAAAAACGGAAGACATATCGTTTCTGATATC
SEQ1405	-----CACCAGCTAATAATTTCAAATATTTTAAACCTGATTCTGTGGTTATT
SEQ1406	-----GGGCAATTGAGACCAATACTTTAGAAAAACGGAAGACATATCGTTTCTGATATC
SEQ1407	-----GGCAATTGAGACCAATACTTTAGAAAAACGGAAGACATATCGTTTCTGATATC
SEQ1408	ACCTTGGAAGTGGCAGCAGCTAATAATTTCAAATATTTTAAACCTGATTCTGTGGTTATT
SEQ1409	AAAAATGGGCAATTGAGACCA - TACTT - AGAAAAACGGAAGACATATCGTTTCTGATATC
SEQ1410	-----
SEQ1411	AAAA - TGGGCAATTGAGACCA - TACTT - AGAAAAACGGAAGACATATCGTTTCTGATATC
SEQ1412	ACCTTGGAAGTGGCAGCAGCTAATAATTTCAAATATTTTAAACCTGATTCTGTGGTTATT
SEQ1413	AAAAATGGGCA - TTGAGACCA - TACTT - AGAAAAACGGAAGACATATCGTTTCTGATATC
SEQ1414	ACCTTGGAAGTGGCAGCAGCTAATAATTTCAAATATTTTAAACCTGATTCTGTGGTTATT
SEQ1415	ACCTTGGAAGTGGCAGCAGCTAATAATTTCAAATATTTTAAACCTGATTCTGTGGTTATT
SEQ1416	AAAAATGGGCAATTGAGACCA - TACTT - AGAAAAACGGAAGACATATCGTTTCTGATATC
SEQ1417	-----AGCAGCTAATAATTTCAAATATTTTAAACCTGATTCTGTGGTTATT
SEQ1401	TTGAATCTCTCA - AACATCGTTTGAGCCTCTATGGATTAACAAAAGATGACTTTCTCGG
SEQ1402	TTGAATCTCTCA - AACATCGTTTGAGCCTCTATGGATTAACAAAAGATGACTTTCTCGG
SEQ1403	TTGAATCTCTCA - AACATCGTTTGAGCCTCTATGGATTAACAAAAGATGACTTTCTCGG
SEQ1404	TTGAATCTCTCA - AACATCGTTTGAGCCTCTATGGATTAACAAAAGATGACTTTCTCGG
SEQ1405	GTGGCGGTGTCTCAGCAGCAGGTGAATTTTACGTAGTCGCGTTGAGAAATACTTT - - -
SEQ1406	TTGAATCTCTCA - AACATCGTTTGAGCCTCTATGGATTAACAAAAGATGACTTTCTCGG
SEQ1407	TTGAATCTCTCA - AACATCGTTTGAGCCTCTATGGATTAACAAAAGATGACTTTCTCGG
SEQ1408	GTGGCGGTGTCTCAGCAGCAGGTGAATTTTACGTAGTCGCGTTGAGAAATACTTT - - -
SEQ1409	TTGAATCTCTCA - AACATCGTTTGAGCCTCTATGGATTAACAAAAGATGACTTTCTCGG
SEQ1410	-----CAGCAGCAGGTGAATTTTACGTAGTCGCGTTGAGAAATACTTT - - -
SEQ1411	TTGAATCTCTCA - AACATCGTTTGAGCCTCTATGGATTAACAAAAGATGACTTTCTCGG
SEQ1412	GTGGCGGTGTCTCAGCAGCAGGTGAATTTTACGTAGTCGCGTTGAGAAATACTTT - - -
SEQ1413	TTGAATCTCTCA - AACATCGTTTGAGCCTCTATGGATTAACAAAAGATGACTTTCTCGG
SEQ1414	GTGGCGGTGTCTCAGCAGCAGGTGAATTTTACGTAGTCGCGTTGAGAAATACTTT - - -
SEQ1415	GTGGCGGTGTCTCAGCAGCAGGTGAATTTTACGTAGTCGCGTTGAGAAATACTTT - - -
SEQ1416	TTGAATCTCTCA - AACATCGTTTGAGCCTCTATGGATTAACAAAAGATGACTTTCTCGG
SEQ1417	GTGGCGGTGTCTCAGCAGCAGGTGAATTTTACGTAGTCGCGTTGAGAAATACTTT - - -
SEQ1401	ATCGGTATGGGTTCTCCAGGAGCTGTTGATAGAACTAGTAAAAACAGTAACAGGTGCTTT
SEQ1402	ATCGGTATGGGTTCTCCAGGAGCTGTTGATAGAACTAGTAAAAACAGTAACAGGTGCTTT
SEQ1403	ATCGGTATGGGTTCTCCAGGAGCTGTTGATAGAACTAGTAAAAACAGTAACAGGTGCTTT
SEQ1404	ATCGGTATGGGTTCTCCAGGAGCTGTTGATAGAACTAGTAAAAAC - - - - - - - - -
SEQ1405	GTCACATTTGCTTTCCACAAAGTTAAAAAGTCAACTA - - - - - - - - -
SEQ1406	ATCGGTATGGGTTCTCCAGGAGCTG - - - - - - - - -
SEQ1407	ATCGGTATGGGTTCTCCAGGAGCTGTTGATAGAACTAGTAAAAACAGTAACAGGTGCTTT
SEQ1408	GTCACATTTGCTTTCCACA - - - - - - - - -
SEQ1409	ATCGGTATGGGTTCTCCAGGAGCTGTTGATAGAACTAGTAAAAACAGTAACAGGTGCTTT
SEQ1410	GTCACATTTGCTTTCCACAAGTTAAAAAGTCAACTAAAAATTAAGATTGCTGAAGTAGG
SEQ1411	ATCGGTATGGGTTCTCCAGGAGCTGTTGATAGAACTAGTAAAAACAGTAACAGGTGCTTT
SEQ1412	GTCACATTTGCTTTCCACAAGTTAAAAAGTCAACTAAAAATTAAGATTG - - - - -
SEQ1413	ATCGGTATGGGTTCTCCAGGAGCTGTTGATAGAACTAGTAAAAACAGTAACAGGTGCTTT
SEQ1414	ATCACATTTGCTTTCCACAAGTTAAAAAGTCAACTAAAAATTAAGATTG - - - - -
SEQ1415	GTCACATTTGCTTTCCACAAGTTAAAAAGTCAACTAA - - - - -
SEQ1416	ATCGGTATGGGTTCTCCAGGAGCTGTTGATAGAACTAGTAAAAACAGTCACAGGTGCTTT
SEQ1417	GTCACATTTGTTTCCACAAGGT - - - - -

Table 14: Comparative Sequences relating to SAG0471 (glucokinase)

SEQ1401_	AATCTAAATTGGGCTGATACTCAAGAAGTAGGTTCA GTTATTGAAAAAGAAGTTGGAAT
SEQ1402	AATCTAAATTGGGCTGATACTCAAGAAGTAGGTTCA GTTATTGAAAAAGAAGTTGGAAT
SEQ1403	AATCTAAATTGGGCTGATACTCAAGA-----
SEQ1404	-----
SEQ1405	-----
SEQ1406	-----
SEQ1407	AATCTAAATTGGGCTGATACTCAAGAAGTAGGTTCA GTTATTGAAAAAGAAGTTGGAAT
SEQ1408	-----
SEQ1409	AATCTAAATTGGGCTGATACTCAAGAAGTAGGTTCA GTTATTGAAAAAGAAGTTGGAAT
SEQ1410	AATGAT-----
SEQ1411	AATCTAAATTGGGCTGATACTCAAGAAGTAGGTTCA GTTATTGAAAAAGAAGTTGGAAT
SEQ1412	-----
SEQ1413	AATCTAAATTGGGCTGATACTCAAGAAGTAGGTTCA GTTATTGAAAAAGAAGTTGGAAT
SEQ1414	-----
SEQ1415	-----
SEQ1416	AATCTAAATTGGGCTGATACTCAAGAAGTAGGTTCA GTTATTGAAAAAGAAGTTGGAAT
SEQ1417	-----
SEQ1401_	CCATTTTATTGATAACGATGCTAATGTTGCAGCACTTGGTGAACGCTGGGTAGGTGC
SEQ1402	CCATTTTATTGATAACGATGCTAATGTTGCAGCACTTGGTGAACGCTGGGTAGGTGC
SEQ1403	-----
SEQ1404	-----
SEQ1405	-----
SEQ1406	-----
SEQ1407	CCATTTTATTGATAACGATGCTAATGTTGCAGCACTTGGTGAACGCTGGGTAGGTGC
SEQ1408	-----
SEQ1409	CCATTTTATTGATAACGATGCTAATGTTGCAGCACTTGGTGAACGCTGGGTAGGTGC
SEQ1410	-----
SEQ1411	CCATTTTATTGATAACGATGCTAATGTTGCAGCACTTGGTGAACGCTGGGTAGGTGC
SEQ1412	-----
SEQ1413	CCATTTTATTGATAACGATGCTAATGTTGCAGCACTTGGTGAACGCTGGGTAGGTGC
SEQ1414	-----
SEQ1415	-----
SEQ1416	CCATTTTATTG-----
SEQ1417	-----
SEQ1401_	GGTGCCAATAATCCCGACGTTGTTTTCGTAACCCCTCGGAACAGGAGTAGGTGGAGGTGT
SEQ1402	GGTGCCAATAATCCCGATGTTGTTTTCGTAACCCCTCGGAACAGGAGTAGGTGGAGGTGT
SEQ1403	-----
SEQ1404	-----
SEQ1405	-----
SEQ1406	-----
SEQ1407	GGTGCCAATAATCCCGACGTTGTTTTCGTAACC-----
SEQ1408	-----
SEQ1409	GGTGCCAATAATCCCGATGTTGTTTTCGTAACCCCTCGGAACAGGAGTAGGTGGAGGTGT
SEQ1410	-----
SEQ1411	GGTGCCAATAATCCCGATGTTGTTTTCGTAACCCCTCGGAACAGGAGTA-----
SEQ1412	-----
SEQ1413	GGTGCCAATAATCCCGACGTTGTTTTCGTAACCCCTCGGAACAGGAGTAGGTGGAGG---
SEQ1414	-----
SEQ1415	-----
SEQ1416	-----
SEQ1417	-----

Table 14: Comparative Sequences relating to SAG0471 (glucokinase)

SEQ1401	ATCGCAGATGGTAACCTCATCCATGGTGTTCAGGAGCAGGTGGAGAAATTGGGCATAT
SEQ1402	ATCGCAGATGGTAACCTCATCCATGGTGTTCAGGAGCAGGTGGAGAAATTGGGCATAT
SEQ1403	-----
SEQ1404	-----
SEQ1405	-----
SEQ1406	-----
SEQ1407	-----
SEQ1408	-----
SEQ1409	ATCGCAGATGGTAACCTCATCCATGGTGTTCAGGAGCAGGTGGAGAAATTGGGCATAT
SEQ1410	-----
SEQ1411	-----
SEQ1412	-----
SEQ1413	-----
SEQ1414	-----
SEQ1415	-----
SEQ1416	-----
SEQ1417	-----
SEQ1401	ATTGTTGATCCAGAAAAATGGATTACGTGCACATGTGGTAACAAAGGCTGCCTTGAGAC
SEQ1402	ATTGTTGATCCAGAKAATGGATTACGTGCACATGTGGTAACAAAGGCTGTCTTGAGAC
SEQ1403	-----
SEQ1404	-----
SEQ1405	-----
SEQ1406	-----
SEQ1407	-----
SEQ1408	-----
SEQ1409	ATT-----
SEQ1410	-----
SEQ1411	-----
SEQ1412	-----
SEQ1413	-----
SEQ1414	-----
SEQ1415	-----
SEQ1416	-----
SEQ1417	-----
SEQ1401	GTTGCATCAGCGACAGGTGTTGTTAGAGTAGCACGTCAACTCGCAGAACAAATATGAGGG
SEQ1402	GTTGCATCAGCGACAGGTGTTGTTAGAGTAGCACGTCAACTCGCAGAACAAATATGAAGG
SEQ1403	-----
SEQ1404	-----
SEQ1405	-----
SEQ1406	-----
SEQ1407	-----
SEQ1408	-----
SEQ1409	-----
SEQ1410	-----
SEQ1411	-----
SEQ1412	-----
SEQ1413	-----
SEQ1414	-----
SEQ1415	-----
SEQ1416	-----
SEQ1417	-----

Table 14: Comparative Sequences relating to SAG0471 (glucokinase)

SEQ1401	TCGTCTGCCATTAAAGCAGCGATTGACACCGGTGATACTGTTACAAGTAAAGATATTTT
SEQ1402	TCGTCTGCCATTAAAGCAGCGATTGACAACGGTGATACTGTTACAAGTAAAGATATTTT
SEQ1403	-----
SEQ1404	-----
SEQ1405	-----
SEQ1406	-----
SEQ1407	-----
SEQ1408	-----
SEQ1409	-----
SEQ1410	-----
SEQ1411	-----
SEQ1412	-----
SEQ1413	-----
SEQ1414	-----
SEQ1415	-----
SEQ1416	-----
SEQ1417	-----
SEQ1401	ATAGCAGCAGAAGATGGGGATAAATTGCTAATTCGTTGTTGAACGTGTATCACGTTA
SEQ1402	ATAGCAGCAGAAGATGGGGATAAATTGCTAATTCGTTGTTGAACGTGTATCACGTTA
SEQ1403	-----
SEQ1404	-----
SEQ1405	-----
SEQ1406	-----
SEQ1407	-----
SEQ1408	-----
SEQ1409	-----
SEQ1410	-----
SEQ1411	-----
SEQ1412	-----
SEQ1413	-----
SEQ1414	-----
SEQ1415	-----
SEQ1416	-----
SEQ1417	-----
SEQ1401	CTTGGACTGGCAGCAGCTAATATTTCAAATATTTTAAACCTGATTCTGTGGTTATTGG
SEQ1402	CTTGGACTGGCAGCAGCTAATATTTCAAATATTTTAAACCTGATTCTGTGGTTATTGG
SEQ1403	-----
SEQ1404	-----
SEQ1405	-----
SEQ1406	-----
SEQ1407	-----
SEQ1408	-----
SEQ1409	-----
SEQ1410	-----
SEQ1411	-----
SEQ1412	-----
SEQ1413	-----
SEQ1414	-----
SEQ1415	-----
SEQ1416	-----
SEQ1417	-----

Table 14: Comparative Sequences relating to SAG0471 (glucokinase)

SEQ1401	GGCGGTGTCTCAGCAGCAGGTGAATTTTACGTAGTCGCGTTGAGAAATACTTTGTCAC
SEQ1402	GGCGGTGTCTCAGCAGCAGGTGAATTTTACGTAGTCGCGTTGAGAAATACTTTGTCAC
SEQ1403	-----
SEQ1404	-----
SEQ1405	-----
SEQ1406	-----
SEQ1407	-----
SEQ1408	-----
SEQ1409	-----
SEQ1410	-----
SEQ1411	-----
SEQ1412	-----
SEQ1413	-----
SEQ1414	-----
SEQ1415	-----
SEQ1416	-----
SEQ1417	-----
SEQ1401	TTTGCTTTCCCAAGTTAAAAAGTCAACTAAAATTAAGAT
SEQ1402	TTTG-----
SEQ1403	-----
SEQ1404	-----
SEQ1405	-----
SEQ1406	-----
SEQ1407	-----
SEQ1408	-----
SEQ1409	-----
SEQ1410	-----
SEQ1411	-----
SEQ1412	-----
SEQ1413	-----
SEQ1414	-----
SEQ1415	-----
SEQ1416	-----
SEQ1417	-----

Table 15: Comparative Sequences relating to SAG0492

SEQ ID NO. 1501: SAG0492 FROM THE 1169NT1 GBS NONTYPEABLE STRAIN

TGACTTGGATATTCATCAAGGAGAAGTGGTGGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAACATTTTAAAGAACATGAATCTCT
 TGAAGTACCAACAAAGGGAAACAGTGACTTTTGAAGGAATTGATATAACAGACAAAAAATGATATTTTAAATGCGCGAAAAAATG
 GGCATGGTTTTTCAACAGTTCAATCTATTTCCCAATATGACTGTACTAGAAAAATTAATCTTTATCACCTATTAAAGACAAAGGGACTTTC
 TAAGCTTGATGCTCAGACAAAAGCATACGAGCTACTTGAAAAAGTTGGACTCAAAGAGAAGGCTAATGCTTATCCAGCTAGCTTATCTG
 GAGGACAACAACACGGATTGCTATTGCAAGAGGTCTTGCAATGAATCCTGATGTCTTCTTTTGGATGAACCTACTTCAGCTCTTGAT
 CCTGAAATGGTAGGTGAAGTCTTGACTGTTATGCAAGATTTAGCTAAATCTGGTATGACGATGGTTATTGTCACTCATGAAATGGGTTT
 TGCACGTGAAGTAGCGGATCGTGTCTTTTATGGATAGTAGCGATTATCTGTAGCAAGGGACCCCTAAGGAAGTAT

SEQ ID NO. 1502: SAG0492 FROM THE 18RS21 GBS TYPE II STRAIN

TTGGGAAAAATGAGGTTTAAAGGCAATGACTTGGATATTCATCAAGGAGAAGTAGTGGTTATTATTGGCCCTTCTGGCTCTGGTAAG
 TCAACATTTTAAAGACAATGAATCTCTTGAAGTACCAACAAAGGGAAACAGTGACTTTTGAAGGGATTGATATAACAGACAAAAAGAA
 TGATATTTTAAATGCGCGAAAAAATGGGCATGGTTTTTCAACAGTTCAATCTATTTCCCAATATGACTGTACTAGAAAAATTAATCTT
 TATCACTTAAGACAAAGGGGCTTCTAATCTTGATGCTCAGACAAAAGCATATGAGCTACTTGAAAAAGTTGGACTCAAAGAGAAG
 GCTAATACTTATCCAGCTAGCTTATCTGGAGGACAACAACGAATGCTATTGCAAGAGGTCTTGCAATGAATCCTCATGTCTTCT
 TTTTGTATGAACCTACTTCAGCTCTTGATCCTGAAATGGTAGGTGAAGTCTTGACTGTTATGCAAGATTTAGCTAAATCTGGTATGACGA
 TGGTTATTGTCACTCATGAAATGGGTTTGCACGTGAAGTAGCGGATCGTGTCTTTTATGGATGACGAGAAATTTAT

SEQ ID NO. 1503: SAG0492 FROM THE 2603V/R GBS TYPE V STRAIN (REVERSE COMPLEMENT)

AAAAATGAGGTTTAAAGGCAATGACTTGGATATTCATCAAGGAGAAGTAGTGGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAAC
 ATTTTAAAGACAATGAATCTCTTGAAGTACCAACAAAGGGAAACAGTGACTTTTGAAGGGATTGATATAACAGACAAAAAGAAATGATA
 TTTTAAATGCGCGAAAAAATGGGCATGGTTTTTCAACAGTTCAATCTATTTCCCAATATGACTGTACTAGAAAAATTAATCTTATCA
 CCTATTAAAGACAAAGGGGCTTCTAATCTTGATGCTCAGACAAAAGCATATGAGCTACTTGAAAAAGTTGGACTCAAAGAGAAGGCTAA
 TACTTATCCAGCTAGCTTATCTGGAGGACAACAACGAATGCTATTGCAAGAGGTCTTGCAATGAATCCTCATGTCTTCTTTTGT
 ATGAACCTACTTCAGCTCTTGATCCTGAAATGGTAGGTGAAGTCTTGACTGTTATGCAAGATTTAGCTAAATCTGGTATGACGATGGTTATTGT
 ACTGTCACTCATGAAATGGGTTTGCACGTGAAGTAGCGGATCGTGTCTTTTATGGATGACGAGAAATTTATTGTTGAGCAAGGGGCC

SEQ ID NO. 1504: SAG0492 FROM THE M781 GBS TYPE III STRAIN (REVERSE COMPLEMENT)

GAGGTTTAAAGGCAATGACTTGGATATTCATCAAGGAGAAGTAGTGGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAACATTTT
 AAGAACAATGAATCTCTTGAAGTACCAACAAAGGGAAACAGTGACTTTTGAAGGGATTGATATAACAGACAAAAAGAAATGATATTTT
 AAATGCGCGAAAAAATGGGCATGGTTTTTCAACAGTTCAATCTATTTCCCAATATGACTGTACTAGAAAAATTAATCTTATCACCTATT
 AAGACAAAGGGGCTTCTAAGCTTGATGCTCAGACAAAAGCATATGAGCTACTTGAAAAAGTTGGACTCAAAGAGAAGGCTAATGCTTA
 TCCAGCAAGCTTATCTGGAGGACAACAACGAATGCTATTGCAAGAGGTCTTGCAATGAATCCTCATGTCTTCTTTTGTATGAAC
 CTACTTCAGCTCTTGATCCTGAAATGGTAGGTGAAGTCTTGACTGTTATGCAAGATTTAGCTAAATCTGGTATGACGATGGTTATTGT
 ACTCATGAAATGGGTTTGCACGTGAAGTAGCGGATCGTGTCTTTTATGGATGACGAGGATTATTGTTGAGCAAGGGGCCCTAAGAA
 AGTAT

SEQ ID NO. 1505: SAG0492 FROM THE 090 GBS TYPE Ia STRAIN

TGGTGGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAACATTTTAAAGACAATGAATCTCTTGAAGTACCAACAAAGGGAAACAGTG
 ACTTTTGAAGGGATTGATATAACAGACAAAAAGAAATGATATTTTAAATGCGCGAAAAAATGGGCATGGTTTTTCAACAGTTCAATCT
 ATTTCCCAATATGACTGTACTAGAAAAATTAATCTTATCACCTATTAAAGACAAAGGGGACTTCTAAGCTTGATGCTCAGACAAAAGCAT
 ACGAGCTACTTGAAAAAGTTGGACTCAAAGAGAAGGCTAATGCTTATCCAGCTAGCTTATCTGGAGGGCAACAACAACGAATGCTATT
 GCAAGAGGTCTTGCAATGAATCCTCATGTCTCTTCTTTTGTATGAACCTACTTCAGCTCTTGATCCTGAAATGGTAGGTGAAGTCTTGAC
 TGGTTATGCAAGATTTAGCTAAATCTGGTATGACGATGGTTATTGTCACTCATGAAATGGGTTTGCACGTGAAGTAGCGGATCGTGTCA
 TTTTATGGATGACGAGCATTATTGTTgAsCAAGGGACCCCTAAGGAAGTA

SEQ ID NO. 1506: SAG0492 FROM THE A909 GBS TYPE Ia STRAIN

CAATACAAGGACTTCATAAAAGTTTGGGAAAAATGAGGTTTAAAGGCAATGACTTGGATATTCATCAAGGAGAAGTAGTGGTTATT
 ATTGGCCCTTCTGGCTCTGGTAAGTCAACATTTTAAAGACAATGAATCTCTTGAAGTACCAACAAAGGGAAACAGTGACTTTTGAAGG
 GATTGATATAACAGACAAAAAGAAATGATATTTTAAATGCGCGAAAAAATGGGCATGGTTTTTCAACAGTTCAATCTATTTCCCAATA
 TGAATGCTACTAGAAAAATTAATCTTATCACCTATTAAAGACAAAGGGGCTTCTAAGCTTGATGCTCAGACAAAAGCATATGAGCTACTT
 GAAAAAGTTGGACTCAAAGAGAAGGCTAATACTTATCCAGCTAGCTTATCTGGAGGACAACAACAACGAATGCTATTGCAAGAGGTCT
 TGCAATGAATCCTGATGTCTTCTTTTGTATGAACCTACTTCAGCTCTTGATCCTGAAATGGTAGGTGAAGTCTTGACTGTTATGCAAG
 ATTTAGCTAAATCTGGTATGACGATGGTTATTGTCACTCATGAAATGGGTTTGCACGTGAAGTAGCGGATCGTGTCTTTTATGGAT
 GCAGGAATTATTGTgAGCAAGGGGCCCTAAGGAAGTATTGAGCAGACAAAAAGAAATCCGCACAAGAGATTCTT

SEQ ID NO. 1507: SAG0492 FROM THE CJB110 GBS NONTYPEABLE STRAIN (REVERSE COMPLEMENT)

GACTTGGATATTCATCAAGGAGAAGTGGTGGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAACATTTTAAAGACAATGAATCTCT
 GGAAGTACCAACAAAGGGAAACAGTGACTTTTGAAGGGATTGATATAACAGACAAAAAGAAATGATATTTTAAATGCGCGAAAAAATGG
 GCATGGTTTTTCAACAGTTCAATCTATTTCCCAATATGACTGTACTAGAAAAATTAATCTTTATCACCTATTAAAGACAAAGGGGACTTTCT
 AAGCTTGATGCTCAGACAAAAGCATACGAGCTACTTGAAAAAGTTGGACTCAAAGAGAAGGCTAATGCTTATCCAGCTAGCTTATCTGG
 AGGACAACAACAACGAATGCTATTGCAAGAGGTCTTGCAATGAATCCTCATGTCTTCTTTTGTATGAACCTACTTCAGCTCTTGATC
 CTGAAATGGTAGGTGAAGTCTTGACTGTTATGCAAGATTTAGCTAAATCTGGTATGACGATGGTTATTGTCACTCATGAAATGGGTTT
 GCACGTGAAGTAGCGGATCGTGTCTTTTATGGATGCGGGAATTATTGTGAGCAAGGGGAC

Table 15: Comparative Sequences relating to SAG0492**SEQ ID NO. 1508: SAG0492 FROM THE H36b GBS TYPE Ib STRAIN**

ATGAGGTTTTAAAAGGCATTGACTTGGATATTCATCAAGGAGAAGTAGTGGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAACATTTT
 TTAAGAACAATGAATCTCTTGGGAAGTACCAACAAAGGGGAACAGTGACTTTTGAAGGGATTGATATAACAGACAAAAAGAATGATATTTT
 TAAATGCGCGAAAAAATGGGCATGGTTTTTCAACAGTTCAATCTATTTCCCAATATGACTGTACTAGAAAAATTACTTTTATCACCTA
 TTAAGACAAAGGGGCTTTCTAAGCTTGATGCTCAGACAAAAGCATATGAGCTACTTGAAAAAGTTGGACTCAAAGAGAAGGCTAATACT
 TATCCAGCTAGCTTATCTGGAGGACAACAACAACGAATTGCTATTGCAAGAGGTCTTGCAATGAATCCTGATGTCCTTCTTTTGTATGA
 ACCTACTTCAGCTCTTGATCCTGAAATGGTAGGTGAAGTCTTGACTGTTATGCAAGATTTAGCTAAATCTGGTATGACGATGGTTATTG
 TCATCATGAAATGGGTTTTGCACGTGAAGTAGCGGATCGTGTCATTTTTATGGATGCASGAATTATGTTTGAGCAAGGGGCCCTAAG
 GAAGTAT

SEQ ID NO. 1509: SAG0492 FROM THE JM9130013 GBS TYPE VIII STRAIN (REVERSE COMPLEMENT)

GGTTTTAAAAGGCATTGACTTGGATATTCATCAAGGAGAAGTAGTGGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAACATTTTAA
 GAACAATGAATCTCTTGGGAAGTACCAACAAAGGGGAACAGTGACTTTTGAAGGGATTGATATAACAGACAAAAAGAATGATATTTTAA
 ATGCGCGAAAAAATGGGCATGGTTTTTCAACAGTTCAATCTATTTCCCAATATGACTGTACTAGAAAAATTACTTTTATCACCTATTAA
 GACAAAGGGGCTTTCTAAGCTTGATGCTCAGACAAAAGCATATGAGCTACTTGAAAAAGTTGGACTCAAAGAGAAGGCTAATACTTATC
 CAGCTAGCTTATCTGGAGGACAACAACAACGAATTGCTATTGCAAGAGGTCTTGCAATGAATCCTGATGTCCTTCTTTTGTATGAACCT
 ACTTCAGCTCTTGATCCTGAAATGGTAGGTGAAGTCTTGACTGTTATGCAAGATTTAGCTAAATCTGGTATGACGATGGTTATTGTAC
 TCATGAAATGGGTTTTGCACGTGAAGTAGCGGATCGTGTCATTTTTATGGATGCAGGAATTATGTTTGAGCAAGGGGCCCTAAGGAAG
 TATTTAGCAAAACAAAAGAAAT

SEQ ID NO. 1510: SAG0492 FROM THE M732 GBS TYPE III STRAIN

GGTGGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAACATTTTAAAGAACAATGAATCTCTTGGGAAGTACCAACAAAGGGGAACAGTGA
 CTTTTGAAGGATTGATATAACAGACAAAAAGAATGATATTTTAAATGCGCGAAAAAATGGGCATGGTTTTTCAACAGTTCAATCTA
 TTTCCCAATATGACTGTACTAGAAAAATTACTTTTATCACCTATTAAAGACAAAGGGACTTTCTAAGCTTGATGCTCAGACAAAAGCATA
 CGAGCTACTTGAAAAAGTTGGACTCAAAGAGAAGGCTAATGCTTATCCAGCAAGCTTATCTGG

SEQ ID NO. 1511: SAG0492 FROM THE COH1 GBS TYPE Ia STRAIN

ATTGACTTGGATATTCATCAAGGAGAAGTGGTGGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAACATTTTAAAGAACAATGAATCT
 CTTGGAAGTACCAACAAAGGGGAACAGTGACTTTTGAAGGGATTGATATAACAGACAAAAAGAATGATATTTTAAATGCGCGAAAAA
 TGGGCATGGTTTTTCAACAGTTCAATCTATTTCCCAATATGACTGTACTAGAAAAATTACTTTTATCACCTATTAAAGACAAAGGGACTT
 TCTAAGCTTGATGCTCAGACAAAAGCATACGAGCTACTTGAAAAAGTTGGACTCAAAGAGAAGGCTAATGCTTATCCAGCAAGCTTATC
 TGG

Table 15: Comparative Sequences relating to SAG0492

SEQ1501	-----TGACTTGG
SEQ1502	-----TTGGGAAAAATGAGGTTTAAAAGGCATTGACTTGG
SEQ1503	-----AAAAATGAGGTTTAAAAGGCATTGACTTGG
SEQ1504	-----GAGGTTTAAAAGGCATTGACTTGG
SEQ1505	-----
SEQ1506	AATACAAGGACTTCATAAAAGTTTTGGGAAAAATGAGGTTTAAAAGGCATTGACTTGG
SEQ1507	-----GACTTGG
SEQ1508	-----ATGAGGTTTAAAAGGCATTGACTTGG
SEQ1509	-----GGTTTAAAAGGCATTGACTTGG
SEQ1510	-----
SEQ1511	-----ATTGACTTGG
SEQ1501	TATTCATCAAGGAGAAGTGGTGGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAACAT
SEQ1502	TATTCATCAAGGAGAAGTAGTGGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAACAT
SEQ1503	TATTCATCAAGGAGAAGTAGTGGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAACAT
SEQ1504	TATTCATCAAGGAGAAGTGGTGGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAACAT
SEQ1505	-----TGGTGGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAACAT
SEQ1506	TATTCATCAAGGAGAAGTAGTGGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAACAT
SEQ1507	TATTCATCAAGGAGAAGTGGTGGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAACAT
SEQ1508	TATTCATCAAGGAGAAGTAGTGGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAACAT
SEQ1509	TATTCATCAAGGAGAAGTAGTGGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAACAT
SEQ1510	-----GGTGGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAACAT
SEQ1511	TATTCATCAAGGAGAAGTGGTGGTTATTATTGGCCCTTCTGGCTCTGGTAAGTCAACAT
SEQ1501	TTTTAAGAACAATGAATCTCTTGAAGTACCAACAAAGGGAACAGTGACTTTTGAAGGAA
SEQ1502	TTTTAAGAACAATGAATCTCTTGAAGTACCAACAAAGGGAACAGTGACTTTTGAAGGGA
SEQ1503	TTTTAAGAACAATGAATCTCTTGAAGTACCAACAAAGGGAACAGTGACTTTTGAAGGGA
SEQ1504	TTTTAAGAACAATGAATCTCTTGAAGTACCAACAAAGGGAACAGTGACTTTTGAAGGGA
SEQ1505	TTTTAAGAACAATGAATCTCTTGAAGTACCAACAAAGGGAACAGTGACTTTTGAAGGGA
SEQ1506	TTTTAAGAACAATGAATCTCTTGAAGTACCAACAAAGGGAACAGTGACTTTTGAAGGGA
SEQ1507	TTTTAAGAACAATGAATCTCTTGAAGTACCAACAAAGGGAACAGTGACTTTTGAAGGGA
SEQ1508	TTTTAAGAACAATGAATCTCTTGAAGTACCAACAAAGGGAACAGTGACTTTTGAAGGGA
SEQ1509	TTTTAAGAACAATGAATCTCTTGAAGTACCAACAAAGGGAACAGTGACTTTTGAAGGGA
SEQ1510	TTTTAAGAACAATGAATCTCTTGAAGTACCAACAAAGGGAACAGTGACTTTTGAAGGGA
SEQ1511	TTTTAAGAACAATGAATCTCTTGAAGTACCAACAAAGGGAACAGTGACTTTTGAAGGGA
SEQ1501	TTGATATAACAGACAAAAAATGATATTTTAAAATGCGCGAAAAAATGGGCATGGTTT
SEQ1502	TTGATATAACAGACAAAAAAGATGATATTTTAAAATGCGCGAAAAAATGGGCATGGTTT
SEQ1503	TTGATATAACAGACAAAAAAGATGATATTTTAAAATGCGCGAAAAAATGGGCATGGTTT
SEQ1504	TTGATATAACAGACAAAAAAGATGATATTTTAAAATGCGCGAAAAAATGGGCATGGTTT
SEQ1505	TTGATATAACAGACAAAAAAGATGATATTTTAAAATGCGCGAAAAAATGGGCATGGTTT
SEQ1506	TTGATATAACAGACAAAAAAGATGATATTTTAAAATGCGCGAAAAAATGGGCATGGTTT
SEQ1507	TTGATATAACAGACAAAAAAGATGATATTTTAAAATGCGCGAAAAAATGGGCATGGTTT
SEQ1508	TTGATATAACAGACAAAAAAGATGATATTTTAAAATGCGCGAAAAAATGGGCATGGTTT
SEQ1509	TTGATATAACAGACAAAAAAGATGATATTTTAAAATGCGCGAAAAAATGGGCATGGTTT
SEQ1510	TTGATATAACAGACAAAAAAGATGATATTTTAAAATGCGCGAAAAAATGGGCATGGTTT
SEQ1511	TTGATATAACAGACAAAAAAGATGATATTTTAAAATGCGCGAAAAAATGGGCATGGTTT
SEQ1501	TTCAACAGTTCATCTATTTCCCAATATGACTGTACTAGAAAATATTACTTTATCACCTA
SEQ1502	TTCAACAGTTCATCTATTTCCCAATATGACTGTACTAGAAAATATTACTTTATCACCTA
SEQ1503	TTCAACAGTTCATCTATTTCCCAATATGACTGTACTAGAAAATATTACTTTATCACCTA
SEQ1504	TTCAACAGTTCATCTATTTCCCAATATGACTGTACTAGAAAATATTACTTTATCACCTA
SEQ1505	TTCAACAGTTCATCTATTTCCCAATATGACTGTACTAGAAAATATTACTTTATCACCTA
SEQ1506	TTCAACAGTTCATCTATTTCCCAATATGACTGTACTAGAAAATATTACTTTATCACCTA
SEQ1507	TTCAACAGTTCATCTATTTCCCAATATGACTGTACTAGAAAATATTACTTTATCACCTA
SEQ1508	TTCAACAGTTCATCTATTTCCCAATATGACTGTACTAGAAAATATTACTTTATCACCTA
SEQ1509	TTCAACAGTTCATCTATTTCCCAATATGACTGTACTAGAAAATATTACTTTATCACCTA
SEQ1510	TTCAACAGTTCATCTATTTCCCAATATGACTGTACTAGAAAATATTACTTTATCACCTA
SEQ1511	TTCAACAGTTCATCTATTTCCCAATATGACTGTACTAGAAAATATTACTTTATCACCTA

Table 15: Comparative Sequences relating to SAG0492

SEQ1501	TTAAGACAAAGGGACTTTCTAAGCTTGATGCTCAGACAAAAGCATACGAGCTACTTGAAA
SEQ1502	TTAAGACAAAGGGGCTTTCTAATCTTGATGCTCAGACAAAAGCATATGAGCTACTTGAAA
SEQ1503	TTAAGACAAAGGGGCTTTCTAATCTTGATGCTCAGACAAAAGCATATGAGCTACTTGAAA
SEQ1504	TTAAGACAAAGGGACTTTCTAAGCTTGATGCTCAGACAAAAGCATACGAGCTACTTGAAA
SEQ1505	TTAAGACAAAGGGGACTTTCTAAGCTTGATGCTCAGACAAAAGCATACGAGCTACTTGAAA
SEQ1506	TTAAGACAAAGGGGCTTTCTAAGCTTGATGCTCAGACAAAAGCATATGAGCTACTTGAAA
SEQ1507	TTAAGACAAAGGGGACTTTCTAAGCTTGATGCTCAGACAAAAGCATACGAGCTACTTGAAA
SEQ1508	TTAAGACAAAGGGGCTTTCTAAGCTTGATGCTCAGACAAAAGCATATGAGCTACTTGAAA
SEQ1509	TTAAGACAAAGGGGCTTTCTAAGCTTGATGCTCAGACAAAAGCATATGAGCTACTTGAAA
SEQ1510	TTAAGACAAAGGGACTTTCTAAGCTTGATGCTCAGACAAAAGCATACGAGCTACTTGAAA
SEQ1511	TTAAGACAAAGGGACTTTCTAAGCTTGATGCTCAGACAAAAGCATACGAGCTACTTGAAA
SEQ1501	AAGTTGGACTCAAAGAGAAGGCTAATGCTTATCCAGCTAGCTTATCTGGAGGACAACAAC
SEQ1502	AAGTTGGACTCAAAGAGAAGGCTAATACTTATCCAGCTAGCTTATCTGGAGGACAACAAC
SEQ1503	AAGTTGGACTCAAAGAGAAGGCTAATACTTATCCAGCTAGCTTATCTGGAGGACAACAAC
SEQ1504	AAGTTGGACTCAAAGAGAAGGCTAATGCTTATCCAGCAAGCTTATCTGGAGGACAACAAC
SEQ1505	AAGTTGGACTCAAAGAGAAGGCTAATGCTTATCCAGCTAGCTTATCTGGAGGGACAACAAC
SEQ1506	AAGTTGGACTCAAAGAGAAGGCTAATACTTATCCAGCTAGCTTATCTGGAGGACAACAAC
SEQ1507	AAGTTGGACTCAAAGAGAAGGCTAATGCTTATCCAGCTAGCTTATCTGGAGGACAACAAC
SEQ1508	AAGTTGGACTCAAAGAGAAGGCTAATACTTATCCAGCTAGCTTATCTGGAGGACAACAAC
SEQ1509	AAGTTGGACTCAAAGAGAAGGCTAATACTTATCCAGCTAGCTTATCTGGAGGACAACAAC
SEQ1510	AAGTTGGACTCAAAGAGAAGGCTAATGCTTATCCAGCAAGCTTATCTGG-----
SEQ1511	AAGTTGGACTCAAAGAGAAGGCTAATGCTTATCCAGCAAGCTTATCTGGTABCMARATVS
SEQ1501	ACGGATTGCTATTGCAAGAGGCTTGCAATGAATCCTGATGTCCTTCTTTTTGATGAAC
SEQ1502	ACGAATTGCTATTGCAAGAGGCTTGCAATGAATCCTCATGTCTTCTTTTTGATGAAC
SEQ1503	ACGAATTGCTATTGCAAGAGGCTTGCAATGAATCCTGATGTCCTTCTTTTTGATGAAC
SEQ1504	ACGGATTGCTATTGCAAGAGGCTTGCAATGAATCCTGATGTCCTTCTTTTTGATGAAC
SEQ1505	ACGAATTGCTATTGCAAGAGGCTTGCAATGAATCCTGATGTCCTTCTTTTTGATGAAC
SEQ1506	ACGAATTGCTATTGCAAGAGGCTTGCAATGAATCCTGATGTCCTTCTTTTTGATGAAC
SEQ1507	ACGAATTGCTATTGCAAGAGGCTTGCAATGAATCCTGATGTCCTTCTTTTTGATGAAC
SEQ1508	ACGAATTGCTATTGCAAGAGGCTTGCAATGAATCCTGATGTCCTTCTTTTTGATGAAC
SEQ1509	ACGAATTGCTATTGCAAGAGGCTTGCAATGAATCCTGATGTCCTTCTTTTTGATGAAC
SEQ1510	-----
SEQ1511	NCSRATNGTSAG-----
SEQ1501	TACTTCAGCTCTTGATCCTGAAATGGTAGGTGAAGTCTTGACTGTTATGCAAGATTTAG
SEQ1502	TACTTCAGCTCTTGATCCTGAAATGGTAGGTGAAGTCTTGACTGTTATGCAAGATTTAG
SEQ1503	TACTTCAGCTCTTGATCCTGAAATGGTAGGTGAAGTCTTGACTGTTATGCAAGATTTAG
SEQ1504	TACTTCAGCTCTTGATCCTGAAATGGTAGGTGAAGTCTTGACTGTTATGCAAGATTTAG
SEQ1505	TACTTCAGCTCTTGATCCTGAAATGGTAGGTGAAGTCTTGACTGTTATGCAAGATTTAG
SEQ1506	TACTTCAGCTCTTGATCCTGAAATGGTAGGTGAAGTCTTGACTGTTATGCAAGATTTAG
SEQ1507	TACTTCAGCTCTTGATCCTGAAATGGTAGGTGAAGTCTTGACTGTTATGCAAGATTTAG
SEQ1508	TACTTCAGCTCTTGATCCTGAAATGGTAGGTGAAGTCTTGACTGTTATGCAAGATTTAG
SEQ1509	TACTTCAGCTCTTGATCCTGAAATGGTAGGTGAAGTCTTGACTGTTATGCAAGATTTAG
SEQ1510	-----
SEQ1511	-----
SEQ1501	TAAATCTGGTATGACGATGGTTATTGTCACTCATGAAATGGGTTTTGCACGTGAAGTAG
SEQ1502	TAAATCTGGTATGACGATGGTTATTGTCACTCATGAAATGGGTTTTGCACGTGAAGTAG
SEQ1503	TAAATCTGGTATGACGATGGTTATTGTCACTCATGAAATGGGTTTTGCACGTGAAGTAG
SEQ1504	TAAATCTGGTATGACGATGGTTATTGTCACTCATGAAATGGGTTTTGCACGTGAAGTAG
SEQ1505	TAAATCTGGTATGACGATGGTTATTGTCACTCATGAAATGGGTTTTGCACGTGAAGTAG
SEQ1506	TAAATCTGGTATGACGATGGTTATTGTCACTCATGAAATGGGTTTTGCACGTGAAGTAG
SEQ1507	TAAATCTGGTATGACGATGGTTATTGTCACTCATGAAATGGGTTTTGCACGTGAAGTAG
SEQ1508	TAAATCTGGTATGACGATGGTTATTGTCACTCATGAAATGGGTTTTGCACGTGAAGTAG
SEQ1509	TAAATCTGGTATGACGATGGTTATTGTCACTCATGAAATGGGTTTTGCACGTGAAGTAG
SEQ1510	-----
SEQ1511	-----

Table 15: Comparative Sequences relating to SAG0492

SEQ1501	GGATCGTGTCAATTTTATGGATGCAGGCATTATTGT-GAGCAAGGGACCCCTAAGGAAG
SEQ1502	GGATCGTGTCAATTTTATGGACGCAGAAATTAT-----
SEQ1503	GGATCGTGTCAATTTTATGGATGCAGGAATTATTGTTGAGCAAGGGGCC-----
SEQ1504	GGATCGTGTCAATTTTATGGATGCAGGGATTATTGTTGAGCAAGGGACCCCTAAGAAAG
SEQ1505	GGATCGTGTCAATTTTATGGATGCAGGCATTATTGTTGASCAAGGGACCCCTAAGGAAG
SEQ1506	GGATCGTGTCAATTTTATGGATGCAGGAATTATTGTGAGCAAGGGGCCCTAAGGAAGT
SEQ1507	GGATCGTGTCTCTTTTATGGATGCGGGAATTATTGT-GAGCAAGGGACC-----
SEQ1508	GGATCGTGTCAATTTTATGGATGCASGAATTATTGTTGAGCAAGGGGCCCTAAGGAAG
SEQ1509	GGATCGTGTCAATTTTATGGATGCAGGAATTATTGTTGAGCAAGGGGCCCTAAGGAAG
SEQ1510	-----
SEQ1511	-----
SEQ1501	AT-----
SEQ1502	-----
SEQ1503	-----
SEQ1504	AT-----
SEQ1505	A-----
SEQ1506	TTTGAGCAGACAAAAGAAATCCGCACAAGAGATTCTT
SEQ1507	-----
SEQ1508	AT-----
SEQ1509	ATTTAGCAAAACAAAAGAAAT-----
SEQ1510	-----
SEQ1511	-----

Table 16: Comparative Sequences relating to SAG0767 (D-alanine – D-alanine ligase)**SEQ ID NO. 1601: SAG0767 FROM THE M781 GBS TYPE III STRAIN**

TGGTCGCTCTGTCGGAACGTGAAGTATCTGTACTGTCTGCAGAAAGCGTCATGCGTGTCTATTAATTATGATAAAATTTTTT
 GTTAAAGCTTATTTTATCAGCAAGTAGGTCAATTTATTAACACAAAGATTTGATGAAATGCCATCTTCAGATGAAAA
 GTTAATGACAAACCAACTGTTGATTTAGACAAAATGGTTCGTCGAAGTGATATCTATGATGATAATGCAATTGTTTCC
 CCGTTTACATGGACCAATGGGGGAAGATGGTTCATCCAAGGATTTTATAGAAGTTTAAGGATGCCTTATGTTGGGACT
 AATATTCTATCTTCAAGCGTGGCTATGGATAAAATTACAACAAAACAAGTCCTTGCAACAGTAGGTGTACCTCAGGTGTC
 ATATCAAACCTTATTTTGAGGGTGATGATTTGGAACATGCGATTAAACTCTCTTTAGAACTTTAAGTTTCCCAATTTTG
 TAAACCGGCTAATATGGGGTCATCAGTAGGTATTTCAAAGCGACAGATGAATCCTCACTTCGCTCTGCAATTGACTTA
 GCTCTCAAGTATGATAGCCGATTTTGAATTGAACAAGCGTGACAGCTCGTGAAATGAAGTAGGTATTTTAGGCAATAA
 TGATGTTAAGACAACCTTTCTGGCGAAGTTGTTAAAGACGTCGATTCTATGACTATGACGCCAAATATATTGATAATA
 AAATTACTATGGATATTCAGCTAAAGTTGATGAAGCAACTATGGAAGCAATGCGTCAATATGCAAGTAAAGCTTTTAA
 GCAATCGGGCTTGTGGTTTATCAGCTGTGATTTCTTTTGACGAAAGATGGACAAATCTTCTTAAACGAACGAATAC
 AATGCCCGGTTTTACTCAGTGGTCAATGTATCCTCTGCTTTGGGAAAATATGGGGCTAACTTATAGTGATTGATTG

SEQ ID NO. 1602: SAG0767 FROM THE 090 GBS TYPE Ia STRAIN

AAACCGGCATTGTATTAGTTCGTTTAAAGAGACTTGTCCATCTTTCGTCAAAAAGAAATCACAGCGTGATAAACACACA
 AGCCCCGATTGCTTTAAAGCTTTACTTGCATATTGACGCATTGCTTCCATAGTTGCTTCATCACTTTAGCTGGAATAT
 CCATAGTAATTTTATTATCAATATATTGGCGTCATAGTCATAGAAATCGACGCTTTAAGCACTTCGCCAGGAAAAGTT
 GTCTTAACATCATTATTGCTTAAATACCTACTTCAATTTACAGAGCTGTACGCGCTTGTTCATCAAAATACGGCTATC
 ATACTTGAGAGCTAAGTCAATksCAGAGCGAAGTGAGGATTATCTGTGCTTTTGAAATACCTACTGATGACCCCATAT
 TAGCCGCTTTTACAAAAATTTGGGAACTTAAAGTTCTTAAAGAGAGTTAATCGCATGTTCCAAATCATCACCCCTCAAAA
 TAAGTTTGATATGCAACCTGAGGTACCTACTGTTGCAAGGACTTGTGTTGTAATTTTATCCATAGCCACGCTTGA
 AGATAGAAATATTAGTCCCAACATAAGGCATCCTTAAACTTCTAAAAATCCTTGGATAGAACCATCTTCCCCCATTGGTC
 CATGTAAACGGGGAAAACAATTGCATTATCATCATAGATATCACTTGGACGAACCATTTTGTCTAAATCAACAGTTTGG
 TTTGTCTATTAACCTTTTCTATCTGAAGATGGCATTTCATCAAATCTTGTGTTTTAATAAATTGACCTACTTGCCTG

SEQ ID NO. 1603: SAG0767 FROM THE COH1 TYPE Ia STRAIN

TCGCTCTGCGGAACGTGAAGTATCTGTACTGTCTGCAGAAAGCGTCATGCGTGTCTATTAATTATGATAAAATTTTTGTTA
 AAATTTATTTTATCAGCAAGTAGGTCAATTTATTAACACAAAGATTTGATGAAATGCCATCTTCAGATGAAAAGTTA
 ATGACAAACCAAACTGTTGATTTAGACAAAATGGTTCGTCGAAGTGATATCTATGATGATAATGCAATGTTTTCCCGT
 TTTACATGGACCAATGGGGGAAGATGGTTCATCCAAGGATTTTTAGAAAGTTTTAAGGATGCCTTATGTTGGGACTAATA
 TTCTATCTTCAAGCGTGGCTAT

SEQ ID NO. 1604: SAG0767 FROM THE CJB110 GBS NONTYPEABLE STRAIN (REVERSE COMPLEMENT)

CGTCGATTTCTATGACTATGACGCCAAATATATTGATAATAAAATTACTATGGATATTTCCAGCTAAAGTTGATGAAGCAA
 CTATGGAAGCAATGCGTCAATATGCAAGTAAAGCTTTTAAAGCAATCGGGGCTTGTGGTTTATCAGCTGTGATTTCTTT
 TTGACGAAAGATGGACAAATCTTCTTAAACGAACGAATACATGCC

SEQ ID NO. 1605: SAG0767 FROM THE CJB110 GBS NONTYPEABLE STRAIN

AACGTGAAGTATCTGTACTGCTCTGCAGAAAAGCGTCATGCGTGTCTATTAATTATGATAAAATTTTTGTTAAACTTATT
 TTATCAGCAAGTAGGTCAATTTATTAACACAAAGATTTGATGAAATGCCATCTTCAGATGAAAA

SEQ ID NO. 1606: SAG0767 FROM THE 1169NT1 GBS TYPE V STRAIN (REVERSE COMPLEMENT)

CTAATATGGGGTCATCAGTAGGTATTTCAAAGCGACAGATGAATCCTCACTTCGCTCTGCAATTGACTTAGCTCTCAAG
 TATGATAGCCGATTTTGAATTGAACAAGGCGTGACAGCTCGTGAAATTGAAGTAGGTATTTTAGGCAATAATGATGTTAA
 GACAACTTTCTGCGCAAGTCGTTAAAGACGTCGATTCTATGACTATGACGCCAAATATATTGATAATAAAATTACTA
 TGGATATTCCAGCTAAAGTTGATGAAGCAACTATGGAAGCAATGCGTCAATATGCAAGTAAAGCTTTTAAAGCAATCGGG
 GCTTGTGGTTTATCAGCTGTGATTTCTTTTGACGAAAGATGGACAAATCTTCTTAAACGAACGAATACAATGCCCGG
 TTTTACTCAGTGGTCAATGTATCCTCTGCTTTGGGAAAAT

SEQ ID NO. 1607: SAG0767 FROM THE 18RS21 GBS TYPE II STRAIN (REVERSE COMPLEMENT)

TTGACTTAGCTCTCAAGTATGATAGCCGATTTTGAATTGAACAAGGCGTGACAGCTCGTGAAATTGAAGTAGGTATTTTA
 GGCAATAATGATGTTAAGACAACCTTTCTGCGCAAGTCGTTAAAGACGTCGATTTCTATGACTATGACGCCAAATATAT
 TGATAATAAAATTACTATGGATATTTCCAGCTAAAGTTGATGAAGCAACTATGGAAGCAATGCGTCAATATGCAAGTAAAG
 CTTTTAAAGCAATCGGGGCTTGTGGTTTATCAGCTGTGATTTCTTTTGACGAAAGATGGACAAATCTTCTTAAACGA
 CTGAATACAATGCCCGGTTTTACTCAGTGGTCAATGTATCCCCTGCTTTGGGAAAAGTATGGGGCTAACCTT

SEQ ID NO. 1608: SAG0767 FROM THE 18RS21 GBS TYPE II STRAIN

ATCTGTACTGTCTGCAGAAAAGCGTCATGCGTGTCTATTAATTATGATAAAATTTTTGTTAAACTTATTTTATCAGCAA
 GTAGGTCAATTTATTAACACAAAGATTTGATGAAATGCCATCTTCAGATGAAAAGTTAATGACAAACCAAACTGTTGA
 TTTAGACAAAATGGTTCGTCGAAGTGATATCTATGATGATAATGCAATGTTTTCCCGTTTTACATGGACCAATGGGGG
 AAGATGGTTCATCCAAGGATTTTATAGAAGTTTAAAGGATGCCTTATGTTGGGACTAATATTCTATCTTCAA

Table 16: Comparative Sequences relating to SAG0767 (D-alanine – D-alanine ligase)

SEQ ID NO. 1609: SAG0767 FROM THE 2603V/R GBS TYPE V STRAIN (REVERSE COMPLEMENT)
 GGCTATGGATAAAATTACAACAAAACAGTCCTTGCAACAGTAGGTGTACCTCAGGTTGCATATCAAACCTATTTTGGAGG
 GTGATGATTTGGAAACATGCGATTAACTCTCTTTAGAACTTTAAGTTTCCCAATTTTGTAAAACCGGCTAATATGGGG
 TCATCAGTAGGTATTTCAAAGCGACAGATGAATCCTCACTTCGCTCTGCAATTGACTTAGCTCTCAAGTATGATAGCCG
 TATTTTGATGGAACAAGGCGTGACAGCTCGTGAAATTGAAGTAGGTATTTAGGCAATAATGATGTTAAGACAACCTTTTC
 CTGGCGAAGTCGTTAAAGACGTCGATTCTATGACTATGACGCCAAATATATTGATAATAAAATTACTATGGATATTCCA
 GCTAAAGTTGATGAAGCAACTATGGAAGCAATGCGTCAATATGCAAGTAAAGCTTTTAAAGCAATCGGGGCTTGTGGTTT
 ATCAGCTGTGATTTCTTTTGTACGAAAGAATGGACAAATCTTCTTAAACGAACTGAAATAC

SEQ ID NO. 1610: SAG0767 FROM THE 2603V/R GBS TYPE V STRAIN
 TCTGTACTGTCTGCAGAAAGCGTCATGCGTGCTATTAATTATGATAAAATTTTGTAAAACTTATTTTATCACGCAAGT
 AGGTCAATTTATTAACACAAAGAATTTGATGAAATGCCATCTTCAGATGAAAAGTTAATGACAAACCAAACCTGTTGATT
 TAGACAAAATGGTTTCGTCCAAGTGATATCTATGATGATAAT

SEQ ID NO. 1611: SAG0767 FROM THE H36b GBS TYPE Ib STRAIN (REVERSE COMPLEMENT)
 AAAACCGGCTAATATGGGGTCATCAGTAGGTATTTCAAAGCGACAGATGAATCCTCACTTCGCTCTGCAATTGACTTAG
 CTCTCAAGTATGATAGCCGATTTTGGATTGAACAAGGCGTGACAGCTCGTGAAATTGAAGTAGGTATTTAGGCAATAAT
 GATGTTAAGACAACCTTTCTGGCGAAGTCGTTAAAGACGTCGATTTCTATGACTATGACGCCAAATATATTGATAATAA
 AATTACTATGATATTTCCAGCTAAAGTTGATGAAGCAACTATGGAAGCAATGCGTCAATATGCAAGTAAAGCTTTTAAAG
 CAATCGGGGCTTGTGGTTTATCACGCTGTGATTTCTTTTGCAGAAAGATGGACAAATCTTCTTAAACGAACTGAATACA
 ATGCCCGGTTTACTCAGTGGTCAATGTATCCCCTGCTTTGGGAAAATATGGGGCTAACTTATAG

SEQ ID NO. 1612: SAG0767 FROM THE H36b TYPE Ib STRAIN
 CGTGAAGTATCTGTACTGTCTGCAGAAAGCGTCATGCGTGCTATTAATTATGATAAAATTTTGTAAAACTTATTTTAT
 CACGCAAGTAGGTCAATTTATTAACACAAAGAATTTGATGAAATGCCATCTTCAGATGAAAAGTTAATGACAAACAAA
 CTGTTGATTTAGACAAAATGGTTTCGTCCAAGTGATATCTATGATGATAATGCAATTGTTTCCCCGTTTACATGGACCA
 ATGGGGGAAGATGGTTCTATCCAAGGATTTTGAAGTTTAAAGGATGCCTTATGTTGGGACTAATATTCTATCTTCAAG
 CGTGGCTATGATAAAATTACAACAAAACAGTCCTTGCAACAGTAG

SEQ ID NO. 1613: SAG0767 FROM THE M732 GBS TYPE III STRAIN (REVERSE COMPLEMENT)
 ATGCGATTAACTCTCTTTAGAACCTTTAAGTTTCCCAATTTTGTAAAACCGGCTAATATGGGGTCATCAGTAGGTATT
 TCAAAGCGACAGATGAATCCTCACTTCGCTCTGCAATTGACTTAGCTCTCAAGTATGATAGCCGATTTTGGATTGAACA
 AGGCGTGACAGCTCGTGAAATTGAAGTAGGTATTTAGGCAATAATGATGTTAAGACAACCTTTCTGGCGAAGTTGTTA
 AAGACGTCGATTCTATGACTATGACGCCAAATATATTGATAATAAAATTACTATGGATATCCAGCTAAAGTTGATGAA
 GCAACTATGGAAAGCAATGCGTCAATATGCAAGTAAAGCTTTTAAAGCAATCGGGGCTTGTGGTTTATCACGCTGTGATTT
 CTTTTTGACGAAAGATGGACAAATCTTCTTAAACGAACTGAATACAATGCCCGTTTTACTCAGTGGTCAATGTATCCTC
 TGCTTTGGGAAAATATGGGGCTAACTT

SEQ ID NO. 1614: SAG0767 FROM THE M732 GBS TYPE III STRAIN
 GTCATGCCGTGCTATTAATTATGATAAAATTTTGTAAAACTTATTTTATCACGCAAGTAGGTCAATTTATTAACAC
 AAGAATTTGATGAAATGCCATCTTCAGATGAAAAGTTAATGACAAACCAAACCTGTTGATTAGACAAAATGGTTTCGTCCA
 AGTGATATCTATGATGATAATGCAATTGTTTCCCCGTTTACATGGACCAATGGGGGAAGATGGTTCTATCCAAGGATT
 TTTAGAAGTTTAAAGATGCCTTATGTTGGGACTAATATTCTATCTTCAAGCGTGGCTATGGATAAAATTACAACAAAAC
 AAGTCCTTGCAACAGTAGGTGTACCTCAG

SEQ ID NO. 1615: SAG0767 FROM THE A909 GBS TYPE Ia STRAIN (REVERSE COMPLEMENT)
 TTTTGAGGGTGATGATTTGGAACATGCGATTAACTCTCTTTAGAACTTTAAGTTTCCCAATTTTGTAAAACCGGCTA
 ATATGGGGTCATCAGTAGGTATTTCAAAGCGACAGATGAATCCTCACTTCGCTCTGCAATTGACTTAGCTCTCAAGTAT
 GATAGCCGATTTTGGATTGAACAAGGCGTGACAGCTCGTGAAATTGAAGTAGGTATTTAGGCAATAATGATGTTAAGAC
 AACTTTTCTGGCGAAGTCGTTAAAGACGTCGATTTCTATGACTATGACGCCAAATATATTGATAATAAAATTACTATGG
 ATATTCCAGCTAAAGTTGATGAAGCAACTATGGAAGCAATGCGTCAATATGCAAGTAAAGCTTTTAAAGCAATCGGGGCT
 TGTGGTTTATCACGCTGTGATTTCTTTTGCAGAAAGATGGACAAATCTTCTTAAACGAACTGAATACAATGCCCGGTTT
 TACTCAGTGGTCAATGTATCCCCTGCTTTGGGAAAATATGGGGCTAACTTATAGTGA

SEQ ID NO. 1616: SAG0767 FROM THE A909 GBS TYPE Ia STRAIN
 TGGTCGCTCTGCGGAACGTGAAGTATCTGTACTGTCTGCAGAAAGCGTCATGCGTGCTATTAATTATGATAAAATTTTGT
 TTAAACCTATTTTATCACGCAAGTAGGTCAATTTATTAACACAAAGAATTTGATGAAATGCCATCTTCAGATGAAAAG
 TTAATGACAAACCAAACCTGTTGATTAGACAAAATGGTTTCGTCCAAGTGATATCTATGATGATAATGCAATTGTTTCCC
 CGTTTTACATGGACCAATGGGGGAAGATGGTTCTATCCAAGGATTTTGAAGTTTAAAGGATGCCTTATGTTGGGACTA
 ATATTCTATCTTCAAGCGTGGCTATGGATAAAATTACAACAAAACAAAGTCCTTGCAACAGTAGG

Table 16: Comparative Sequences relating to SAG0767 (D-alanine – D-alanine ligase)

SEQ ID NO. 1617: SAG0767 FROM THE JM9130013 GBS TYPE VIII STRAIN (REVERSE COMPLEMENT)
 AAGCAGGGGATACATTGACCACTGAGTAAAACCGGCATTGTATTTCAGTTCGTTTAAGAAGATCTGTCCATCTTTTCGTCA
 AAAAGAAATCACAGCGTGATAAACCAAGCCCGATTGCTTTAAAGCTTTACTTGATATTGACGCATTGCTTCCATA
 .GATGCTTCATCAACTTTAGCTGGAATATCCATAGCAATTTTATTATCAATATATTTGGCG

SEQ1601	GGTCGCTCTGTCTCGGAACGTGAAGTATCTGTACTGTCTGCAGAAAGCGTCATGCGTGCTA
SEQ1602	-----
SEQ1603	-----
SEQ1604	-----
SEQ1605	-----
SEQ1606	-----
SEQ1607	-----
SEQ1608	-----
SEQ1609	-----
SEQ1610	-----
SEQ1611	-----
SEQ1612	-----
SEQ1613	-----
SEQ1614	-----
SEQ1615	-----
SEQ1616	-----
SEQ1617	-----

SEQ1601	TAATTATGATAAAATTTTTGTTAAACTTATTTTATCACGCAAGTAGGTCAATTTATTA
SEQ1602	-----
SEQ1603	-----
SEQ1604	-----
SEQ1605	-----
SEQ1606	-----
SEQ1607	-----
SEQ1608	-----
SEQ1609	-----
SEQ1610	-----
SEQ1611	-----
SEQ1612	-----
SEQ1613	-----
SEQ1614	-----
SEQ1615	-----
SEQ1616	-----
SEQ1617	-----

SEQ1601	AACACAAGAATTTGATGAAATGCCATCTTCAGATGAAAAGTTAATGACAAACCAAACTG
SEQ1602	-----
SEQ1603	-----
SEQ1604	-----
SEQ1605	-----
SEQ1606	-----
SEQ1607	-----
SEQ1608	-----
SEQ1609	-----
SEQ1610	-----
SEQ1611	-----
SEQ1612	-----
SEQ1613	-----
SEQ1614	-----
SEQ1615	-----
SEQ1616	-----
SEQ1617	-----

Table 16: Comparative Sequences relating to SAG0767 (D-alanine – D-alanine ligase)

SEQ1601	TGATTTAGACAAAATGGTTCGTTCCAAGTGATATCTATGATGATAATGCAATTGTTTTCC
SEQ1602	-----
SEQ1603	-----
SEQ1604	-----
SEQ1605	-----
SEQ1606	-----
SEQ1607	-----
SEQ1608	-----
SEQ1609	-----
SEQ1610	-----
SEQ1611	-----
SEQ1612	-----
SEQ1613	-----
SEQ1614	-----
SEQ1615	-----
SEQ1616	-----
SEQ1617	-----
SEQ1601	CGTTTTACATGGACCAATGGGGGAAGATGGTTCTATCCAAGGATTTTTAGAAAGTTTTAA
SEQ1602	-----
SEQ1603	-----
SEQ1604	-----
SEQ1605	-----
SEQ1606	-----
SEQ1607	-----
SEQ1608	-----
SEQ1609	-----
SEQ1610	-----
SEQ1611	-----
SEQ1612	-----
SEQ1613	-----
SEQ1614	-----
SEQ1615	-----
SEQ1616	-----
SEQ1617	-----
SEQ1601	GATGCCTTATGTTGGGACTAATATTCTATCTTCAAGCGTGGCTATGGATAAAATTACAA
SEQ1602	-----
SEQ1603	-----
SEQ1604	-----
SEQ1605	-----
SEQ1606	-----
SEQ1607	-----
SEQ1608	-----
SEQ1609	-----GGCTATGGATAAAATTACAA
SEQ1610	-----
SEQ1611	-----
SEQ1612	-----
SEQ1613	-----
SEQ1614	-----
SEQ1615	-----
SEQ1616	-----
SEQ1617	-----

Table 16: Comparative Sequences relating to SAG0767 (D-alanine – D-alanine ligase)

SEQ1601	AAAAACAAGTCCTTGCAACAGTAGGTGTACCTCAGGTTGCATATCAAACCTATTTTGAGG
SEQ1602	-----
SEQ1603	-----
SEQ1604	-----
SEQ1605	-----
SEQ1606	-----
SEQ1607	-----
SEQ1608	-----
SEQ1609	AAAAACAAGTCCTTGCAACAGTAGGTGTACCTCAGGTTGCATATCAAACCTATTTTGAGG
SEQ1610	-----
SEQ1611	-----
SEQ1612	-----
SEQ1613	-----
SEQ1614	-----
SEQ1615	-----TTTTGAGG
SEQ1616	-----
SEQ1617	-----
SEQ1601	TGATGATTTGGAACATGCGATTAAACTCTCTTTAGAACTTTAAGTTTCCCAATTTTTG
SEQ1602	-----
SEQ1603	-----
SEQ1604	-----
SEQ1605	-----
SEQ1606	-----
SEQ1607	-----
SEQ1608	-----
SEQ1609	TGATGATTTGGAACATGCGATTAAACTCTCTTTAGAACTTTAAGTTTCCCAATTTTTG
SEQ1610	-----
SEQ1611	-----
SEQ1612	-----
SEQ1613	-----ATGCGATTAAACTCTCTTTAGAACCTTTAAGTTTCCCAATTTTTG
SEQ1614	-----
SEQ1615	TGATGATTTGGAACATGCGATTAAACTCTCTTTAGAACTTTAAGTTTCCCAATTTTTG
SEQ1616	-----
SEQ1617	-----
SEQ1601	AAAACCGGCTAATATGGGGTCATCAGTAGGTATTTCAAAGCGACAGATGAATCCTCAC
SEQ1602	-----AAACCGGGC
SEQ1603	-----TCGCTCTGCGGAACGTGAAGTATCTGTACTG-TCTGCAGAAA-GCGT
SEQ1604	-----
SEQ1605	-----AACGTGAAGTATCTGTACTGCTCTGCAGAAAAGCGT
SEQ1606	-----CTAATATGGGGTCATCAGTAGGTATTTCAAAGCGACAGATGAATCCTCAC
SEQ1607	-----
SEQ1608	-----ATCTGTACTG-TCTGCAGAAAAGCGT
SEQ1609	AAAACCGGCTAATATGGGGTCATCAGTAGGTATTTCAAAGCGACAGATGAATCCTCAC
SEQ1610	-----TCTGTACTG-TCTGCAGAAA-GCGT
SEQ1611	AAAACCGGCTAATATGGGGTCATCAGTAGGTATTTCAAAGCGACAGATGAATCCTCAC
SEQ1612	-----CGTGAAGTATCTGTACTG-TCTGCAGAAA-GCGT
SEQ1613	AAAACCGGCTAATATGGGGTCATCAGTAGGTATTTCAAAGCGACAGATGAATCCTCAC
SEQ1614	-----GT
SEQ1615	AAAACCGGCTAATATGGGGTCATCAGTAGGTATTTCAAAGCGACAGATGAATCCTCAC
SEQ1616	-----TGGTCGCTCTGCGGAACGTGAAGTATCTGTACTG-TCTGCAGAAA-GCGT
SEQ1617	-----AAGCAGGGGATACATTGACCACTGAGTAAACCGGGC
SEQ1601	TCGCTCTGCAATTGACTTAGCTCTCAAGTATGATAGCCGTATTTTGATTGAACAAGGCG
SEQ1602	TTGT-ATTCAAGTTCGTTTAAGAAGACTTGTCATCTTTCGTCAAAAAGAAATCACAGCG
SEQ1603	ATGC-GTGCTATTAATTATGATAAATTTTTGTTAAACTTATTTTATCACGCAAGTAG
SEQ1604	-----
SEQ1605	ATGC-GTGCTATTAATTATGATAAATTTTTGTTAAACTTATTTTATCACGCAAGTAG
SEQ1606	TCGCTCTGCAATTGACTTAGCTCTCAAGTATGATAGCCGTATTTTGATTGAACAAGGCG
SEQ1607	-----TTGACTTAGCTCTCAAGTATGATAGCCGTATTTTGATTGAACAAGGCG
SEQ1608	ATGC-GTGCTATTAATTATGATAAATTTTTGTTAAACTTATTTTATCACGCAAGTAG
SEQ1609	TCGCTCTGCAATTGACTTAGCTCTCAAGTATGATAGCCGTATTTTGATTGAACAAGGCG

Table 16: Comparative Sequences relating to SAG0767 (D-alanine – D-alanine ligase)

SEQ1610	ATGC-GTGTCTATTAATTATGATAAAATTTTGTGTTAAACTTATTTTATCACGCAAGTAG
SEQ1611	TCGCTCTGCAATTGACTTAGCTCTCAAGTATGATAGCCGTATTTTGATTGAACAAGGCG
SEQ1612	ATGC-GTGTCTATTAATTATGATAAAATTTTGTGTTAAACTTATTTTATCACGCAAGTAG
SEQ1613	TCGCTCTGCAATTGACTTAGCTCTCAAGTATGATAGCCGTATTTTGATTGAACAAGGCG
SEQ1614	ATGCCGTGCTATTAATTATGATAAAATTTTGTGTTAAACTTATTTTATCACGCAAGTAG
SEQ1615	TCGCTCTGCAATTGACTTAGCTCTCAAGTATGATAGCCGTATTTTGATTGAACAAGGCG
SEQ1616	ATGC-GTGTCTATTAATTATGATAAAATTTTGTGTTAAACTTATTTTATCACGCAAGTAG
SEQ1617	TTGT-ATTCAGTTTCGTTTAAAGAAGATCTGTCCATCTTTCGTCAAAAAGAAATCACAGCG
SEQ1601	GACAGCTCGTGAAATTGAAGTAGGTATTTTAGGCAATAATGATGTTAAGACAACCTTTTC
SEQ1602	GATAAACCAACAAGC---CCCGATTGCTTTAAAAGCTTTACTTGCATATTGACGCATTG
SEQ1603	GTCAATTTATTAAA---ACACAAGAATTTGATGAAATGCCATCTTCAGATGAAAAGTTA
SEQ1604	-----
SEQ1605	GTCAATTTATTAAA---ACACAAGAATTTGATGAAATGCCATCTTCAGATGAAA---
SEQ1606	GACAGCTCGTGAAATTGAAGTAGGTATTTTAGGCAATAATGATGTTAAGACAACCTTTTC
SEQ1607	GACAGCTCGTGAAATTGAAGTAGGTATTTTAGGCAATAATGATGTTAAGACAACCTTTTC
SEQ1608	GTCAATTTATTAAA---ACACAAGAATTTGATGAAATGCCATCTTCAGATGAAAAGTTA
SEQ1609	GACAGCTCGTGAAATTGAAGTAGGTATTTTAGGCAATAATGATGTTAAGACAACCTTTTC
SEQ1610	GTCAATTTATTAAA---ACACAAGAATTTGATGAAATGCCATCTTCAGATGAAAAGTTA
SEQ1611	GACAGCTCGTGAAATTGAAGTAGGTATTTTAGGCAATAATGATGTTAAGACAACCTTTTC
SEQ1612	GTCAATTTATTAAA---ACACAAGAATTTGATGAAATGCCATCTTCAGATGAAAAGTTA
SEQ1613	GACAGCTCGTGAAATTGAAGTAGGTATTTTAGGCAATAATGATGTTAAGACAACCTTTTC
SEQ1614	GTCAATTTATTAAA---ACACAAGAATTTGATGAAATGCCATCTTCAGATGAAAAGTTA
SEQ1615	GACAGCTCGTGAAATTGAAGTAGGTATTTTAGGCAATAATGATGTTAAGACAACCTTTTC
SEQ1616	GTCAATTTATTAAA---ACACAAGAATTTGATGAAATGCCATCTTCAGATGAAAAGTTA
SEQ1617	GATAAACCAACAAGC---CCCGATTGCTTTAAAAGCTTTACTTGCATATTGACGCATTG
SEQ1601	TGGCGAAGTTGTTAAAGACGTCGATTTCTATGA--CTATGACGCCAAAT-ATATTGATA
SEQ1602	TTCCATAGTT---GCTTCATCAACTTTAGCTGGAATATCCATAGTAATTTTATTATCA
SEQ1603	TGACAAACC---AACTGTTGATTTAGACAAAATGGTTCGTCCAAGTGATATCTATG
SEQ1604	-----CGTCGATTTCTATGA--CTATGACGCCAAAT-ATATTGATA
SEQ1605	-----
SEQ1606	TGGCGAAGTCGTTAAAGACGTCGATTTCTATGA--CTATGACGCCAAAT-ATATTGATA
SEQ1607	TGGCGAAGTCGTTAAAGACGTCGATTTCTATGA--CTATGACGCCAAAT-ATATTGATA
SEQ1608	TGACAAACC---AACTGTTGATTTAGACAAAATGGTTCGTCCAAGTGATATCTATG
SEQ1609	TGGCGAAGTCGTTAAAGACGTCGATTTCTATGA--CTATGACGCCAAAT-ATATTGATA
SEQ1610	TGACAAACC---AACTGTTGATTTAGACAAAATGGTTCGTCCAAGTGATATCTATG
SEQ1611	TGGCGAAGTCGTTAAAGACGTCGATTTCTATGA--CTATGACGCCAAAT-ATATTGATA
SEQ1612	TGACAAACC---AACTGTTGATTTAGACAAAATGGTTCGTCCAAGTGATATCTATG
SEQ1613	TGGCGAAGTTGTTAAAGACGTCGATTTCTATGA--CTATGACGCCAAAT-ATATTGATA
SEQ1614	TGACAAACC---AACTGTTGATTTAGACAAAATGGTTCGTCCAAGTGATATCTATG
SEQ1615	TGGCGAAGTCGTTAAAGACGTCGATTTCTATGA--CTATGACGCCAAAT-ATATTGATA
SEQ1616	TGACAAACC---AACTGTTGATTTAGACAAAATGGTTCGTCCAAGTGATATCTATG
SEQ1617	TTCCATAGAT---GCTTCATCAACTTTAGCTGGAATATCCATAGCAATTTTATTATCA
SEQ1601	TAAAATTACTAT--GGATATTCAGCTAAAGTTGATGAAGCAACTATGGAAGCAATGCG
SEQ1602	TATATTTGGCGTCATAGTCATAGAAATCGACGCTCTTAAACGACTTCGCCAGG--AAAAG
SEQ1603	TGATAATGCAAT--TGTTTTCCCGTTTTTAC---ATGGACCAATGGGGGAAG--ATGGT
SEQ1604	TAAAATTACTAT--GGATATTCAGCTAAAGTTGATGAAGCAACTATGGAAGCAATGCG
SEQ1605	-----
SEQ1606	TAAAATTACTAT--GGATATTCAGCTAAAGTTGATGAAGCAACTATGGAAGCAATGCG
SEQ1607	TAAAATTACTAT--GGATATTCAGCTAAAGTTGATGAAGCAACTATGGAAGCAATGCG
SEQ1608	TGATAATGCAAT--TGTTTTCCCGTTTTTAC---ATGGACCAATGGGGGAAG--ATGGT
SEQ1609	TAAAATTACTAT--GGATATTCAGCTAAAGTTGATGAAGCAACTATGGAAGCAATGCG
SEQ1610	TGATAAT--
SEQ1611	TAAAATTACTAT--GGATATTCAGCTAAAGTTGATGAAGCAACTATGGAAGCAATGCG
SEQ1612	TGATAATGCAAT--TGTTTTCCCGTTTTTAC---ATGGACCAATGGGGGAAG--ATGGT
SEQ1613	TAAAATTACTAT--GGATATTCAGCTAAAGTTGATGAAGCAACTATGGAAGCAATGCG
SEQ1614	TGATAATGCAAT--TGTTTTCCCGTTTTTAC---ATGGACCAATGGGGGAAG--ATGGT
SEQ1615	TAAAATTACTAT--GGATATTCAGCTAAAGTTGATGAAGCAACTATGGAAGCAATGCG
SEQ1616	TGATAATGCAAT--TGTTTTCCCGTTTTTAC---ATGGACCAATGGGGGAAG--ATGGT
SEQ1617	TATATTTGGCGT---ABLECMPARATIVESEQUENCESRELA-TINGTSAGD--ALANI

Table 16: Comparative Sequences relating to SAG0767 (D-alanine – D-alanine ligase)

SEQ1601	CAATATGCAAGTAAAGCTTTTAAAGCAATCGGGGCTTGTGGTTTATCACGCTGTGATTT
SEQ1602	T--GTCCTAACATCATTATTGCCTAAAATACCTACTTCAATTTACAGAGCTGTACAGCC
SEQ1603	C--TATCCAAG--GATTTT TAGAAGTTTAAAGGATGCCTTATGTTGGGACTAATATTCT
SEQ1604	CAATATGCAAGTAAAGCTTTTAAAGCAATCGGGGCTTGTGGTTTATCACGCTGTGATTT
SEQ1605	-----
SEQ1606	CAATATGCAAGTAAAGCTTTTAAAGCAATCGGGGCTTGTGGTTTATCACGCTGTGATTT
SEQ1607	CAATATGCAAGTAAAGCTTTTAAAGCAATCGGGGCTTGTGGTTTATCACGCTGTGATTT
SEQ1608	C--TATCCAAG--GATTTT TAGAAGTTTAAAGGATGCCTTATGTTGGGACTAATATTCT
SEQ1609	CAATATGCAAGTAAAGCTTTTAAAGCAATCGGGGCTTGTGGTTTATCACGCTGTGATTT
SEQ1610	-----
SEQ1611	CAATATGCAAGTAAAGCTTTTAAAGCAATCGGGGCTTGTGGTTTATCACGCTGTGATTT
SEQ1612	C--TATCCAAG--GATTTT TAGAAGTTTAAAGGATGCCTTATGTTGGGACTAATATTCT
SEQ1613	CAATATGCAAGTAAAGCTTTTAAAGCAATCGGGGCTTGTGGTTTATCACGCTGTGATTT
SEQ1614	C--TATCCAAG--GATTTT TAGAAGTTTAAAGGATGCCTTATGTTGGGACTAATATTCT
SEQ1615	CAATATGCAAGTAAAGCTTTTAAAGCAATCGGGGCTTGTGGTTTATCACGCTGTGATTT
SEQ1616	C--TATCCAAG--GATTTT TAGAAGTTTAAAGGATGCCTTATGTTGGGACTAATATTCT
SEQ1617	E--DALANINELIGASE-----
SEQ1601	TTTTTGACGAAAGA--TGGACAAATCTTCTTAAACGAACTGAA-TACAATGCCCGGTTT
SEQ1602	TGTTCAATCAAAATACGGCTATCATACTGAGAGCTAAGTCAATKSCAGAGCGAAGTGA
SEQ1603	TCTTCAAGCGTGGCTAT-----
SEQ1604	TTTTTGACGAAAGA--TGGACAAATCTTCTTAAACGAACTGAA-TACAATGCC-----
SEQ1605	-----
SEQ1606	TTTTTGACGAAAGA--TGGACAAATCTTCTTAAACGAACTGAA-TACAATGCCCGGTTT
SEQ1607	TTTTTGACGAAAGA--TGGACAAATCTTCTTAAACGAACTGAA-TACAATGCCCGGTTT
SEQ1608	TCTTCAA-----
SEQ1609	TTTTTGACGAAAGAA-TGGACAAATCTTCTTAAACGAACTGAAATAC-----
SEQ1610	-----
SEQ1611	TTTTTGACGAAAGA--TGGACAAATCTTCTTAAACGAACTGAA-TACAATGCCCGGTTT
SEQ1612	TCTTCAAGCGTGGCTATGGATAAAATTACAACAAAACAAGTCCTTGCAACAGTAG----
SEQ1613	TTTTTGACGAAAGA--TGGACAAATCTTCTTAAACGAACTGAA-TACAATGCCCGGTTT
SEQ1614	TCTTCAAGCGTGGCTATGGATAAAATTACAACAAAACAAGTCCTTGCAACAGTAGGTGT
SEQ1615	TTTTTGACGAAAGA--TGGACAAATCTTCTTAAACGAACTGAA-TACAATGCCCGGTTT
SEQ1616	TCTTCAAGCGTGGCTATGGATAAAATTACAACAAAACAAGTCCTTGCAACAGTAGG----
SEQ1617	-----
SEQ1601	ACTCAGTGGTCAATGTATCCTCTGCTTTGGGAAAA-TATGGGGCTAACTTATAGTGATT
SEQ1602	GATTATCTGTGCGCTTTTGAAATACCTACTGATGACCCCATATTAGCCGGTTTACAAA
SEQ1603	-----
SEQ1604	-----
SEQ1605	-----
SEQ1606	ACTCAGTGGTCAATGTATCCTCTGCTTTGGGAAAA-T-----
SEQ1607	ACTCAGTGGTCAATGTATCCCTGCTTTGGGAAAAGTATGGGGCTAACCTT-----
SEQ1608	-----
SEQ1609	-----
SEQ1610	-----
SEQ1611	ACTCAGTGGTCAATGTATCCCTGCTTTGGGAAAA-TATGGGGCTAACTTATAG-----
SEQ1612	-----
SEQ1613	ACTCAGTGGTCAATGTATCCTCTGCTTTGGGAAAA-TATGGGGCTAACTT-----
SEQ1614	CCTCAGG-----
SEQ1615	ACTCAGTGGTCAATGTATCCCTGCTTTGGGAAAA-TATGGGGCTAACTTATAGTGA--
SEQ1616	-----
SEQ1617	-----

Table 16: Comparative Sequences relating to SAG0767 (D-alanine – D-alanine ligase)

SEQ1601	GATTG-----
SEQ1602	ATTGGGAAACTTAAAGTTTCTAAAGAGAGTTTAATCGCATGTTCCAAATCATCACCTC
SEQ1603	-----
SEQ1604	-----
SEQ1605	-----
SEQ1606	-----
SEQ1607	-----
SEQ1608	-----
SEQ1609	-----
SEQ1610	-----
SEQ1611	-----
SEQ1612	-----
SEQ1613	-----
SEQ1614	-----
SEQ1615	-----
SEQ1616	-----
SEQ1617	-----
SEQ1601	-----
SEQ1602	AAATAAGTTTGATATGCAACCTGAGGTACACCTACTGTTGCAAGGACTTGTTTTGTTGT
SEQ1603	-----
SEQ1604	-----
SEQ1605	-----
SEQ1606	-----
SEQ1607	-----
SEQ1608	-----
SEQ1609	-----
SEQ1610	-----
SEQ1611	-----
SEQ1612	-----
SEQ1613	-----
SEQ1614	-----
SEQ1615	-----
SEQ1616	-----
SEQ1617	-----
SEQ1601	-----
SEQ1602	ATTTTATCCATAGCCACGCTTGAAGATAGAATATTAGTCCCAACATAAGGCATCCTTAA
SEQ1603	-----
SEQ1604	-----
SEQ1605	-----
SEQ1606	-----
SEQ1607	-----
SEQ1608	-----
SEQ1609	-----
SEQ1610	-----
SEQ1611	-----
SEQ1612	-----
SEQ1613	-----
SEQ1614	-----
SEQ1615	-----
SEQ1616	-----
SEQ1617	-----

Table 16: Comparative Sequences relating to SAG0767 (D-alanine – D-alanine ligase)

SEQ1601	-----
SEQ1602	ACTTCTAAAAATCCTTGGATAGAACCATCTTCCCCATTGGTCCATGTAAACGGGGAA
SEQ1603	-----
SEQ1604	-----
SEQ1605	-----
SEQ1606	-----
SEQ1607	-----
SEQ1608	-----
SEQ1609	-----
SEQ1610	-----
SEQ1611	-----
SEQ1612	-----
SEQ1613	-----
SEQ1614	-----
SEQ1615	-----
SEQ1616	-----
SEQ1617	-----
SEQ1601	-----
SEQ1602	ACAATTGCATTATCATCATAGATATCACTTGGACGAACCATTTGTCTAAATCAACAGT
SEQ1603	-----
SEQ1604	-----
SEQ1605	-----
SEQ1606	-----
SEQ1607	-----
SEQ1608	-----
SEQ1609	-----
SEQ1610	-----
SEQ1611	-----
SEQ1612	-----
SEQ1613	-----
SEQ1614	-----
SEQ1615	-----
SEQ1616	-----
SEQ1617	-----
SEQ1601	-----
SEQ1602	TGGTTTGTCATTAACTTTTCATCTGAAGATGGCATTCATCAAATCTTGTGTTTAAAT
SEQ1603	-----
SEQ1604	-----
SEQ1605	-----
SEQ1606	-----
SEQ1607	-----
SEQ1608	-----
SEQ1609	-----
SEQ1610	-----
SEQ1611	-----
SEQ1612	-----
SEQ1613	-----
SEQ1614	-----
SEQ1615	-----
SEQ1616	-----
SEQ1617	-----

Table 16: Comparative Sequences relating to SAG0767 (D-alanine – D-alanine ligase)

SEQ1601	-----
SEQ1602	AATTGACCTACTTGCGTG
SEQ1603	-----
SEQ1604	-----
SEQ1605	-----
SEQ1606	-----
SEQ1607	-----
SEQ1608	-----
SEQ1609	-----
SEQ1610	-----
SEQ1611	-----
SEQ1612	-----
SEQ1613	-----
SEQ1614	-----
SEQ1615	-----
SEQ1616	-----
SEQ1617	-----

Table 17: Comparative Sequences relating to SAG1086 (xanthine phosphoribosyltransferase)

SEQ ID NO. 1701: SAG1086 FROM THE1169NT1 GBS NONTYPEABLE STRAIN
 TTTAAAGGTTGATTCCTTTTGAATCATCAGGTAGATTTTGAGTTAATGCAGGAAATAGGTAAAGTTTTGCTGATAAATATAAAGAAG
 CCGGCATTACGAAGGTTGTTACGATTGAAGCATCTGGAATTGCGCCAGCAGTGTACGCAGCTCAAGCATTGGGCGTACCAATGATATTT
 GCTAAAAAGGCTAAGAACATTACTATGACTGAAGGTATCTTAACCTGCTGAAGTGTATTTCTTTACAAAGCAAGWTACGAGTCAAGTTTC
 TATTGTGAGTCGCTTTTATCTAACGATGATACTGTACTCATCATTGATGACTTTTGTAGCAAACGGTCAAGCGGCTAAAGGATTACTTG
 AAATTATTGGTCAAGCTGGAGCTAAGGTTGCTGGTATCGGAATCGTTATTGAAAAATCTTTCCAAGATGGGCGTGATTTGTTAGAAAAA
 ACAGGTGTTCCAGT

SEQ ID NO. 1702: SAG0767 FROM THE 18RS21 GBS TYPE II STRAIN
 TTTAGGTGAGAACATTTTAAAGGTTGATTCCTTTTGAATCATCAGGTAGATTTTGAGTTAATGCAGGAAATAGGTAAAGTTTTGCTG
 ATAAATATAAAGAAGCCGGCATTACGAAGGTTGTTACGATTGAAGCATCTGGAATTGCACCAGCAGTGTACGCAGCTCAAGCATTGGGC
 GKACCAATGATATTTGCTAAAAAGCTAAGAACATTACTATGACTGAAGGTATCTTAACCTGCTGAAGTGTATTTCTTTACAAAGCAAGT
 TACGAGTCAAGTTTCTATTGTGAGTCGCTTTTATCTAACGATGATACTGTACTCATCATTGATGACTTTTGTAGCAAACGGTCAAGCGG
 CTAAGGATTACTTGAATATTATTGGTCAAGCTGGAGCTAAGGTTGCTGGTATCGGAATCGTTATTGAAAAATCTTTCCAAGATGGGCGT
 GATTGTTAGAAAAACA

SEQ ID NO. 1703: SAG0767 FROM THE H36b1 GBS TYPE Ib STRAIN
 AAGAACGTATTTCTTAAAGATGGTGATGTTTAAAGTGAGAACATTTTAAAGTTGATTCCTTTTGAATCATCAGGTAGATTTTGAGTTA
 ATGCAGGAAATAGGTAAAGTTTTGCTGATAAATATAAAGAAGCCGGCATTACGAAGGTTGTTACAAATGAAGCATCTGGAATTGCGCC
 AGCAGTGTACGCAGCTCAAGCATTGGGCGTACCAATGATATTTGCTAAAAAGCTAAGAACATTACTATGACTGAAGGTATCTTAACCT
 CTGAAGTGTATTTCTTTACAAAGCAAGTTACGAGTCAAGTTTCTATTGTGAGTCGCTTTTATCTAACGATGATACTGTACTCATCATT
 GATGACTTTTGTAGCAAACGGTCAAGCGGCTAAGGATTACTTGAATATTATTGGTCAAGCTGGAGCTAAGGTTGCTGGTATCGGAATCTY
 TATTGAAAAATCTTTCCAAGATGGGCGTGATT

SEQ ID NO. 1704: SAG0767 FROM THE M732 GBS TYPE III STRAIN
 ATTCCTTTTGAATCATCAGGTAAATTTGAGTTAATGCAGGAAATAGGTAAAGTTTTGCTGATAAATATAAAGAAGCCGGCATTACGA
 AGGTTTGTACAAATTTGAAGCATCTGGAATTGCGCCAGCAGTGTACGCAGCTCAAGCATTGGGCGTACCAATGATATTTGTAAAAAGCT
 AAGAACATTACTATGACTGAAGGTATCTTAACCTGCTGAAGTGTATTTCTTTACAAAGCAAGTTACGAGTCAAGTTTCTATTGTGAGTCG
 CTTTTATCTAACGATGATACTGTACTCATCATTGATGACTTTTGTAGCAAACGGTCAAGCGGCTAAGGATTACTTGAATATTATTGGT
 AAGCTGAAGCTAAGGTTGCTGGTATCGGAATCGTTATTGAAAAATCTTTCCAAGATGGGCGTGATTTGTTAGAAAAACAGGTGTTCCG
 GTTACTTCTCTGCTCGT

SEQ ID NO. 1705: SAG0767 FROM THE M781 GBS TYPE III STRAIN (REVERSE COMPLEMENT)
 GAACGTATTTCTTAAAGATGGTGATGTTTAAAGTGAGAACATTTTAAAGTTGATTCCTTTTGAATCATCAGGTAAATTTGAGTTAAT
 GCAGGAAATAGGTAAAGTTTTGCTGATAAATATAAAGAAGCCGGCATTACGAAGGTTGTTACAAATGAAGCATCTGGAATTGCGCCAG
 CAGTGTACGCAGCTCAAGCATTGGGCGTACCAATGATATTTGCTAAAAAGCTAAGAACATTACTATGACTGAAGGTATRTTAACTGCT
 GAAGTGTATTTCTTTACAAAGCAAGTTACGAGTCAAGTTTCTATTGTGAGTCGCTTTTATCTAACGATGATACTGTACTCATCATTGA
 TGACTTTTAAACAAACGGTCAAGC

SEQ ID NO. 1706: SAG0767 FROM THE 090 GBS TYPE Ia STRAIN (REVERSE COMPLEMENT)
 ACATTTTAAAGTTGATTCCTTTTGAATCATCAGGTAGATTTTGAGTTAATGCAGGAAATAGGTAAAGTTTTGCTGATAAATATAA
 GAAGCCGGCATTACGAAGGTTGTTACGATTGAAGCATCTGGAATTGCGCCAGCAGTGTACGCAGCTCAAGCATTGGGCGTACCAATGAT
 ATTTGCTAAAAAGCTAAGAACATTACTATGACTGAAGGTATCTTAACCTGCTGAAGTGTATTTCTTTACAAAGCAAGTTACGAGTCAAG
 TTTCTATTGTGAGTCGCTTTTATCTAACGATGATACTGTACTCATCATTGATGACTTTTGTAGCAAACMGTCYAGCGGCTAAGGATT
 CTTGAATATTATTGGTCAAGCTGGAGCTAAGGTTGCTGGTATCGGAATCGTTATTGAAAAATCTTTCCAAGATGGGCGTGATTTGTTAG
 AAA

SEQ ID NO. 1707: SAG0767 FROM THE A909 GBS TYPE Ia STRAIN (REVERSE COMPLEMENT)
 ACGTATTTCTTAAAGATGGTGATGTTTAAAGTGAGAACATTTTAAAGTTGATTCCTTTTGAATCATCAGGTAGATTTTGAGTTAATGC
 AGGAAATAGGTAAAGTTTTGCTGATAAATATAAAGAAGCCGGCATTACGAAGGTTGTTACAAATGAAGCATCTGGAATTGCGCCAGCA
 GTGTACGCAGCTCAAGCATTGGGCGTACCAATGATATTTGCTAAAAAGCTAAGAACATTACTATGACTGAAGGTATCTTAACCTGCTGA
 AGTGTATTTCTTTACAAAGCAAGTTACGAGTCAAGTTTCTATTGTGAGTCGCTTTTATCTAACGATGATACTGTACTCATCATTGATG
 ACTTTTGTAGCAAACGGKCAAGCGGSTAAGGATTACTTGAAATATTGGTCAAGCTGGAGCTA

SEQ ID NO. 1708: SAG0767 FROM THE COH1 GBS TYPE Ia STRAIN
 TTTAAAGTTGATTCCTTTTGAATCATCAGGTAAATTTGAGTTAATGCAGGAAATAGGTAAAGTTTTGCTGATAAATATAAAGAAG
 CCGGCATTACGAAGGTTGTTACAAATGAAGCATCTGGAATTGCGCCAGCAGTGTACGCAGCTCAAGCATTGGGCGTACCAATGATATTT
 GCTAAAAAGCTAAGAACATTACTATGACTGAAGGTATCTTAACCTGCTGAAGTGTATTTCTTTACAAAGCAAGTTACGAGTCAAGTTTC
 TATTGTGAGTCGCTTTTATCTAACGATGATACTGTACTCATCATTGATGACTTTTGTAGCAAACGGTCAAGCGGCTAAGGATTACTTG
 AAATTATTGGTCAAGCTGAAGCTAAGGTTGCTGGTATCGGAATCGTTATTGAAAAATCTTTCCAAGATGGGCGTGATTTGTTAGAAAAA
 ACAGGTGTTCCGGTTAC

SEQ ID NO. 1709: SAG0767 FROM THE CJB110 GBS NONTYPEABLE STRAIN (REVERSE COMPLEMENT)
 GCTGATAAATATAAAGAAGCCGGCATTACGAAGGTTGTTACAAATGAAGCATCTGGAATTGCGCCAGCAGTGTACGCAGCTCAAGCATT
 GGGCGTACCAATGATATTTGCTAAAAAGCTAAGAACATTACTATGACTGAAGGTATCTTAACCTGCTGAAGTGTATTTCTTTACAAAGC
 AAGTTACGAGTCAAGTTTCTATTGTGAGTCGCTTTTATCTAACGATGATACTGTACTCATCATTGATGACTTTTGTAGCAAACGGTCAA
 GCGGCTAAGGATTACTTGAAATTTATTGGTCAAGCTGGAGCTAAGGTTGCTGGTATCGGAATCGTTATTGAAAAATCTTTCCAAGATG
 GCGTGATTTGTTAGAAAAACAGGTGTTCCAGT

Table 17: Comparative Sequences relating to SAG1086 (xanthine phosphoribosyltransferase)

SEQ ID NO. 1710: SAG0767 FROM THE 2603 V/R GBS TYPE V STRAIN
 AACGTATTCTTAAAGATGGTGATGTTTTAGGTGAGAACATTTTAAAGTTGATTCTTTTTTGACTCATCAGGTAGATTTTGAGTTAATG
 CAGGAAATAGGTAAAGTTTTGCTGATAAATATAAAGAAGCCGGCATTACGAAGGTTGTTACAATTGAAGCATCTGGAATTGCGCCAGC
 AGTGTACGCAGCTCAAGCATTGGGCGTACCAATGATATTTGCTAAAAAGCTAAGAACATTACTATGACTGAAGGTATCTTAAGTCTG
 AAGTGTATTCTTTTACAAAGCAAGTTACGAGTCAAGTTCTATTGTGAGTCGCTTTTTATCTAACGATGATACTGTACTCATCATTGAT
 GACTTTTTAGCAACCGGTCAAGCGGCTAAAGGATTACTTGAAATATTGGTCAAGCTGGAGCTAAGGTTGCTGGTATCGGAATCGTTAT
 TGAAAAATCTTTCCAAGATGGGCGTGATTTGTAGAAAAAACAGGTGTTCCAG

SEQ ID NO. 1711: SAG0767 FROM THE JM9130013 GBS TYPE VIII STRAIN (REVERSE
 COMPLEMENT)
 ACGAAGTTGTTTACAATTGAAGCATCTGGAATTGCGCCAGCAGTGTACGCAGCTCAAGCATTGGGCGTACCAATGATATTTGCTAAAA
 AGCTAAGAACATTACTATGACTGAAGGTATCTTAAGTCTGAAAGTGTATTCTTTTACAAAGCAAGTTACGAGTCAAGTTTCTATTGTGA
 GTCGCTTTTTATCTAACGATGATACTGTACTCATCATTGATGACTTTTTAGCAACCGGTCAAGCGGCTAAAGGATTACTTGAAATATT
 GGTCAAGCTGGAGCTAAGGTTGCTGGTATCGGA

SEQ1701 -----TTTAAAGGTTGATTCTCT
 SEQ1702 -----TTTAGGTGAGAACATTTTAAAGGTTGATTCTT
 SEQ1703 AGAACGTATTCTTAAAGATGGTGATGTTTTAGGTGAGAACATTTTAAAGTTGATTCTT
 SEQ1704 -----ATTCT
 SEQ1705 -GAACGTATTCTTAAAGATGGTGATGTTTTAGGTGAGAACATTTTAAAGTTGATTCTT
 SEQ1706 -----ACATTTTAAAGGTTGATTCTT
 SEQ1707 ---ACGTATTCTTAAAGATGGTGATGTTTTAGGTGAGAACATTTTAAAGTTGATTCTT
 SEQ1708 -----TTTAAAGTTGATTCTT
 SEQ1709 -----
 SEQ1710 --AACGTATTCTTAAAGATGGTGATGTTTTAGGTGAGAACATTTTAAAGTTGATTCTT
 SEQ1711 -----

SEQ1701 TTTGACTCATCAGGTAGATTTTGAGTTAATGCAGGAAATAGGTAAAGTTTTTGCTGATA
 SEQ1702 TTTGACTCATCAGGTAGATTTTGAGTTAATGCAGGAAATAGGTAAAGTTTTTGCTGATA
 SEQ1703 TTTGACTCATCAGGTAGATTTTGAGTTAATGCAGGAAATAGGTAAAGTTTTTGCTGATA
 SEQ1704 TTTTGACTATCAGGTAAATTTTGAGTTAATGCAGGAAATAGGTAAAGTTTTTGCTGATA
 SEQ1705 TTTGACTCATCAGGTAAATTTTGAGTTAATGCAGGAAATAGGTAAAGTTTTTGCTGATA
 SEQ1706 TTTGACTCATCAGGTAGATTTTGAGTTAATGCAGGAAATAGGTAAAGTTTTTGCTGATA
 SEQ1707 TTTGACTCATCAGGTAGATTTTGAGTTAATGCAGGAAATAGGTAAAGTTTTTGCTGATA
 SEQ1708 TTTGACTCATCAGGTAAATTTTGAGTTAATGCAGGAAATAGGTAAAGTTTTTGCTGATA
 SEQ1709 -----GCTGATA
 SEQ1710 TTTGACTCATCAGGTAGATTTTGAGTTAATGCAGGAAATAGGTAAAGTTTTTGCTGATA
 SEQ1711 -----

SEQ1701 ATATAAAGAAGCCGGCATTACGAAGGTTGTTACGATTGAAGCATCTGGAATTGCGCCAG
 SEQ1702 ATATAAAGAAGCCGGCATTACGAAGGTTGTTACGATTGAAGCATCTGGAATTGCGCCAG
 SEQ1703 ATATAAAGAAGCCGGCATTACGAAGGTTGTTACAATTGAAGCATCTGGAATTGCGCCAG
 SEQ1704 ATATAAAGAAGCCGGCATTACGAAGGTTGTTACAATTGAAGCATCTGGAATTGCGCCAG
 SEQ1705 ATATAAAGAAGCCGGCATTACGAAGGTTGTTACAATTGAAGCATCTGGAATTGCGCCAG
 SEQ1706 ATATAAAGAAGCCGGCATTACGAAGGTTGTTACGATTGAAGCATCTGGAATTGCGCCAG
 SEQ1707 ATATAAAGAAGCCGGCATTACGAAGGTTGTTACAATTGAAGCATCTGGAATTGCGCCAG
 SEQ1708 ATATAAAGAAGCCGGCATTACGAAGGTTGTTACAATTGAAGCATCTGGAATTGCGCCAG
 SEQ1709 ATATAAAGAAGCCGGCATTACGAAGGTTGTTACAATTGAAGCATCTGGAATTGCGCCAG
 SEQ1710 ATATAAAGAAGCCGGCATTACGAAGGTTGTTACAATTGAAGCATCTGGAATTGCGCCAG
 SEQ1711 -----ACGAAGGTTGTTACAATTGAAGCATCTGGAATTGCGCCAG

SEQ1701 CAGTGTACGCAGCTCAAGCATTGGGCGTACCAATGATATTTGCTAAAAAGGCTAAGAACA
 SEQ1702 CAGTGTACGCAGCTCAAGCATTGGGCGKACCAATGATATTTGCTAAAAAGCTAAGAACA
 SEQ1703 CAGTGTACGCAGCTCAAGCATTGGGCGTACCAATGATATTTGCTAAAAAGCTAAGAACA
 SEQ1704 CAGTGTACGCAGCTCAAGCATTGGGCGTACCAATGATATTTGCTAAAAAGCTAAGAACA
 SEQ1705 CAGTGTACGCAGCTCAAGCATTGGGCGTACCAATGATATTTGCTAAAAAGCTAAGAACA
 SEQ1706 CAGTGTACGCAGCTCAAGCATTGGGCGTACCAATGATATTTGCTAAAAAGCTAAGAACA
 SEQ1707 CAGTGTACGCAGCTCAAGCATTGGGCGTACCAATGATATTTGCTAAAAAGCTAAGAACA
 SEQ1708 CAGTGTACGCAGCTCAAGCATTGGGCGTACCAATGATATTTGCTAAAAAGCTAAGAACA
 SEQ1709 CAGTGTACGCAGCTCAAGCATTGGGCGTACCAATGATATTTGCTAAAAAGCTAAGAACA
 SEQ1710 CAGTGTACGCAGCTCAAGCATTGGGCGTACCAATGATATTTGCTAAAAAGCTAAGAACA
 SEQ1711 CAGTGTACGCAGCTCAAGCATTGGGCGTACCAATGATATTTGCTAAAAAGCTAAGAACA

Table 17: Comparative Sequences relating to SAG1086 (xanthine phosphoribosyltransferase)

SEQ1701	TTACTATGACTGAAGGTATCTTAACTGCTGAAGTGTATTCTTTTACAAAGCAAGWTACGA
SEQ1702	TTACTATGACTGAAGGTATCTTAACTGCTGAAGTGTATTCTTTTACAAAGCAAGTTACGA
SEQ1703	TTACTATGACTGAAGGTATCTTAACTGCTGAAGTGTATTCTTTTACAAAGCAAGTTACGA
SEQ1704	TTACTATGACTGAAGGTATCTTAACTGCTGAAGTGTATTCTTTTACAAAGCAAGTTACGA
SEQ1705	TTACTATGACTGAAGGTATCTTAACTGCTGAAGTGTATTCTTTTACAAAGCAAGTTACGA
SEQ1706	TTACTATGACTGAAGGTATCTTAACTGCTGAAGTGTATTCTTTTACAAAGCAAGTTACGA
SEQ1707	TTACTATGACTGAAGGTATCTTAACTGCTGAAGTGTATTCTTTTACAAAGCAAGTTACGA
SEQ1708	TTACTATGACTGAAGGTATCTTAACTGCTGAAGTGTATTCTTTTACAAAGCAAGTTACGA
SEQ1709	TTACTATGACTGAAGGTATCTTAACTGCTGAAGTGTATTCTTTTACAAAGCAAGTTACGA
SEQ1710	TTACTATGACTGAAGGTATCTTAACTGCTGAAGTGTATTCTTTTACAAAGCAAGTTACGA
SEQ1711	TTACTATGACTGAAGGTATCTTAACTGCTGAAGTGTATTCTTTTACAAAGCAAGTTACGA
SEQ1701	GTCAAGTTTCTATTGTGAGTCGCTTTTATCTAACGATGATACTGTACTCATCATTGATG
SEQ1702	GTCAAGTTTCTATTGTGAGTCGCTTTTATCTAACGATGATACTGTACTCATCATTGATG
SEQ1703	GTCAAGTTTCTATTGTGAGTCGCTTTTATCTAACGATGATACTGTACTCATCATTGATG
SEQ1704	GTCAAGTTTCTATTGTGAGTCGCTTTTATCTAACGATGATACTGTACTCATCATTGATG
SEQ1705	GTCAAGTTTCTATTGTGAGTCGCTTTTATCTAACGATGATACTGTACTCATCATTGATG
SEQ1706	GTCAAGTTTCTATTGTGAGTCGCTTTTATCTAACGATGATACTGTACTCATCATTGATG
SEQ1707	GTCAAGTTTCTATTGTGAGTCGCTTTTATCTAACGATGATACTGTACTCATCATTGATG
SEQ1708	GTCAAGTTTCTATTGTGAGTCGCTTTTATCTAACGATGATACTGTACTCATCATTGATG
SEQ1709	GTCAAGTTTCTATTGTGAGTCGCTTTTATCTAACGATGATACTGTACTCATCATTGATG
SEQ1710	GTCAAGTTTCTATTGTGAGTCGCTTTTATCTAACGATGATACTGTACTCATCATTGATG
SEQ1711	GTCAAGTTTCTATTGTGAGTCGCTTTTATCTAACGATGATACTGTACTCATCATTGATG
SEQ1701	ACTTTT TAGCAAACGGTCAAGCGGCTAAAGGATTACTTGAAATT-ATTGGTCAAGCTGGA
SEQ1702	ACTTTT TAGCAAACGGTCAAGCGGCTAAAGGATTACTTGAAATT-ATTGGTCAAGCTGGA
SEQ1703	ACTTTT TAGCAAACGGTCAAGCGGCTAAAGGATTACTTGAAATT-ATTGGTCAAGCTGGA
SEQ1704	ACTTTT TAGCAAACGGTCAAGCGGCTAAAGGATTACTTGAAATT-ATTGGTCAAGCTGGA
SEQ1705	ACTTTT TAGCAAACGGTCAAGC-----
SEQ1706	ACTTTT TAGCAAACMGTCYAGCGGCTAAAGGATTACTTGAAATT-ATTGGTCAAGCTGGA
SEQ1707	ACTTTT TAGCAAACGGKCAAGCGGSTAAAGGATTACTTGAAATT-ATTGGTCAAGCTGGA
SEQ1708	ACTTTT TAGCAAACGGTCAAGCGGCTAAAGGATTACTTGAAATT-ATTGGTCAAGCTGGA
SEQ1709	ACTTTT TAGCAAACGGTCAAGCGGCTAAAGGATTACTTGAAATTATTGGTCAAGCTGGA
SEQ1710	ACTTTT TAGCAAACGGTCAAGCGGCTAAAGGATTACTTGAAATT-ATTGGTCAAGCTGGA
SEQ1711	ACTTTT TAGCAAACGGTCAAGCGGCTAAAGGATTACTTGAAATT-ATTGGTCAAGCTGGA
SEQ1701	CTAAGGTTGCTGGTATCGGAATCGTTATTGAAAAATCTTTCCAAGATGGGCGTGATTG
SEQ1702	CTAAGGTTGCTGGTATCGGAATCGTTATTGAAAAATCTTTCCAAGATGGGCGTGATTG
SEQ1703	CTAAGGTTGCTGGTATCGGAATCYTTATTGAAAAATCTTTCCAAGATGGGCGTGATT--
SEQ1704	CTAAGGTTGCTGGTATCGGAATCGTTATTGAAAAATCTTTCCAAGATGGGCGTGATTG
SEQ1705	-----
SEQ1706	CTAAGGTTGCTGGTATCGGAATCGTTATTGAAAAATCTTTCCAAGATGGGCGTGATTG
SEQ1707	CTA-----
SEQ1708	CTAAGGTTGCTGGTATCGGAATCGTTATTGAAAAATCTTTCCAAGATGGGCGTGATTG
SEQ1709	CTAAGGTTGCTGGTATCGGAATCGTTATTGAAAAATCTTTCCAAGATGGGCGTGATTG
SEQ1710	CTAAGGTTGCTGGTATCGGAATCGTTATTGAAAAATCTTTCCAAGATGGGCGTGATTG
SEQ1711	CTAAGGTTGCTGGTATCGGA-----TABCMARATVSTNCSR--ATNGTSAGXANTHN
SEQ1701	TAGAAAAAACAGGTGTTCCAGT-----
SEQ1702	TAGAAAAACA-----
SEQ1703	-----
SEQ1704	TAGAAAAAACAGGTGTTCCGGTTACTTCTCTTGCTCGT
SEQ1705	-----
SEQ1706	TAGAAAA-----
SEQ1707	-----
SEQ1708	TAGAAAAAACAGGTGTTCCGGTTAC-----
SEQ1709	TAGAAAAAACAGGTGTTCCAGT-----
SEQ1710	TAGAAAAAACAGGTGTTCCAG-----
SEQ1711	HRBSYTRANSRAS-----

Table 18: Comparative Sequences relating to SAG1600 (glutamate racemase)**SEQ ID NO. 1801: SAG1600 FROM THE H36b GBS TYPE Ib STRAIN (REVERSE COMPLEMENT)**

AATCTTCATTGGAGATCAGGCTAGAGCTCCGTATGGTCTAGACCTGCTCAACAGATTAGAGAGTTTACCTGGCAGATGGTTAATTTCT
TATTGACTAAAAATGTTAAGATGATTGTTATAGCTTGTAAATACAGCAACTGCAGTTGCCTGGCAAGAAATTAAAGAAAACTAGACGTG
CCTGTTTTAGGCGTTATTTTACCAGGAGCTAGCGCAGCTATCAAATCAACTAATTCAGGGAAGTTGGTATTATAGGTACTCCCATGAC
TGTTAAATCAGATGCTTATCGTCAAAAAATTCAAGCTTTGTCTCCAAATACTGCTGTGGTATCCCTTGTCTCCGAAATTTGTTCCAA
TTGTGGAATCAAATCAGATGCTTCTAGTTTAGCCAAAAAGGTGGTTTATGAAACGTTGTCCCATTAGTTGGTAAATTAGATACTTTA
ATTTTAGGTTGCACGCATTATCCCTTATTACGTCCCATCATTCAAATGTTATGGGGGCTGAGGTTAAATTAATTGATAGTGGCGCAGA
AACCGTTTCGTGATATTTCTGTTTTATTGAACATTTTTGAGATAAACCATAAATTGGCAAAATAAACACGGTGGTCATCACTTTTACACAA
CCGCCAGCCCAA

SEQ ID NO. 1802: SAG1600 FROM THE M732 GBS TYPE III STRAIN (REVERSE COMPLEMENT)

AAATGTTCCGTCACCTCCAGAAGAGGAAGTAATCTTCATTGGAGATCAGGCTAGAGCTCCGTATGGTCTAGACCTGCTCAACAGATT
AGAGAGTTTACCTGGCAGATGGTTAACTTCTTATTGACTAAAAATGTTAAGATGATTGTTATAGCTTGTAAATACAGCAACTGCAGTTGC
CTGGCAAGAAATTAAAGAAAACTAGACATCCCTGTTTTAGGCGTTATTTTACCAGGAGCTAGCGCAGCTATCAAATCAACTAATTTAG
GGAAAGTTGGTATTATAGGTACTCCCATGACTGTTAAATCAGATGCTTATCGTCAAAAAATTCAAGCTTTGTCTCCAAATACTGCTGTG
GTATCCCTTGTCTGTCGAAATTTGTTCCAATGTGGAATCAAATCAGATGCTTCTAGTTTAGCCAAAAAGGTGGTTTATGAAACGTT
GTCCCATTAGTTGGTAAATTAGATACTTTAATTTTAGGTTGCACGCATTATCCCTTATTACGTCCCATCATTCAAATGTTATGGGGG
CTGAGGTTAAATTAATTGATAGTGGCGCAGAAACCGTTTCGTGATATTTCTGTTTTATTGAACATTTTTGAGATAAACCATAAATTGGCAA
AATAAACACGGTGGTCATCACTTTTACACAACCGCCAGCCCAAAGGTTTTAAAGAAA

SEQ ID NO. 1803: SAG1600 FROM THE 090 GBS TYPE Ia STRAIN

AATCTTCATTGGAGACCGGCTAGAGCTCCGTATGGTCTAGACCTGCTCAACAGATTAGAGAGTTACCTGGCAGATGGTTAATTTCTT
ATTGACTAAAAATGTTAAGATGATTGTTATAGCTTGTAAATACAGCAACTGCAGTTGCCTGGCAAGAAATTAAAGAAAACTAGACATAC
CTGTTTTAGGCGTTATTTTACCAGGAGCTAGCGCAGCTATCAAATCAACTAATTCAGGGAAGTTGGTATTATAGGTACTCCCATGACT
GTTAAATCAGATGCTTATCGTCAAAAAATTCAAGCTTTGTCTCCAAATACTGCTGTGGTATCCCTTGTCTCCGAAATTTGTTCCAAT
TGTGGAATCAAATCAGATGCTTCTAGTTTAGCCAAAAAGGTGGTTTATGAAACGCTGTCCCATTAGTTGGTAAATTAGATACTTTAA
TTTTAGGTTGCACGCATTATCCCTTATTACGTCCCATCATTCAAATGTTATGGGGGCTGAGGTTAAATTAATTGATAGTGGCGCAGAA
ACCGTTTCGTGATATTTCTGTTTTATTGAACATTTTTGAGATAAACCATAAATTGGGsmAAATAAACACGGTGGTCATCACTTTTACACAAC
CGsCAGCCCAAAGGTTTTTAAGGAAATTCAGAACCAATGGCTTAATCAAGAAATAAT

SEQ ID NO. 1804: SAG1600 FROM THE A909 GBS TYPE Ia STRAIN

GCGGTTGTGTAAAGTGTGACCAACCGTGTATTTTGGCAATTATGGTTTATCTCAAAATAGTTCAATAAAACAGAAATATCAGGAAC
GGTTTCTGCGCCACTATCAATTAATTTAACCTCAGCCCCCATAACATTTGAATGATGGGACGTAATAGGGGATAATGCGTGCAACCTA
AAATTAAGTATCTAATTTTACCACTAATGGGGACAACGTTTTCATAAACACACCTTTTGGCTAAACTAGAAGACATCTGATTTGATTCC
ACAATTGGGAACAAATTTCCGACAAGCAAGGGATACCAACAGCAGTATTTGGAGACAAAGCTTGAATTTTTTGACGATAAGCATCTGATTT
AACAGTCATGGGAGTACCTATAATACCAACTTTCCCTAAATTAGTTGATTTGATAGCTGCGCTAGCTCCTGGTAAATAACGCCTAAAA
CAGGGATGCTAGTTTCTTTAATTTCTGCCAGGCAACTGCAGTTGCTGTATTACAAGCTATAACAATCATCTTAACATTTTGTGTC
AATAAGAAAGTTAACCATCTGCCAGGTAAACTCTCTAATCTGTTGAGCAGGTCTAGGACCATAACGGAGCTTAGCCTGATCTCCAATGAA
GATTACTTCTCTCTGGAAGTTGACGGAACATTTCTTAAACAACCGTTAAACACCT

SEQ ID NO. 1805: SAG1600 FROM THE COH1 GBS TYPE Ia STRAIN

TTCCGTCACCTTCCAAATATGAAGTAATCTTCATTGGAGATCAGGCTAGAGCTCCGTATGGTCTAGACCTGCTCAACAGATTAGAGA
GTTTACCTGGCAGATGGTTAACTTCTTATTGACTAAAAATGTTAAGATGATTGTTATAGCTTGTAAATACAGCAACTGCAGTTGCCTGGC
AAGAAATTAAAGAAAACTAGACATCCCTGTTTTAGGCGTTATTTTACCAGGAGCTAGCGCAGTATCAAATCAACTAATTTAGGGAAA
GTTGGTATTATAGGTACTCCCATGACTGTTAAATCAGATGCTTATCGTCAAAAAATTCAAGCTTTGTCTCCAAATACTGCTGTGGTATC
CCTGCTTGTCCGAAAT

SEQ ID NO. 1806: SAG1600 FROM THE CJB110 GBS NONTYPEABLE STRAIN

GTAATCTTCATTGGAGATCAGGCTAGAGCTCCGTATGGTCTAGACCTGCTCAACAGATTAGAGAGTTTACCTGGCAGATGGTTAATTT
CTTATTGACTAAAAATGTTAAGATGATTGTTATAGCTTGTAAATACAGCAACTGCAGTTGCCTGGCAAGAAATTAAAGAAAACTAGACA
TAC

SEQ ID NO. 1807: SAG1600 FROM THE 1169NT1 GBS TYPE V STRAIN

CTTTTGGGCTGGCGTTGTGTAAATTTGATGACCACCGTGTATTTTGGCAATTATGGTTTATCTCAAAATAGTTCAATAAAACAGAA
ATATCAGAACCGTTTCTGCGCCACTATCAATTAATTTAACCTCAGCCCCCATAACATTTTGAATAATGGGACGTAATAGGGGATAATG
CGTGCAACCTAAAAATTAAAGTATCTAATTTACCACTAATGGGGACAATGTTTCATAAACACACCTTTTGGCTAAACTAGAAGACATCT
GATTTGATTTCCACAATTGGAACAAATTTCCGACAAGCAAGGATACCAACAGCAGTATTTGGAGACAAAGCTTGAATTTTTTGGACGATAA
GCATCTGATTTAACAGTCATGGGAGTACCTATA

SEQ ID NO. 1808: SAG1600 FROM THE 1169NT1 GBS TYPE V STRAIN

GTAATCTTCATTGGGATCAGGCTAGAGCTCCGTATGGTCTAGACCTGCTCAACAGATTAGAGAGTTTACCTGGCAGATGGTTAATTT
CTTATTGACTAAAAATGTTAAGATGATTGTTATAGCTTGTAAATACAGCAACTGCAGTT

SEQ ID NO. 1809: SAG1600 FROM THE 18RS21 GBS TYPE II STRAIN

GAAATGTTCCGTCACCTTCCAGAAGAGGAAGTAATCTTCATTGGAGATCAGGCTAGAGCTCCGTATGGTCTAGACCTGCTCAACAGAT
TAGAGAGTTTACCTGGCAGATGGTTAACTTCTTATTGACTAAAAATGTTAAGATGATTGTTATAGCTTGTAAATACAGCAACTGCAGTTG
CCTGGCAAGAAATTAAAGAAAACTAGACATCCCTGTTTTAGGCGTTATTTTACCAGGAGCTAGCGCAGCTATCAAATCAACTAATTTA
GGGAAAGTTGGTATTATAGGTACTCCCATGACTGTTAAATCAGATGCTTATCGTCAAAAAATTCAAGC

Table 18: Comparative Sequences relating to SAG1600 (glutamate racemase)

SEQ ID NO. 1810: SAG1600 FROM THE 18RS21 TYPE II STRAIN
 ATTTCTTTAAAACCTTTTGGGCTGGCGGTTGTGTAATATTGATGACCACCGTGTATTTTGGCCAATTATGGTTTATCTCAAAATAGTT
 CAATAAAACAGAAATATCACGAACGGTTTCTGCGCCACTATCAATTAATTTAACCTCAGCCCCCATAACATTTTGAATGATGGGACGT
 ATATGGGATAATGCGTGCAACCTAAATTAAGTA

SEQ ID NO. 1811: SAG1600 FROM THE 2603 V/R GBS TYPE V STRAIN
 ATTTCTTTAAAACCTTTTGGGCTGGCGGTTGTGTAATAAGTGATGACCACCGTGTATTTTGGCCAATTATGGTTTATCTCAAAATAGTT
 TCAATAAAACAGAAATATCACGAACGGTTTCTGCGCCACTATCAATTAATTTAACCTCAGCCCCCATAACATTTTGAATGATGGGACGT
 AATAGGGGATAATGCGTGCAACCTAAATTAAGTATCTAATTTACCACTAATGGGGACAACGTTTCATAAACCACCTTTTGGCTAA
 ACTAGAAGACATCTGATTTGATTCCACAATTGGAACAA

SEQ ID NO. 1812: SAG1600 FROM THE M781 GBS TYPE III STRAIN
 GGCGGTTGTGTAAGTGATGACCACCGTGTATTTTGGCCAATTATGGTTTATCTCAAAATAGTTCAATAAAACAGAAATATCACGA
 CGGTTTCTGCGCCACTATCAATTAATTTAACCTCAGCCCCCATAACATTTTGAATGATGGGACGTAATAGGGGATAATGCGTGCAACCT
 AAAATTAAGTATCTAATTTACCACTAATGGGGACAACGTTTCATAAACCACCTTTTGGCTAAACTAGAAGA

SEQ ID NO. 1813: SAG1600 FROM THE M 781 GBS TYPE III STRAIN
 AATCTTCATTGGAGATCAGGCTAGAGCTCCGTATGGTCCTAGACCTGCTCAACAGATTAGAGAGTTTACCTGGCAGATGGTTAACTTCT
 TATTGACTAAAAATGTTAAGATGATTGTTATAGCTTGTAATACAGCAACTGC

SEQ ID NO. 1814: SAG1600 FROM THE JM9130013 GS TYPE VIII STRAIN
 TGGGCTGGCGGTTGTGTAAGTGATGACCACCGTGTATTTTGGCCAATTATGGTTTATCTCAAAATAGTTCAATAAAACAGAAATAT
 CACGAACGGTTTCTGCGCCACTATCAATTAATTTAACCTCAGCCCCCATAACATTTTGAATGATGGGACGTAATAAGGGATAATGCGTG
 CAACCTAAAAATTAAGTATCTAATTTACCACTAATGGGGACAACGTTTCATAAACCACCTTTTGGCTAAACTAGAAGACATCTGATT
 TGATTCACAAATTGGAAACAAATTTTCGGACAAGCAAGGGATACCAACAGCAGTATTTGGAGACAAAGCTTGAATTTTGGACGATAAGCAT
 CTGATTTAACAGTCATGGGAGTACCTATAATACCAACTTTCCCTGAA

SEQ1801 -----AATCTTCATTGGAGATCAGGCTAGAGCT
 SEQ1802 AAATGTTCCGTCAACTTCCAGAAGAGGAAGTAATCTTCATTGGAGATCAGGCTAGAGCT
 SEQ1803 -----AATCTTCATTGGAGACCAGGCTAGAGCT
 SEQ1804 -----GCGGTTGTGTAAG-T
 SEQ1805 ----TTCCGTCAACTTCCAAAATATGAAGTAATCTTCATTGGAGATCAGGCTAGAGCT
 SEQ1806 -----GTAATCTTCATTGGAGATCAGGCTAGAGCT
 SEQ1807 -----CTTTTGGGCTGGCGGTTGTGTAAG-T
 SEQ1808 -----GTAATCTTCATTGGGATCAGGCTAGAGCT
 SEQ1809 AAATGTTCCGTCAACTTCCAGAAGAGGAAGTAATCTTCATTGGAGATCAGGCTAGAGCT
 SEQ1810 -----ATTTCTTTAAAACCTTTTGGGCTGGCGGTTGTGTAAT-T
 SEQ1811 -----ATTTCTTTAAAACCTTTTGGGCTGGCGGTTGTGTAATAAGT
 SEQ1812 -----GGCGGTTGTGTAAG-T
 SEQ1813 -----AATCTTCATTGGAGATCAGGCTAGAGCT
 SEQ1814 -----TGGGCTGGCGGTTGTGTAAG-T

SEQ1801 CGTATGGTC-CTAGACCTGCTCAACAGATTAGAGAGTTTACCTGGCAGATGGTTAACTT
 SEQ1802 CGTATGGTC-CTAGACCTGCTCAACAGATTAGAGAGTTTACCTGGCAGATGGTTAACTT
 SEQ1803 CGTATGGTC-CTAGACCTGCTCAACAGATTAGAGAGTT-ACCTGGCAGATGGTTAACTT
 SEQ1804 --GATGACCACCGTGTATTTTGGCCAATTATGG--TTTATCTCA-AAATAGTTCA--
 SEQ1805 CGTATGGTC-CTAGACCTGCTCAACAGATTAGAGAGTTTACCTGGCAGATGGTTAACTT
 SEQ1806 CGTATGGTC-CTAGACCTGCTCAACAGATTAGAGAGTTTACCTGGCAGATGGTTAACTT
 SEQ1807 --GATGACCACCGTGTATTTTGGCCAATTATGG--TTTATCTCA-AAATAGTTCA--
 SEQ1808 CGTATGGTC-CTAGACCTGCTCAACAGATTAGAGAGTTTACCTGGCAGATGGTTAACTT
 SEQ1809 CGTATGGTC-CTAGACCTGCTCAACAGATTAGAGAGTTTACCTGGCAGATGGTTAACTT
 SEQ1810 --GATGACCACCGTGTATTTTGGCCAATTATGG--TTTATCTCA-AAATAGTTCA--
 SEQ1811 --GATGACCACCGTGTATTTTGGCCAATTATGG--TTTATCTCA-AAATAGTTCA--
 SEQ1812 --GATGACCACCGTGTATTTTGGCCAATTATGG--TTTATCTCA-AAATAGTTCA--
 SEQ1813 CGTATGGTC-CTAGACCTGCTCAACAGATTAGAGAGTTTACCTGGCAGATGGTTAACTT
 SEQ1814 --GATGACCACCGTGTATTTTGGCCAATTATGG--TTTATCTCA-AAATAGTTCA--

Table 18: Comparative Sequences relating to SAG1600 (glutamate racemase)

SEQ1801	TTATTGACTAAAAATGTTAAGATGATTGTTATAGCTTGTAATACAGCAACTGCAGTTGC
SEQ1802	TTATTGACTAAAAATGTTAAGATGATTGTTATAGCTTGTAATACAGCAACTGCAGTTGC
SEQ1803	TTATTGACTAAAAATGTTAAGATGATTGTTATAGCTTGTAATACAGCAACTGCAGTTGC
SEQ1804	--ATAAACAGAAATATCACGAACGGT-TTCTGCGCCACTATCAATTAATTTAACCTCA
SEQ1805	TTATTGACTAAAAATGTTAAGATGATTGTTATAGCTTGTAATACAGCAACTGCAGTTGC
SEQ1806	TTATTGACTAAAAATGTTAAGATGATTGTTATAGCTTGTAATACAGCAACTGCAGTTGC
SEQ1807	--ATAAACAGAAATATCACGAACGGT-TTCTGCGCCACTATCAATTAATTTAACCTCA
SEQ1808	TTATTGACTAAAAATGTTAAGATGATTGTTATAGCTTGTAATACAGCAACTGCAGTT--
SEQ1809	TTATTGACTAAAAATGTTAAGATGATTGTTATAGCTTGTAATACAGCAACTGCAGTTGC
SEQ1810	--ATAAACAGAAATATCACGAACGGT-TTCTGCGCCACTATCAATTAATTTAACCTCA
SEQ1811	--ATAAACAGAAATATCACGAACGGT-TTCTGCGCCACTATCAATTAATTTAACCTCA
SEQ1812	--ATAAACAGAAATATCACGAACGGT-TTCTGCGCCACTATCAATTAATTTAACCTCA
SEQ1813	TTATTGACTAAAAATGTTAAGATGATTGTTATAGCTTGTAATACAGCAACTGC-----
SEQ1814	--ATAAACAGAAATATCACGAACGGT-TTCTGCGCCACTATCAATTAATTTAACCTCA
SEQ1801	TGGCAAGAAATTAAAGAAAAACTAGACGTGCCTGTTTTAGGCGTTATTTTACCAGGAGC
SEQ1802	TGGCAAGAAATTAAAGAAAAACTAGACATCCCTGTTTTAGGCGTTATTTTACCAGGAGC
SEQ1803	TGGCAAGAAATTAAAGAAAAACTAGACATACCTGTTTTAGGCGTTATTTTACCAGGAGC
SEQ1804	CCCCCATAACATTTTGAATGATGGGACGTAATAGGGGATAATGC-GTGCAACCTAAAAT
SEQ1805	TGGCAAGAAATTAAAGAAAAACTAGACATCCCTGTTTTAGGCGTTATTTTACCAGGAGC
SEQ1806	TGGCAAGAAATTAAAGAAAAACTAGACATAC-----
SEQ1807	CCCCCATAACATTTTGAATAATGGGACGTAATAGGGGATAATGC-GTGCAACCTAAAAT
SEQ1808	-----
SEQ1809	TGGCAAGAAATTAAAGAAAAACTAGACATCCCTGTTTTAGGCGTTATTTTACCAGGAGC
SEQ1810	CCCCCATAACATTTTGAATGATGGGACGTAATATGGGATAATGC-GTGCAACCTAAAAT
SEQ1811	CCCCCATAACATTTTGAATGATGGGACGTAATAGGGGATAATGC-GTGCAACCTAAAAT
SEQ1812	CCCCCATAACATTTTGAATGATGGGACGTAATAGGGGATAATGC-GTGCAACCTAAAAT
SEQ1813	-----
SEQ1814	CCCCCATAACATTTTGAATGATGGGACGTAATAAGGGATAATGC-GTGCAACCTAAAAT
SEQ1801	AGCGCAGCTATCAAATCAACTAATTCAGGGAAAGTTGGTATTATAGGTACTCCCATGAC
SEQ1802	AGCGCAGCTATCAAATCAACTAATTTAGGGAAAGTTGGTATTATAGGTACTCCCATGAC
SEQ1803	AGCGCAGCTATCAAATCAACTAATTCAGGGAAAGTTGGTATTATAGGTACTCCCATGAC
SEQ1804	AAAGTATCTAATTTACCAACTAATGGGGACAACGTTTCATAAACCACCTTTTGGCTAA
SEQ1805	AGCGCAGCTATCAAATCAACTAATTTAGGGAAAGTTGGTATTATAGGTACTCCCATGAC
SEQ1806	-----
SEQ1807	AAAGTATCTAATTTACCAACTAATGGGGACAATGTTTCATAAACCACCTTTTGGCTAA
SEQ1808	-----
SEQ1809	AGCGCAGCTATCAAATCAACTAATTTAGGGAAAGTTGGTATTATAGGTACTCCCATGAC
SEQ1810	AAAGTA-----
SEQ1811	AAAGTATCTAATTTACCAACTAATGGGGACAACGTTTCATAAACCACCTTTTGGCTAA
SEQ1812	AAAGTATCTAATTTACCAACTAATGGGGACAACGTTTCATAAACCACCTTTTGGCTAA
SEQ1813	-----
SEQ1814	AAAGTATCTAATTTACCAACTAATGGGGACAACGTTTCATAAACCACCTTTTGGCTAA
SEQ1801	GTTAAATCAGATGCTTATCGTCAAAAAATTCAAGCTTTGTCTCCAAATACTGCTGTGGT
SEQ1802	GTTAAATCAGATGCTTATCGTCAAAAAATTCAAGCTTTGTCTCCAAATACTGCTGTGGT
SEQ1803	GTTAAATCAGATGCTTATCGTCAAAAAATTCAAGCTTTGTCTCCAAATACTGCTGTGGT
SEQ1804	CTAGAAGACATCTGATTTGATTCCACAATTGGAACAAATTCGGACAAGCAAGGGATAC
SEQ1805	GTTAAATCAGATGCTTATCGTCAAAAAATTCAAGCTTTGTCTCCAAATACTGCTGTGGT
SEQ1806	-----
SEQ1807	CTAGAAGACATCTGATTTGATTCCACAATTGGAACAAATTCGGACAAGCAAGGGATAC
SEQ1808	-----
SEQ1809	GTTAAATCAGATGCTTATCGTCAAAAAATTCAAGC-----
SEQ1810	-----
SEQ1811	CTAGAAGACATCTGATTTGATTCCACAATTGGAACAA-----
SEQ1812	CTAGAAGA-----
SEQ1813	-----
SEQ1814	CTAGAAGACATCTGATTTGATTCCACAATTGGAACAAATTCGGACAAGCAAGGGATAC

Table 18: Comparative Sequences relating to SAG1600 (glutamate racemase)

SEQ1801	TCCCTTGCTTGTCCGAAATTTGTTCCAATTGTGGAATCAAATCAGATGTCCTTCTAGTTT
SEQ1802	TCCCTTGCTTGTCCGAAATTTGTTCCAATTGTGGAATCAAATCAGATGTCCTTCTAGTTT
SEQ1803	TCCCTTGCTTGTCCGAAATTTGTTCCAATTGTGGAATCAAATCAGATGTCCTTCTAGTTT
SEQ1804	ACAGCAGTATTTGGAGACAAAGCTTGAATTTTTTGACGATAAGCATCTGATTAAACAGT
SEQ1805	TCCCTTGCTTGTCCGAAAT-----
SEQ1806	-----
SEQ1807	ACAGCAGTATTTGGAGACAAAGCTTGAATTTTTTGACGATAAGCATCTGATTAAACAGT
SEQ1808	-----
SEQ1809	-----
SEQ1810	-----
SEQ1811	-----
SEQ1812	-----
SEQ1813	-----
SEQ1814	ACAGCAGTATTTGGAGACAAAGCTTGAATTTTTTGACGATAAGCATCTGATTAAACAGT
SEQ1801	GCCAAAAAGGTGGTTTATGAAACGTTGTCCCCATTAGTTGGTAAATTAGATACTTTAAT
SEQ1802	GCCAAAAAGGTGGTTTATGAAACGTTGTCCCCATTAGTTGGTAAATTAGATACTTTAAT
SEQ1803	GCCAAAAAGGTGGTTTATGAAACGCTGTCCCCATTAGTTGGTAAATTAGATACTTTAAT
SEQ1804	ATGGGAGTACCTATAATAACCACTTTCCCTAAATTAGTTGATTGATAGCTGCGCTAGC
SEQ1805	-----
SEQ1806	-----
SEQ1807	ATGGGAGTACCTATAA-----
SEQ1808	-----
SEQ1809	-----
SEQ1810	-----
SEQ1811	-----
SEQ1812	-----
SEQ1813	-----
SEQ1814	ATGGGAGTACCTATAATAACCACTTTCCCTGAATABC MARATVSTNCSRATNGTSAGGT
SEQ1801	TTAGGTTGCACGCATTATCCCTTATTACGTCCCATCATTCAAATGTTATGGGGGCTGA
SEQ1802	TTAGGTTGCACGCATTATCCCTTATTACGTCCCATCATTCAAATGTTATGGGGGCTGA
SEQ1803	TTAGGTTGCACGCATTATCCCTTATTACGTCCCATCATTCAAATGTTATGGGGGCTGA
SEQ1804	CCTGGTAAATAACGCCTAAACAGGGATGTCTAGTTTTCTTTAATTTCTTGCCAGGC
SEQ1805	-----
SEQ1806	-----
SEQ1807	-----
SEQ1808	-----
SEQ1809	-----
SEQ1810	-----
SEQ1811	-----
SEQ1812	-----
SEQ1813	-----
SEQ1814	AMATRACMAS-----
SEQ1801	GTAAATTAATTGATAGTGGCGCAGAAACCGTTCGTGATATTTCTGTTTTATTGAACTA
SEQ1802	GTTAAATTAATTGATAGTGGCGCAGAAACCGTTCGTGATATTTCTGTTTTATTGAACTA
SEQ1803	GTTAAATTAATTGATAGTGGCGCAGAAACCGTTCGTGATATTTCTGTTTTATTGAACTA
SEQ1804	ACTGCAGTTGCTGTATTACAAGCTATAACAATCATCTTAACATTTTTAGTCAATAAGAA
SEQ1805	-----
SEQ1806	-----
SEQ1807	-----
SEQ1808	-----
SEQ1809	-----
SEQ1810	-----
SEQ1811	-----
SEQ1812	-----
SEQ1813	-----
SEQ1814	-----

Table 18: Comparative Sequences relating to SAG1600 (glutamate racemase)

SEQ1801	TTTGAGATAAACCATAATTGGCAAATAAACACGGTGGTCATCACTTTTACACAACCGC
SEQ1802	TTTGAGATAAACCATAATTGGCAAATAAACACGGTGGTCATCACTTTTACACAACCGC
SEQ1803	TTTGAGATAAMCCATAATTGGSMAAATAAACACGGTGGTCATCACTTTTACACAACCGS
SEQ1804	TTAACCATCTGCCAGGTAAACTCTCTAATCTGTTGAGCAGGTCTAGGACCATACGGAGC
SEQ1805	-----
SEQ1806	-----
SEQ1807	-----
SEQ1808	-----
SEQ1809	-----
SEQ1810	-----
SEQ1811	-----
SEQ1812	-----
SEQ1813	-----
SEQ1814	-----
SEQ1801	AGCCCAA-----
SEQ1802	AGCCCAAAGGTTTAAAGAAA-----
SEQ1803	AGCCCAAAGGTTTAAAGGAAATTGCAGAACAAATGGCTTAATCAAGAAATAAAT----
SEQ1804	CTAGCCTGATCTCCAATGAAGATTACTTCCTCTTCTGGAAGTTGACGGAACATTTTCCTT
SEQ1805	-----
SEQ1806	-----
SEQ1807	-----
SEQ1808	-----
SEQ1809	-----
SEQ1810	-----
SEQ1811	-----
SEQ1812	-----
SEQ1813	-----
SEQ1814	-----
SEQ1801	-----
SEQ1802	-----
SEQ1803	-----
SEQ1804	ACAACCGTTAAACCACCT
SEQ1805	-----
SEQ1806	-----
SEQ1807	-----
SEQ1808	-----
SEQ1809	-----
SEQ1810	-----
SEQ1811	-----
SEQ1812	-----
SEQ1813	-----
SEQ1814	-----

Table 19: Comparative Sequences relating to SAG1680 (shikimate 5-dehydrogenase)**SEQ ID NO. 1901: SAG1680 FROM THE 2603 V/R GBS TYPE V STRAIN**

ATCCCTAGACCATTATAAGCATGTTTCACTCCATTTTGTCTAACAAATCGTAACAATGCTGTTTCTTTAGGCTTGTAAC
 CAAGTCGACAACTACTAAATTCGGTGTAAATTTCTGGATCGTTAATTAACTATAATTATCTAATGGCCTCATTCCTA
 AACTAGTAGCATCAATATAAAAAATGACTAGTTCTAATAGCGTCTTTAAATGCTGTCTTATTTCTAGATAATCAACGACT
 ACCTTTATTTGAACTGTTTAAATTTTATCTGATAAGTCAATGACCTTATCGTAATTTGAGCTGTTACGATTAAATAA
 TCTAATTTCCGCAACTCCCTCCATAGCTGCTTGAAGTGAACCTGCTTTACCTGAACCACCAATACCAGCTATTGTAATTA
 TTTTATTTTGTAGCACTGAAACCTTGAGCTGTAAAGCTTTAAACAACCAATGCCATCTGTCAATATGGCCTACTAAACGT
 CCGGTTCCACCTTGATTAAACGATAGTATTTACAGCACCCTAATTTAGCTTGAGGAGATAAATCATCTAGCAAAGGGAT
 AACACTCTGTTTAAATGGCATTGAAACATTAAACACCACGAATACCCAATGCCCTGACACCTCGAACAGCTTCTGTTAATT
 TACCCTCTTCTACTTCAAATGTGAGATAGGCATAATTCATGTTTTTTCTTGAAAAGAGGTATTCCACATTAACGGGGAT
 AGAGAGTGGCGTGCAGG

SEQ ID NO. 1902: SAG1680 FROM THE H36b GBS TYPE Ib STRAIN

GTTATTAATTGAAATGCTTCTGCTCCTTGATAAATCAGCATCCCTAGACCATTATAAGCATGTTTCACTCCATTTTGTCT
 AACAAATCGTAACAATGCTGTTCTTTAGGCTTGTAACCAAGTCGACAACTACTAAATTCGGTGTAAATTTCTGGAT
 CGTTAATTAACCTATAAATTCTAATGGCCTCATTCCTAACTAGTAGCATCAATATAAAAAATGACTAGTTCTAATAGCG
 TCTTTAAATGCTGTCTTATTTCTAGATAATCAACGACTACCTTTATTTGAACTGTTTAAATTTTATCTGATAAGTC
 AATGACCTTATCGTAATTTGAGCTGTTACGATTAAATAATCTAATTTCCGCAACTCCCTCCATAGCTGCTTGAAGTGA
 CTGCTTTACCTGAACCACCAATACCAGCTATTGTAATTTATTTTATTTTGTAGCACTGAAACCTTGAGCTGTAAAGCTTTA
 AAACAACCAATGCCATCTGTCAATATGGCCTACTAAACGTCCGGTTCACCTTGATTAAAGATAGTATTTACAGCACCAC
 TAATTTAGCTTGAGGAGATAAATCATCTAGCAAAGGGATAACACTCTGTTTAAATGGCATTGAAACATTAAACACCAGAA
 TACCCAATGCCCTGACACCTCGAACAGCTTCTGTTAATTTACCTCTTCTACTTCAAATGTGAGATAGGCATAATTCATG
 TTTTTTTCTTGAAAAGAGGTATTCCACATTAACGGGGATAGAGAGTGGCGTGCAGGA

SEQ ID NO. 1903: SAG1680 FROM THE M732 GBS TYPE III STRAIN

CTGGTCTAATTGCCAATCCTGCACGCCACTCTCTATCCCCGTTAATGTGGAATACCTCTTTTCAAGAAAAAATCATGAAT
 TATGCCATCTGACATTTGAAGTAGAAGAGGGTAAATTAACAGAAGCTGTTTCGAGGTGTCAGGGCATTGAGTATTCGTGG
 TGTTAATGTTTCAATGCCATTTAAACAGAGTGTTATCCCTTGTCTAGATGATTTATCTCTCAAGCTAAATTAGTGGGTG
 CTGTAATACTATCGTTAATCAAGGTGGAACCGGACGTTTAGTAGGCCATATGACAGATGGCATTGGTTGTTTAAAGCT
 TTAGCAGCTCAAGGTTTCAGTGCTAAAAATAAAATAAATTACAATAGCTGTTATGGTGGTTTCAGGTAAGCAGTTGCACT
 TCAAGCAGCTATGGAGGGAGTTGCGGAAATTAGATTATTTAATCGTAACAGCTCAAATTACGATAAGGTCATTGACTTAT
 CAGATAAAATTAATAAACAGTTTCAAATAAAGGTAGTCGTTGATTATCTAGAAAATAAGACAGCATTAAAGACGCTATT
 AGAACTAGTCATTTTTATATTGATGCTACTAGTTTAGGAATGAGGCCATTAGATAATTATAGTTTAAATTAACGATCCAGA
 TATTTTAACACCGAATTTAGTAGTTGTGCACTT

SEQ ID NO. 1904: SAG1680 FROM THE M781 GBS TYPE III STRAIN

AAATCAGCATCCCTAGACATTATAAGCATGTTTCACTCCATTTTGTCTAACAAATCGTAACAATGCTGTTTCTTTAGGCT
 TGTAACCAAGTCGACAACTACTAAATTCGGTGTAAATTTCTGGATCGTTAATTAACTATAATTATCTAATGGCCTC
 ATTCTTAACTAGTAGCATCAATATAAAAAATGACTAGTTCTAATAGCGTCTTTAAATGCTGTCTTATTTTCTAGATAATC
 AACGACTACCTTTATTTGAACTGTTTAAATTTTATCTGATAAGTCAATGACCTTATCGTAATTTGAGCTGTTACGAT
 TAAATAATCTAATTTCCGCAACTCCCTCCATAGCTGCTTGAAGTGAACCTGCTTTACCTGAACCACCAATACCAGCTATT
 GTAATTATTTTATTTTGTAGCACTGAAACCTTGAGCTGTAAAGCTTTAAACAACCAATGCCATCTGTCAATATGGCCTAC
 TAAACGTCCGGTTCACCTTGATTAAAGATAGTATTTACAGCACCCTAATTTAGCTTGAGGAGATAAATCATCTAGCA
 AAGGGATAACACTCTGTTTAAATGGCATTGAAACATTAAACACCACGAATACTCAATGCCCTGACACCTCGAACAGCTTCT
 GTTAATTTACCTCTTCTACTTCAAATGTGAGATAGGCATAATTCATGTTTTTTCTTGAAAAGAGGTATTCCACATTAA
 CGGGATAGAGAGTGGCGTGCA

SEQ ID NO. 1905: SAG1680 FROM THE 090 GBS TYPE Ia STRAIN

GTTTCAGAGTGTGAGGGCATTGGGTATTCTGGTGTAAATGTTTCAATGCCATTTAAACAGAGTGTTATCCCTTTGCTArA
 TGATTTATCTCTCAAGCTAAATTAGTGGGTGCTGTAAATACTATCGTTAATCAAGGTGGAACCGsACGTTTAGTAGGCC
 ATATGACAGATGGCATTGGTTGTTTAAAGCTTTAGCAGCTCAAGGTTTCAGTGCTAAAAATAAAATAGTTACAATAGCT
 GGTATTGGTGGTTTCAGGTAAAGCAGTTGCAGTTCAAGCAGCTATGGAGGAGTTGCGGAAATTAGATTATTTAATCGTAA
 TAGCTCAAATTAGCATAAGGTCACTTATCAGATAAAATTAATAAACAGTTTCAAATAAAGGTAGTCGTTGATTATC
 TAGAAAATAAGACAGCATTTAAAGACGCTATTAGAAGTAGTCATTTTATATTGATGCTACTAGTTTAGGAATGARGCCA
 TTAGATAAATTATAGTTTAAATTAACGATCCAGAAATTTTACACCCAATTTAGTAGTTGTGCACTTGGTTTACAAGCCTAA
 AGAAACAGCATTTGATACGATTGTTAGACAAAATGGAGTGAAACATGCTTATAATGGTCTAGGGATGCTGATTATCAAG
 GAGCAGA

Table 19: Comparative Sequences relating to SAG1680 (shikimate 5-dehydrogenase)**SEQ ID NO. 1906: SAG1680 FROM THE A909 GBS TYPE Ia STRAIN**

CCCTAGACCATTATAATCATGTTTCACTCCATTTTGTCTAACAAATCGTAACAATGCTGTTTCTTTAGGCTTGTAACCA
 AGTCGACAACCTACTAAATTCGGTGTAAAATTTCTGGATCGTTAATTAACCTATAATTATCTAATGGCCTCATTCTAAA
 CTAGTAGCATCAATATAAAATGACTAGTTCTAATAGCGTCTTTAAATGCTGTCTTATTTTCTAGATAATCAACGACTAC
 CTTTATTTGAAACTGTTTTTAATTTTATCTGATAAGTCAATGACCTTATCGTAATTTGAGCTGTTACGATTAAATAATC
 TAATTTCCGCAACTCCCTCCATAGCTGCTTGAACCTGCAACTGCTTTACCTGAACCACCAATACCAGCTATTGTAATTATT
 TTATTTTGTAGCACTGAAACCTTGAGCTGCTAAAGCTTTAAACCAACCAATGCCATCTGTCTATATGGCCTACTAAACGTCC
 GGTTCACCTTGATTAAACGATAGTATTTACAGCACCCTAATTTAGCTTGAGGAGATAAATCATCTAGCAAAGGGATAA
 CACTCTGTTTAAATGGCATTGAAACATTAAACACCAGCAATACCCAATGCCCTGACACCTCGAACAGCTTCTGTTAATTTA
 CCCTCTTCTACTTCAATGTCTAGATAGGCATAATTCATGTTTTTTTCTTGAAAAGAGGTATTCCACATTAACGGGGATAG

SEQ ID NO. 1907: SAG1680 FROM THE COH1 GBS TYPE Ia STRAIN

TGCACGCCACTCTCTATCCCCGTTAATGTGGAATACCTCTTTTAAAGAAAAAACATGAATTATGCCTATCTGACATTTGA
 AGTAGAAGAGGGTAAATTAACAGAAGCTGTTTCGAGGTGTGAGGGCATTGAGTATTCGTGGTGTAAATGTTTCAATGCCAT
 TTAACAGAGTGTATCCCTTTGCTAGATGATTATCTCCTCAAGCTAAATTAGTGGGTGCTGTAAATACT

SEQ ID NO. 1908: SAG1680 FROM THE CJB110 GBS NONTYPEABLE STRAIN

ATTGCTTATTAATTGAAATGCTTCTGCTCCTTGATAAATCAGCATCCCTAGACCATTATAAGCATGTTTCACTCCATTTT
 GTCTAACAAATCGTAACAATGCTGTTTCTTTAGGCTTGTAACCAAGTCGACAACCTACTAAATTGGGTGTTAAAATTTCT
 GGATCGTTAATTAACCTATAATTATCTAATGGCCTCATTCTAACTAGTAGCATCAATATAAAATGACTAGTTCTAAT
 AGCGTCTTTAAATGCTGTCTTATTTTCTAGATAATCAACGACTACCTTTATTTGAAACTGTTTTTAATTTTATCTGATA
 AGTCAATGACCTTATCGTAATTTGAGCTATTACGATTAAATAATCTAATTTCCGCAACTCCCTCCATAACTGCTTGAAC
 GCAACTGCTTTACCTGAACCACCAATACCAGCTATTGTAATTTT

SEQ ID NO. 1909: SAG1680 FROM THE CJB110 GBS NONTYPEABLE STRAIN

ACTCTCTATCCCCGTTAATGTGGAATACCTCTTTTCAAGAAAAAACATGAATTATGCCTATCTGACATTTGAAGTAGAA
 GAGGTAAATTAACAGAAGCTGTTTCGAGGTGTGAGGGCATTGGGTATTCTGTTGTTAATGTTTCAATGCCATTAAACA
 GAGTGTATCCCTTTGCTAGATGATTATCTCCTCAAGCTAAATTAGTGGGTGCTGTAAATACTATCGTTAATCAAGGTG
 GAACCGGACGTTTAGTAGGCCATATGACAGATGGCATTGTTGTTTTAAAGCTTTAGCAGCTCAAGGTTTCAGTGCTAAA
 AATAAAATAGTTACAAATAGCTGGTATTGGTG

SEQ ID NO. 1910: SAG1680 FROM THE 1169NT1 GBS TYPE V STRAIN

ATTGCTTATTAATTGAAATGCTTCTGCTCCTTGATAAATCAGCATCCCTAGACCATTATAAGCATGTTTCACTCCATTTT
 GTCTAACAAATCGTAACAATGCTGTTTCTTTAGGCTTGTAACCAAGTCGACAACCTACTAAATTCGGGTGTTAAAATTTCT
 GGATCGTTAATTAACCTATAATTATCTAATGGCCTCATTCTAACTAGTAGCATCAATATAAAATGACTAGTTCTAAT
 AGCGTCTTTAAATGCTGTCTTATTTTCTAGATAATCAACGACTACCTTTATTTGAAACTGTTTTTAATTTTATCTGATA
 AGTCAATGACCTTATCGTAATTTGAGCTGTTACGAT

SEQ ID NO. 1911: SAG1680 FROM THE 1169NT1 GBS TYPE V STRAIN

ACTTCTCTATTCCCCGTTAATGTGGAATACCTCTTTTCAAGAAAAAACATGAATTATGCCTATCTGACATTTGAAGTAG
 AAGAGGGTAAATTAACAGAAGCTGTTTCGAGGTGTGAGGGCATTGGGTATTCTGTTGTTAATGTTTCAATGCCATTAAAC
 CAGAGTGTATCCCTTTGCTAGATGATTATCTCCTCAAGCTAAATTAGTGGGTGCTGTAAATACTATCGTTAATCAAGG
 TGGAACC

SEQ ID NO. 1912: SAG1680 FROM THE 18RS21 GBS TYPE II STRAIN

TCGTATTATAATTGAAATGCTTCTGCTCCTTGATAAATCATCATCCCTAGACCATTATAAGCATGTTTCACTCCATTTTGT
 CTAACAAATCGTAACAATGCTGTTTCTTTAGGCTTGTAACCAAGTCGACAACCTACTAAATTCGGGTGTTAAAATTTCTGG
 ATCGTTAATTAACCTATAATTATCTAATGGCCTCATTCTAACTAGTAGCATCAATATAAAATGACTAGTTCTAATAG
 CGTCTTTAAATGCTGTCTTATTTTCTAGATAATCAACGACTACCTTTATTTGAAACTGTTTTTAATTTTATCTGATAAG
 TCAATGACCTTATCGTAATTTGAGCTGTTACGATTAAATAATCTAATTTCCGCAAC

SEQ ID NO. 1913: SAG1680 FROM THE 18RS21 GBS TYPE II STRAIN

ATGCCTATCTGACATTTGAAGTAGAAGAGGGTAAATTAACAGAAGCTGTTTCGAGGTGTGAGGGCATTGGGTATTCTGGT
 GTTAATGTTTCAATGCCATTAAACAGAGTGTATCCCTTTGCTAGATGATTATCTCCTCAAGCTAAATTAGTGGGTGCT
 TGTAATACTATCGTTAATCAAGGTGAACCGGACGTTTAGTAGCCATATGACAGATGGCATTGGTTGTTTTAAAGCTT
 TAGCAGCTCAAGGTTTCAGTGCTAAAAATAAATAATTAACAATAGCTGGTATTGGTGGTTTCAGGTAAAGCAGTTGCAGTT
 CAAGCAGCTATGGAGGGAGTTGCGG

Table 19: Comparative Sequences relating to SAG1680 (shikimate 5-dehydrogenase)

SEQ ID NO. 1914: SAG1680 FROM THE JM9130013 GBS TYPE VIII STRAIN

CCCTAGACCATTATAAGTCATGTTTCACTCCATTTTGTCTAACAAATCGTAACAATGCTGTTTCTTTAGGCTTGTAACCC
 AAGTCGACAACACTACTAAATTGGGTGTTAAAATTTCTGGATCGTTAATTAACTATAATTATCTAATGGCCTCATTCTCTAA
 ACTAGTAGCATCAATATAAAAATGACTAGTTCTAATAGCGTCTTTAAATGCTGTCTTATTTTCTAGATAATCAACGACTA
 CCTTATTTGAAACTGTTTTTTAATTTTATCTGATAAGTCAATGACCTTATCGTAATTTGAGCTATTACGATTAAATAAT
 CTAATTTCCGCAACTCCCTCCATAGCTGCTTGAAGTCAACTGCTTTACCTGAACCACCAATACCAGCTATTGTAACATAT
 TTTATTTTGTAGCACTGAAACCTTGAGCTGCTAAAGCTTTAAACAACCAATGCCATCTGTCTAT

SEQ1901 -----ATCCCT
 SEQ1902 -----GTTATTAATTGAAATGCTTCTGCTCCTTGATAAATCAGCATCCCT
 SEQ1903 TGGTCTAATTGCCAATCCTGCAGCCACTCTCTAT-CCCCGTTAATGTGGAATACCTCT
 SEQ1904 -----AAATCAGCATCCCT
 SEQ1905 -----
 SEQ1906 -----CCCT
 SEQ1907 -----TGCACGCCACTCTCTAT-CCCCGTTAATGTGGAATACCTCT
 SEQ1908 -----ATTGTTTAAATTGAAATGCTTCTGCTCCTTGATAAATCAGCATCCCT
 SEQ1909 -----ACTCTCTAT-CCCCGTTAATGTGGAATACCTCT
 SEQ1910 -----ATTGTTTAAATTGAAATGCTTCTGCTCCTTGATAAATCAGCATCCCT
 SEQ1911 -----ACTTCTCTATCCCCGTTAATGTGGAATACCTCT
 SEQ1912 -----TCGTTATTAATTGAAATGCTTCTGCTCCTTGATAAATCATCATCCCT
 SEQ1913 -----
 SEQ1914 -----CCCT

SEQ1901 GACCATTATAAG-CATGTTTCACTCCATTTTGTCTAACAAATCGTAACAATGCTGTTTC
 SEQ1902 GACCATTATAAG-CATGTTTCACTCCATTTTGTCTAACAAATCGTAACAATGCTGTTTC
 SEQ1903 TTCAAGAAAAAACATGAATTATGCCTATCTGACATTGAAGTAGAAGAGGGTAAATTA
 SEQ1904 GAC-ATTATAAG-CATGTTTCACTCCATTTTGTCTAACAAATCGTAACAATGCTGTTTC
 SEQ1905 -----
 SEQ1906 GACCATTATAAT-CATGTTTCACTCCATTTTGTCTAACAAATCGTAACAATGCTGTTTC
 SEQ1907 TT-AAGAAAAAACATGAATTATGCCTATCTGACATTGAAGTAGAAGAGGGTAAATTA
 SEQ1908 GACCATTATAAG-CATGTTTCACTCCATTTTGTCTAACAAATCGTAACAATGCTGTTTC
 SEQ1909 TTCAAGAAAAAACATGAATTATGCCTATCTGACATTGAAGTAGAAGAGGGTAAATTA
 SEQ1910 GACCATTATAAG-CATGTTTCACTCCATTTTGTCTAACAAATCGTAACAATGCTGTTTC
 SEQ1911 TTCAAGAAAAAACATGAATTATGCCTATCTGACATTGAAGTAGAAGAGGGTAAATTA
 SEQ1912 GACCATTATAAG-CATGTTTCACTCCATTTTGTCTAACAAATCGTAACAATGCTGTTTC
 SEQ1913 -----ATGCCTATCTGACATTGAAGTAGAAGAGGGTAAATTA
 SEQ1914 GACCATTATAAGTCATGTTTCACTCCATTTTGTCTAACAAATCGTAACAATGCTGTTTC

SEQ1901 TTAGGCTTGTAACCAAGTC--GACAACTACTAAATTCGGTGTTAAAATTTCTGGATCG
 SEQ1902 TTAGGCTTGTAACCAAGTC--GACAACTACTAAATTCGGTGTTAAAATTTCTGGATCG
 SEQ1903 CAGAAGCTGTTTCGAGGTGTCAGGGCATTGAGTATTCGTGGTGTTAATGTTTCAATGCCA
 SEQ1904 TTAGGCTTGTAACCAAGTC--GACAACTACTAAATTCGGTGTTAAAATTTCTGGATCG
 SEQ1905 -----GTTTCGAGGTGTCAGGGCATTGGGTATTCGTGGTGTTAATGTTTCAATGCCA
 SEQ1906 TTAGGCTTGTAACCAAGTC--GACAACTACTAAATTCGGTGTTAAAATTTCTGGATCG
 SEQ1907 CAGAAGCTGTTTCGAGGTGTCAGGGCATTGAGTATTCGTGGTGTTAATGTTTCAATGCCA
 SEQ1908 TTAGGCTTGTAACCAAGTC--GACAACTACTAAATTCGGTGTTAAAATTTCTGGATCG
 SEQ1909 CAGAAGCTGTTTCGAGGTGTCAGGGCATTGGGTATTCGTGGTGTTAATGTTTCAATGCCA
 SEQ1910 TTAGGCTTGTAACCAAGTC--GACAACTACTAAATTCGGTGTTAAAATTTCTGGATCG
 SEQ1911 CAGAAGCTGTTTCGAGGTGTCAGGGCATTGGGTATTCGTGGTGTTAATGTTTCAATGCCA
 SEQ1912 TTAGGCTTGTAACCAAGTC--GACAACTACTAAATTCGGTGTTAAAATTTCTGGATCG
 SEQ1913 CAGAAGCTGTTTCGAGGTGTCAGGGCATTGGGTATTCGTGGTGTTAATGTTTCAATGCCA
 SEQ1914 TTAGGCTTGTAACCAAGTC--GACAACTACTAAATTCGGTGTTAAAATTTCTGGATCG

Table 19: Comparative Sequences relating to SAG1680 (shikimate 5-dehydrogenase)

SEQ1901	TT-AATTAACTATAATTATCT-----AATGGCCTCATTCT-AACTAGTAGCATCAAT
SEQ1902	TT-AATTAACTATAATTATCT-----AATGGCCTCATTCT-AACTAGTAGCATCAAT
SEQ1903	TTTAAACAGAGTGTTATCCCTTTGCTAGATGATTTATCTCCTCAAGCTAAATTAGTGGGT
SEQ1904	TT-AATTAACTATAATTATCT-----AATGGCCTCATTCT-AACTAGTAGCATCAAT
SEQ1905	TTTAAACAGAGTGTTATCCCTTTGCTARATGATTTATCTCCTCAAGCTAAATTAGTGGGT
SEQ1906	TT-AATTAACTATAATTATCT-----AATGGCCTCATTCT-AACTAGTAGCATCAAT
SEQ1907	TTTAAACAGAGTGTTATCCCTTTGCTAGATGATTTATCTCCTCAAGCTAAATTAGTGGGT
SEQ1908	TT-AATTAACTATAATTATCT-----AATGGCCTCATTCT-AACTAGTAGCATCAAT
SEQ1909	TTTAAACAGAGTGTTATCCCTTTGCTAGATGATTTATCTCCTCAAGCTAAATTAGTGGGT
SEQ1910	TT-AATTAACTATAATTATCT-----AATGGCCTCATTCT-AACTAGTAGCATCAAT
SEQ1911	TTTAAACAGAGTGTTATCCCTTTGCTAGATGATTTATCTCCTCAAGCTAAATTAGTGGGT
SEQ1912	TT-AATTAACTATAATTATCT-----AATGGCCTCATTCT-AACTAGTAGCATCAAT
SEQ1913	TTTAAACAGAGTGTTATCCCTTTGCTAGATGATTTATCTCCTCAAGCTAAATTAGTGGGT
SEQ1914	TT-AATTAACTATAATTATCT-----AATGGCCTCATTCT-AACTAGTAGCATCAAT
SEQ1901	TAAAAATGACTAGTTCTAATAGCGTCTTTAAATGCTGTCTTATTTTCTAGATAATCAAC
SEQ1902	TAAAAATGACTAGTTCTAATAGCGTCTTTAAATGCTGTCTTATTTTCTAGATAATCAAC
SEQ1903	CTGTAAATACTATCGTTAATCAAGGTGGAACCGGACGTTTAGTAGGCCATATGACAGAT
SEQ1904	TAAAAATGACTAGTTCTAATAGCGTCTTTAAATGCTGTCTTATTTTCTAGATAATCAAC
SEQ1905	CTGTAAATACTATCGTTAATCAAGGTGGAACCGSACGTTTAGTAGGCCATATGACAGAT
SEQ1906	TAAAAATGACTAGTTCTAATAGCGTCTTTAAATGCTGTCTTATTTTCTAGATAATCAAC
SEQ1907	CTGTAAATACT-----
SEQ1908	TAAAAATGACTAGTTCTAATAGCGTCTTTAAATGCTGTCTTATTTTCTAGATAATCAAC
SEQ1909	CTGTAAATACTATCGTTAATCAAGGTGGAACCGGACGTTTAGTAGGCCATATGACAGAT
SEQ1910	TAAAAATGACTAGTTCTAATAGCGTCTTTAAATGCTGTCTTATTTTCTAGATAATCAAC
SEQ1911	CTGTAAATACTATCGTTAATCAAGGTGGAACCGGACGTTTAGTAGGCCATATGACAGAT
SEQ1912	TAAAAATGACTAGTTCTAATAGCGTCTTTAAATGCTGTCTTATTTTCTAGATAATCAAC
SEQ1913	CTGTAAATACTATCGTTAATCAAGGTGGAACCGGACGTTTAGTAGGCCATATGACAGAT
SEQ1914	TAAAAATGACTAGTTCTAATAGCGTCTTTAAATGCTGTCTTATTTTCTAGATAATCAAC
SEQ1901	ACTACCTTTATTTGAAACTGTTTTTAAATTTTATCTGATAAGTCAATGACCTTATCGTA
SEQ1902	ACTACCTTTATTTGAAACTGTTTTTAAATTTTATCTGATAAGTCAATGACCTTATCGTA
SEQ1903	GCATTGGTTGTTTTAAAGCTTTAGCAGCTCAAGGTTTCAGTGCTAAAAATAAAATAATT
SEQ1904	ACTACCTTTATTTGAAACTGTTTTTAAATTTTATCTGATAAGTCAATGACCTTATCGTA
SEQ1905	GCATTGGTTGTTTTAAAGCTTTAGCAGCTCAAGGTTTCAGTGCTAAAAATAAAATAGTT
SEQ1906	ACTACCTTTATTTGAAACTGTTTTTAAATTTTATCTGATAAGTCAATGACCTTATCGTA
SEQ1907	-----
SEQ1908	ACTACCTTTATTTGAAACTGTTTTTAAATTTTATCTGATAAGTCAATGACCTTATCGTA
SEQ1909	GCATTGGTTGTTTTAAAGCTTTAGCAGCTCAAGGTTTCAGTGCTAAAAATAAAATAGTT
SEQ1910	ACTACCTTTATTTGAAACTGTTTTTAAATTTTATCTGATAAGTCAATGACCTTATCGTA
SEQ1911	-----
SEQ1912	ACTACCTTTATTTGAAACTGTTTTTAAATTTTATCTGATAAGTCAATGACCTTATCGTA
SEQ1913	GCATTGGTTGTTTTAAAGCTTTAGCAGCTCAAGGTTTCAGTGCTAAAAATAAAATAATT
SEQ1914	ACTACCTTTATTTGAAACTGTTTTTAAATTTTATCTGATAAGTCAATGACCTTATCGTA
SEQ1901	TTTGAGCTGTTACGATTAAATAATCTAATTTCCGCAACTCCCTCCATAGCTGCTTGAAC
SEQ1902	TTTGAGCTGTTACGATTAAATAATCTAATTTCCGCAACTCCCTCCATAGCTGCTTGAAC
SEQ1903	CAATAGCTGGTATTGGTGGTTCAAGGTAAAGCAGTTGCAGTTCAAGCAGCTATGGAGGGA
SEQ1904	TTTGAGCTGTTACGATTAAATAATCTAATTTCCGCAACTCCCTCCATAGCTGCTTGAAC
SEQ1905	CAATAGCTGGTATTGGTGGTTCAAGGTAAAGCAGTTGCAGTTCAAGCAGCTATGGAGGGA
SEQ1906	TTTGAGCTGTTACGATTAAATAATCTAATTTCCGCAACTCCCTCCATAGCTGCTTGAAC
SEQ1907	-----
SEQ1908	TTTGAGCTATTACGATTAAATAATCTAATTTCCGCAACTCCCTCCATAACTGCTTGAAC
SEQ1909	CAATAGCTGGTATTGGTG-----
SEQ1910	TTTGAGCTGTTACGAT-----
SEQ1911	-----
SEQ1912	TTTGAGCTGTTACGATTAAATAATCTAATTTCCGCAAC-----
SEQ1913	CAATAGCTGGTATTGGTGGTTCAAGGTAAAGCAGTTGCAGTTCAAGCAGCTATGGAGGGA
SEQ1914	TTTGAGCTATTACGATTAAATAATCTAATTTCCGCAACTCCCTCCATAGCTGCTTGAAC

Table 19: Comparative Sequences relating to SAG1680 (shikimate 5-dehydrogenase)

SEQ1901	GCAACTGCTTTACCTGAACCACCAATACCAGCTATTGTAATTATTTTATTTTAGCACT
SEQ1902	GCAACTGCTTTACCTGAACCACCAATACCAGCTATTGTAATTATTTTATTTTAGCACT
SEQ1903	TTGCGGAAATTAGATTATTTAATCGTAACAGCTCAAATTACGATAAGGTCATTGACTTA
SEQ1904	GCAACTGCTTTACCTGAACCACCAATACCAGCTATTGTAATTATTTTATTTTAGCACT
SEQ1905	TTGCGGAAATTAGATTATTTAATCGTAATAGCTCAAATTACGATAAGGTCATTGACTTA
SEQ1906	GCAACTGCTTTACCTGAACCACCAATACCAGCTATTGTAATTATTTTATTTTAGCACT
SEQ1907	-----
SEQ1908	GCAACTGCTTTACCTGAACCACCAATACCAGCTATTGTAATTATTTT-----
SEQ1909	-----
SEQ1910	-----
SEQ1911	-----
SEQ1912	-----
SEQ1913	TTGCGG-----
SEQ1914	GCAACTGCTTTACCTGAACCACCAATACCAGCTATTGTAATTATTTTATTTTAGCACT
SEQ1901	AAACCTTGAGCTGCTAAAGCTTTAAAACAACCAATGCCATCTGTCATATGGCCTACTAA
SEQ1902	AAACCTTGAGCTGCTAAAGCTTTAAAACAACCAATGCCATCTGTCATATGGCCTACTAA
SEQ1903	CAGATAAAATTAAAAACAGTTTCAAATAAAGGTAGTCGTTGATTATCTAGAAAATAAG
SEQ1904	AAACCTTGAGCTGCTAAAGCTTTAAAACAACCAATGCCATCTGTCATATGGCCTACTAA
SEQ1905	CAGATAAAATTAAAAACAGTTTCAAATAAAGGTAGTCGTTGATTATCTAGAAAATAAG
SEQ1906	AAACCTTGAGCTGCTAAAGCTTTAAAACAACCAATGCCATCTGTCATATGGCCTACTAA
SEQ1907	-----
SEQ1908	-----
SEQ1909	-----
SEQ1910	-----
SEQ1911	-----
SEQ1912	-----
SEQ1913	-----
SEQ1914	AAACCTTGAGCTGCTAAAGCTTTAAAACAACCAATGCCATCTGTCAT-TABCMARAT--
SEQ1901	CGTCCGGTTCCACCTTGATTAAACGATAGTATTTACAGCACCCACTAATTTAGCTTGAGG
SEQ1902	CGTCCGGTTCCACCTTGATTAAACGATAGTATTTACAGCACCCACTAATTTAGCTTGAGG
SEQ1903	CAGCATTTAAAGACGCTATTAGAAGTAGTCATTTTATATTGATGCTACTAGTTTAGGA
SEQ1904	CGTCCGGTTCCACCTTGATTAAACGATAGTATTTACAGCACCCACTAATTTAGCTTGAGG
SEQ1905	CAGCATTTAAAGACGCTATTAGAAGTAGTCATTTTATATTGATGCTACTAGTTTAGGA
SEQ1906	CGTCCGGTTCCACCTTGATTAAACGATAGTATTTACAGCACCCACTAATTTAGCTTGAGG
SEQ1907	-----
SEQ1908	-----
SEQ1909	-----
SEQ1910	-----
SEQ1911	-----
SEQ1912	-----
SEQ1913	-----
SEQ1914	STNCSRATNGTSASHKMATDHYDRGNAS-----
SEQ1901	GATAAATCATCTAGCAAAGGGATAACACTCTGTTTAAATGGCATTGAAACATTAAACACC
SEQ1902	GATAAATCATCTAGCAAAGGGATAACACTCTGTTTAAATGGCATTGAAACATTAAACACC
SEQ1903	TGAGGCCATTAGATAATTATAGTTTAATTAACGATCCAGATATTTTAACACCGAATTTA
SEQ1904	GATAAATCATCTAGCAAAGGGATAACACTCTGTTTAAATGGCATTGAAACATTAAACACC
SEQ1905	TGARGCCATTAGATAATTATAGTTTAATTAACGATCCAGAAATTTTAACACCCAATTTA
SEQ1906	GATAAATCATCTAGCAAAGGGATAACACTCTGTTTAAATGGCATTGAAACATTAAACACC
SEQ1907	-----
SEQ1908	-----
SEQ1909	-----
SEQ1910	-----
SEQ1911	-----
SEQ1912	-----
SEQ1913	-----
SEQ1914	-----

Table 19: Comparative Sequences relating to SAG1680 (shikimate 5-dehydrogenase)

SEQ1901	CGAATACCCAATGCCCTGACACCTCGAACAGCTTCTGTTAATTTACCCCTCTTCTACTTC
SEQ1902	CGAATACCCAATGCCCTGACACCTCGAACAGCTTCTGTTAATTTACCCCTCTTCTACTTC
SEQ1903	TAGTTGTCGACTT-----
SEQ1904	CGAATACTCAATGCCCTGACACCTCGAACAGCTTCTGTTAATTTACCCCTCTTCTACTTC
SEQ1905	TAGTTGTCGACTTGGTTTACAAGCCTAAAGAAACAGCATTGTTACGATTGTTAGACAA
SEQ1906	CGAATACCCAATGCCCTGACACCTCGAACAGCTTCTGTTAATTTACCCCTCTTCTACTTC
SEQ1907	-----
SEQ1908	-----
SEQ1909	-----
SEQ1910	-----
SEQ1911	-----
SEQ1912	-----
SEQ1913	-----
SEQ1914	-----
SEQ1901	AATGTCAGATAGGCATAATTCATGTTTTTTTCTTGAAAAGAGGTATTCACATTAAACGG
SEQ1902	AATGTCAGATAGGCATAATTCATGTTTTTTTCTTGAAAAGAGGTATTCACATTAAACGG
SEQ1903	-----
SEQ1904	AATGTCAGATAGGCATAATTCATGTTTTTTTCTTGAAAAGAGGTATTCACATTAAACGG
SEQ1905	ATGGAGTGAAACATGCTTATAATGGTCTAGGGATGCTGATTTATCAAGGAGCAGA----
SEQ1906	AATGTCAGATAGGCATAATTCATGTTTTTTTCTTGAAAAGAGGTATTCACATTAAACGG
SEQ1907	-----
SEQ1908	-----
SEQ1909	-----
SEQ1910	-----
SEQ1911	-----
SEQ1912	-----
SEQ1913	-----
SEQ1914	-----
SEQ1901	GATAGAGAGTGGCGTGCAGG-
SEQ1902	GATAGAGAGTGGCGTGCAGGA
SEQ1903	-----
SEQ1904	GATAGAGAGTGGCGTGCA---
SEQ1905	-----
SEQ1906	GATAG-----
SEQ1907	-----
SEQ1908	-----
SEQ1909	-----
SEQ1910	-----
SEQ1911	-----
SEQ1912	-----
SEQ1913	-----
SEQ1914	-----

Table 20: Comparative Sequences relating to SAG1723 (signal peptidase I)**SEQ ID NO. 2001: SAG1723 FROM THE COH1 GBS TYPE Ia STRAIN**

ATCGATTTCGATATTGTAGTGGCTAACGAAGAAGAAGGCGGCCAAAAGAAAAAATTGTTAAACGTGTCTATTGGTATGCCAGGTGATGTC
ATCAAATATAAAAATGACACCTTAACCTATTAAACAATAAAAAACAGAAGAACCTTACCTCAAGGAATATACTAAATTATTTAAAAAGGA
TAAATTAACAGAAAAATATTTCGTATAACCCACTTTTCCAAGACCTAGCACAAAGCTCTACCGCTTTCACCACTGACAGCAATGGCAGCA
GCGAATTACTACTGTCTGTCCTAAAGGCCACTACTATCTTGTGGTGATGACCGAATTGTCTCTAAAGATAGTCGTGCCGTGCGTTCC
TTCAAAA

SEQ ID NO. 2002: SAG1680 FROM THE CJB110 GBS NONTYPEABLE STRAIN (REVERSE COMPLEMENT)

TAAAGTTGACGGACACTCCATGGATCCAACCTTTAGCTGACAAGGAACAGCTAGTAGTTCTCAAACAAACAAAAATCAATCGATTTCGATA
TTGTAGTGGCTAACGAAGAAGAAGGCGGCCAAAAGAAAAAATTGTTAAACGTGTCTATTGGTATGCCAGGTGATGTCATCAAATATAAAA
AATGACACCTTAACCTATTAAACAATAAAAAACAGAAGAACCTTACCTCAAGGAATATACTAAATTATTTAAAAAGGATAAAATTACAGGA
AAAAATTTCGTATAACCCACTTTTCCAAGACCTAGCACAAAGCTCTACCGCTTTCACCTACTGACAGCAATGGCAGCAGCGAATTACTA
CTGTCTGTCCTAAAGGCCACTATTATCTTGTGGTGATGACCGAATTGTCTCTAAAGATAGTCGTGCCGTGCGTCCCTTCAA AAAATCA
ACAATTGTGGGAG

SEQ ID NO. 2003: SAG1680 FROM THE 18RS21 GBS TYPE II STRAIN

TTGACGGACACTCCATGGATCCAACCTTTAGCTGACAAGGAACAGCTAGTAGTTCTCAAACAAACAAAAATCAATCGATTTCGATATTGTA
GTGGCTAACGAAGAAGAAGGCGGCCAAAAGAAAAAATTGTTAAACGTGTCTATTGGTATGCCAGGTGATGTCATCAAATATAAAAATGA
CACCTTAACCTATTAAACAATAAAAAACAGAAGAACCTTACCTCAAGGAATATACTAAATTATTTAAAAAGGATAAAATTACAGGAAAAAT
ATTCGTATAACCCACTTTTCCAAGACCTAGCACAAAGCTCTACCGCTTTCACCACTGACAGCAATGGCAGCAGCGAATTACTACTGTC
GTGCCCTAAAGGCCACTACTATCTTGTGGTGATGACCGAATTGTCTCTAAAGATAGTCGTGCCGTGCGTCCCTTCAA AAAATCAACGAT
TGTGGGAGAGGT

SEQ ID NO. 2004: SAG1680 FROM THE 2603 V/R GBS TYPE V STRAIN (REVERSE COMPLEMENT)

AAGTTGACGGACACTCCATGGATCCAACCTTTAGCTGACAAGGAACAGCTAGTAGTTCTCAAACAAACAAAAATCAATCGATTTCGATATT
GTAGTGGCTAACGAAGAAGAAGGCGGCCAAAAGAAAAAATTGTTAAACGTGTCTATTGGTATGCCAGGTGATGTCATCAAATATAAAAAT
TGACACCTTAACCTATTAAACAATAAAAAACAGAAGAACCTTACCTCAAGGAATATACTAAATTATTTAAAAAGGATAAAATTACAGGAAA
AATATTTCGTATAACCCACTTTTCCAAGACCTAGCACAAAGCTCTACCGCTTTCACCACTGACAGCAATGGCAGCAGCGAATTACTACT
GTCTGTCCTAAAGGCCACTACTATCTTGTGGTGATGACCGAATTGTCTCTAAAGATAGTCGTGCCGTGCGTCCCTTCAA AAAATCAACGAT

SEQ ID NO. 2005: SAG1680 FROM THE M732 GBS TYPE III STRAIN (REVERSE COMPLEMENT)

TTGACGGACACTCCATGGATCCAACCTTTAGCTGACAAGGAACAGCTAGTAGTTCTCAAACAAACAAAAATCAATCGATTTCGATATTGTA
GGCTAACGAAGAAGAAGGCGGCCAAAAGAAAAAATTGTTAAACGTGTCTATTGGTATGCCAGGTGATGTCATCAAATATAAAAATGACA
CCTTAACCTATTAAACAATAAAAAACAGAAGAACCTTACCTCAAGGAATATACTAAATTATTTAAAAAGGATAAAATTACAGGAAAAATAT
TCGTATAACCCACTTTTCCAAGACCTAGCACAAAGCTCTACCGCTTTCACCACTGACAGCAATGGCAGCAGCGAATTACTACTGTCTG
GCCTAAAGGCCACTACTATCTTGTGGTGATGACCGA

SEQ ID NO. 2006: SAG1680 FROM THE M781 GBS TYPE III STRAIN

TTGACGGACACTCCATGGATCCAACCTTTAGCTGACAAGGAACAGCTAGTAGTTCTCAAACAAACAAAAATCAATCGATTTCGATATTGTA
GTGGCTAACGAAGAAGAAGGCGGCCAAAAGAAAAAATTGTTAAACGTGTCTATTGGTATGCCAGGTGATGTCATCAAATATAAAAATGA
CACCTTAACCTATTAAACAATAAAAAACAGAAGAACCTTACCTCAAGGAATATACTAAATTATTTAAAAAGGATAAAATTACAGGAAAAA
TATTTCGTATAACCCACTTTTCCAAGACCTAGCACAAAGCTCTACCGCTTTCACCACTGACAGCAATGGCAGCAGCGAATTACT

SEQ ID NO. 2007: SAG1680 FROM THE 1169NT1 GBS TYPE V STRAIN (REVERSE COMPLEMENT)

TTGGTAAAGTTGACGGACACTCCATGGATCCAACCTTTAGCTGACAAGGAACAGCTAGTAGTTCTCAAACAAACAAAAATCAATCGATTTC
GATATTGTAGTGGCTAACGAAGAAGAAGGCGGCCAAAAGAAAAAATTGTTAAACGTGTCTATTGGTATGCCAGGTGATGTCATCAAATA
TAAAAATGACACCTTAACCTATTAAACAATAAAAAACAGAAGAACCTTACCTCAAGGAATATACTAAATTATTTAAAAAGGATAAAATTAC
AGGAAAAATATTTCGTATAACCCACTTTTCCAAGACCTAGCACAAAGCTCTACCGCTTTCACCTACTGACAGCAATGGCAGCAGCGAATTT
ACCACTGTCTGCTAAAGGCCACTACTATCTTGTGGTGATGACCGAATTGTCTCTAAAGATAGTCGTGCCGTGCGGCCCTTCAA AAAA
ATCAACG

SEQ ID NO. 2008: SAG1680 FROM THE H36b GBS TYPE Ib STRAIN (REVERSE COMPLEMENT)

TTGACGGACACTCCATGGATCCAACCTTTAGCTGACAAGGAACAGCTAGTAGTTCTCAAACAAACAAAAATCAATCGATTTCGATATTGTA
GTGGCTAACGAAGAAGAAGGCGGCCAAAAGAAAAAATTGTTAAACGTGTCTATTGGTATGCCAGGTGATGTCATCAAATATAAAAATGA
CACCTTAACCTATTAAACAATAAAAAACAGAAGAACCTTACCTCAAGGAATATACTAAATTATTTAAAAAGGATAAAATTACAGGAAAAAT
ATTCGTATAACCCACTTTTCCAAGACCTAGCACAAAGCTCTACCGCTTTCACCACTGACAGCAATGGCAGCAGCGAATTACTACTGTC
GTGCCCTAAAGGCCACTACTATCTTGTGGTGATGACCGA

SEQ ID NO. 2009: SAG1680 FROM THE 090 GBS TYPE Ia STRAIN (REVERSE COMPLEMENT)

TAAAGTTGACGGACACTCCATGGATCCAACCTTTAGCTGACAAGGAACAGCTAGTAGTTCTCAAACAAACAAAAATCAATCGATTTCGATA
TTGTAGTGGCTAACGAAGAAGAAGGCGGCCAAAAGAAAAAATTGTTAAACGTGTCTATTGGTATGCCAGGTGATGTCATCAAATATAAAA
AATGACACCTTAACCTATTAAACAATAAAAAACAGAAGAACCTTACCTCAAGGAATATACTAAATTATTTAAAAAGGATAAAATTACAGGA
AAAAATTTCGTATAACCCACTTTTCCAAGACCTAGCACAAAGCTCTACCGCTTTCACCTACTGACAGCAATGGCAGCAGCGAATTACTA
CTGTCTGTCCTAAAGGCCACTATTATCTTGTGGTGATGACCGAATTGTCTCTAAAGATAGTCGTGCCGTGCGT

Table 20: Comparative Sequences relating to SAG1723 (signal peptidase I)

SEQ ID NO. 2010: SAG1680 FROM THE A909 GBS TYPE Ia STRAIN (REVERSE COMPLEMENT)
 AAAGTTGACGGACACTCCATGGATCCAACCTTTAGCTGACAAGGAACAGCTAGTCTCAACAAACAAAAATCAATCGATTTCGATAT
 TGTAGTGGCTAACGAAGAAGGCGGCCAAAAGAAAAAATGTTAAACGTGTCATTGGTATGCCAGGTGATGTCATCAAAATATAAAA
 ATGACACCTTAACCTATTAACAATAAAAAACAGAAGAACCTTACCTCAAGGAATATACTAAATTATTAAAAAGGATAAATTACAGGAA
 AAATATTCGTATAACCCACTTTTCCAAGACCTAGCACAAAGCTCTACCGCTTTACCACTGACAGCAATGGCAGCAGCGAATTTACTAC
 TGTGCTGCCTAAAGGCCACTACTATCTTGTGGTGTGACCGAATGTCTCTAAAGATAGTCGTGCCGTCCGTTCAAAAAATCAA
 CG

SEQ2001 -----
 SEQ2002 ---TAAAGTTGACGGACACTCCATGGATCCAACCTTTAGCTGACAAGGAACAGCTAGTAG
 SEQ2003 -----TTGACGGACACTCCATGGATCCAACCTTTAGCTGACAAGGAACAGCTAGTAG
 SEQ2004 -----AAGTTGACGGACACTCCATGGATCCAACCTTTAGCTGACAAGGAACAGCTAGTAG
 SEQ2005 -----TTGACGGACACTCCATGGATCCAACCTTTAGCTGACAAGGAACAGCTAGTAG
 SEQ2006 -----TTGACGGACACTCCATGGATCCAACCTTTAGCTGACAAGGAACAGCTAGTAG
 SEQ2007 TGGTAAAGTTGACGGACACTCCATGGATCCAACCTTTAGCTGACAAGGAACAGCTAGTAG
 SEQ2008 -----TTGACGGACACTCCATGGATCCAACCTTTAGCTGACAAGGAACAGCTAGTAG
 SEQ2009 ---TAAAGTTGACGGACACTCCATGGATCCAACCTTTAGCTGACAAGGAACAGCTAGTAG
 SEQ2010 ---AAAGTTGACGGACACTCCATGGATCCAACCTTTAGCTGACAAGGAACAGCTAGTAG

SEQ2001 -----ATCGATTTCGATATTGTAGTGGCTAACGAAGAAGAAGGCG
 SEQ2002 TCTCAAACAAACAAAAATCAATCGATTTCGATATTGTAGTGGCTAACGAAGAAGAAGGCG
 SEQ2003 TCTCAAACAAACAAAAATCAATCGATTTCGATATTGTAGTGGCTAACGAAGAAGAAGGCG
 SEQ2004 TCTCAAACAAACAAAAATCAATCGATTTCGATATTGTAGTGGCTAACGAAGAAGAAGGCG
 SEQ2005 TCTCAAACAAACAAAA--TAATCGATTTCGATATTGTAGTGGCTAACGAAGAAGAAGGCG
 SEQ2006 TCTCAAACAAACAAAAATCAATCGATTTCGATATTGTAGTGGCTAACGAAGAAGAAGGCG
 SEQ2007 TCTCAAACAAACAAAAATCAATCGATTTCGATATTGTAGTGGCTAACGAAGAAGAAGGCG
 SEQ2008 TCTCAAACAAACAAAAATCAATCGATTTCGATATTGTAGTGGCTAACGAAGAAGAAGGCG
 SEQ2009 TCTCAAACAAACAAAAATCAATCGATTTCGATATTGTAGTGGCTAACGAAGAAGAAGGCG
 SEQ2010 TCTCAAACAAACAAAAATCAATCGATTTCGATATTGTAGTGGCTAACGAAGAAGAAGGCG

SEQ2001 GCCAAAAGAAAAAATGTTAAACGTGTCATTGGTATGCCAGGTGATGTCATCAAATATA
 SEQ2002 GCCAAAAGAAAAAATGTTAAACGTGTCATTGGTATGCCAGGTGATGTCATCAAATATA
 SEQ2003 GCCAAAAGAAAAAATGTTAAACGTGTCATTGGTATGCCAGGTGATGTCATCAAATATA
 SEQ2004 GCCAAAAGAAAAAATGTTAAACGTGTCATTGGTATGCCAGGTGATGTCATCAAATATA
 SEQ2005 GCCAAAAGAAAAAATGTTAAACGTGTCATTGGTATGCCAGGTGATGTCATCAAATATA
 SEQ2006 GCCAAAAGAAAAAATGTTAAACGTGTCATTGGTATGCCAGGTGATGTCATCAAATATA
 SEQ2007 GCCAAAAGAAAAAATGTTAAACGTGTCATTGGTATGCCAGGTGATGTCATCAAATATA
 SEQ2008 GCCAAAAGAAAAAATGTTAAACGTGTCATTGGTATGCCAGGTGATGTCATCAAATATA
 SEQ2009 GCCAAAAGAAAAAATGTTAAACGTGTCATTGGTATGCCAGGTGATGTCATCAAATATA
 SEQ2010 GCCAAAAGAAAAAATGTTAAACGTGTCATTGGTATGCCAGGTGATGTCATCAAATATA

SEQ2001 AAAATGACACCTTAACCTATTAACAATAAAAAACAGAAGAACCTTACCTCAAGGAATATA
 SEQ2002 AAAATGACACCTTAACCTATTAACAATAAAAAACAGAAGAACCTTACCTCAAGGAATATA
 SEQ2003 AAAATGACACCTTAACCTATTAACAATAAAAAACAGAAGAACCTTACCTCAAGGAATATA
 SEQ2004 AAAATGACACCTTAACCTATTAACAATAAAAAACAGAAGAACCTTACCTCAAGGAATATA
 SEQ2005 AAAATGACACCTTAACCTATTAACAATAAAAAACAGAAGAACCTTACCTCAAGGAATATA
 SEQ2006 AAAATGACACCTTAACCTATTAACAATAAAAAACAGAAGAACCTTACCTCAAGGAATATA
 SEQ2007 AAAATGACACCTTAACCTATTAACAATAAAAAACAGAAGAACCTTACCTCAAGGAATATA
 SEQ2008 AAAATGACACCTTAACCTATTAACAATAAAAAACAGAAGAACCTTACCTCAAGGAATATA
 SEQ2009 AAAATGACACCTTAACCTATTAACAATAAAAAACAGAAGAACCTTACCTCAAGGAATATA
 SEQ2010 AAAATGACACCTTAACCTATTAACAATAAAAAACAGAAGAACCTTACCTCAAGGAATATA

SEQ2001 CTAAATTATTT-AAAAAGGATAAATTACAGGAAAAATATTTCGTATAACCCACTTTTCCAA
 SEQ2002 CTAAATTATTT-AAAAAGGATAAATTACAGGAAAAATATTTCGTATAACCCACTTTTCCAA
 SEQ2003 CTAAATTATTT-AAAAAGGATAAATTACAGGAAAAATATTTCGTATAACCCACTTTTCCAA
 SEQ2004 CTAAATTATTT-AAAAAGGATAAATTACAGGAAAAATATTTCGTATAACCCACTTTTCCAA
 SEQ2005 CTAAATTATTT-AAAAAGGATAAATTACAGGAAAAATATTTCGTATAACCCACTTTTCCAA
 SEQ2006 CTAAATTATTTTAAAAAGGATAAATTACAGGAAAAATATTTCGTATAACCCACTTTTCCAA
 SEQ2007 CTAAATTATTT-AAAAAGGATAAATTACAGGAAAAATATTTCGTATAACCCACTTTTCCAA
 SEQ2008 CTAAATTATTT-AAAAAGGATAAATTACAGGAAAAATATTTCGTATAACCCACTTTTCCAA
 SEQ2009 CTAAATTATTT-AAAAAGGATAAATTACAGGAAAAATATTTCGTATAACCCACTTTTCCAA
 SEQ2010 CTAAATTATTT-AAAAAGGATAAATTACAGGAAAAATATTTCGTATAACCCACTTTTCCAA

Table 20: Comparative Sequences relating to SAG1723 (signal peptidase I)

SEQ2001	GACCTAGCACAAAGCTCTACCGCTTTCCACCACTGACAGCAATGGCAGCAGCGAATTTACT
SEQ2002	GACCTAGCACAAAGCTCTACCGCTTTCCACCACTGACAGCAATGGCAGCAGCGAATTTACT
SEQ2003	GACCTAGCACAAAGCTCTACCGCTTTCCACCACTGACAGCAATGGCAGCAGCGAATTTACT
SEQ2004	GACCTAGCACAAAGCTCTACCGCTTTCCACCACTGACAGCAATGGCAGCAGCGAATTTACT
SEQ2005	GACCTAGCACAAAGCTCTACCGCTTTCCACCACTGACAGCAATGGCAGCAGCGAATTTACT
SEQ2006	GACCTAGCACAAAGCTCTACCGCTTTCCACCACTGACAGCAATGGCAGCAGCGAATTTACT
SEQ2007	GACCTAGCACAAAGCTCTACCGCTTTCCACCACTGACAGCAATGGCAGCAGCGAATTTACC
SEQ2008	GACCTAGCACAAAGCTCTACCGCTTTCCACCACTGACAGCAATGGCAGCAGCGAATTTACT
SEQ2009	GACCTAGCACAAAGCTCTACCGCTTTCCACCACTGACAGCAATGGCAGCAGCGAATTTACT
SEQ2010	GACCTAGCACAAAGCTCTACCGCTTTCCACCACTGACAGCAATGGCAGCAGCGAATTTACT
SEQ2001	CTGTCGTGCCTAAAGGCCACTACTATCTTGTGGTGATGACCGAATTGTCTCTAAAGAT
SEQ2002	CTGTCGTGCCTAAAGGCCACTATTATCTTGTGGTGATGACCGAATTGTCTCTAAAGAT
SEQ2003	CTGTCGTGCCTAAAGGCCACTACTATCTTGTGGTGATGACCGAATTGTCTCTAAAGAT
SEQ2004	CTGTCGTGCCTAAAGGCCACTACTATCTTGTGGTGATGACCGAATTGTCTCTAAAGAT
SEQ2005	CTGTCGTGCCTAAAGGCCACTACTATCTTGTGGTGATGACCGA-----
SEQ2006	-----
SEQ2007	CTGTCGTGCCTAAAGGCCACTACTATCTTGTGGTGATGACCGAATTGTCTCTAAAGAT
SEQ2008	CTGTCGTGCCTAAAGGCCACTACTATCTTGTGGTGATGACCGA-----
SEQ2009	CTGTCGTGCCTAAAGGCCACTATTATCTTGTGGTGATGACCGAATTGTCTCTAAAGAT
SEQ2010	CTGTCGTGCCTAAAGGCCACTACTATCTTGTGGTGATGACCGAATTGTCTCTAAAGAT
SEQ2001	GTCGTGCCGTCGGTTCCCTTCAAAA-----
SEQ2002	GTCGTGCCGTCGGTCCCTTCAAAAAATCAACAATTGTGGGAG-----
SEQ2003	GTCGTGCCGTCGGTCCCTTCAAAAAATCAACGATTGTGGGAGAGGT-----
SEQ2004	GTCGTGCCGTCGGT-----
SEQ2005	-----
SEQ2006	-----
SEQ2007	GTCGTGCCGTCGGCCCCCTTCAAAAAATCAACG-----
SEQ2008	-----
SEQ2009	GTCGTGCCGTCGGT-----
SEQ2010	GTCGTGCCGTCGGTCCCTTCAAAAAATCAACGTABCMARATVSTNCSRATNGTSAGSGN
SEQ2001	----
SEQ2002	----
SEQ2003	----
SEQ2004	----
SEQ2005	----
SEQ2006	----
SEQ2007	----
SEQ2008	----
SEQ2009	----
SEQ2010	TDAS

Table 21: Comparative Sequences relating to SAG0079 (adenylate kinase)

SEQ ID NO. 2101: SAG0079 FROM THE 2603V/R GBS TYPE V STRAIN

AATCTTTTAATTATGGGTTTGCCTGGTGTCTGGTAAAGGTACTCAAGCAGCTAAGATCGTTGAAGAATTGGTGTGCTCACATCTCA
ACAGGGGATATGTTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTT
CCTGATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAGGTTTTTACTTGTGATGGATATCCA
CGTACTATTGAACAAGCACACGCCTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGAT
CCATCATGTCTTATAGAGCGTTTGAGTGGTGTGATTATCAATCGTAAAACCTGGTGAACTTTCCACAAAGTGTTCACCCACCAGTA
GATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGA
GAACCTATTCTTGAACACTATCGTAAGCTTGGTCTTGTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTTGCAGATGTT
GAAAAAGCGTTG

SEQ ID NO. 2102: SAG0079 FROM THE 090 GBS TYPE Ia STRAIN (REVERSE COMPLEMENT)

AATCTTTTAATTATGGGTTTGCCTGGTGTCTGGTAAAGGTACTCAAGCAGCTAAGATCGTTGAAGAATTGGTGTGCTCACATCTCA
ACAGGGGATATGTTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTT
CCTGATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAGGTTTTTACTTGTGATGGATATCCA
CGTACTATTGAACAAGCACACGCCTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGAT
CCATCATGTCTTATAGAGCGTTTGAGTGGTGTGATTATCAATCGTAAAACCTGGTGAACTTTCCACAAAGTGTTCACCCACCAGTA
GATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGA
GAACCTATTCTTGAACACTATCGTAAGCTTGGTCTTGTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTTGCAGATGTT
GAAAAAGCGTTGCTAGAACTCAA

SEQ ID NO. 2103: SAG0079 FROM THE 1169NT1 GBS TYPE V STRAIN (REVERSE COMPLEMENT)

TGGTAAAGGGACTCAAGCAGCTAAGATGTTGAAGAATTTGGTGTTCGCACATCTCAACAGGGGATATGTTCCGCGCCGCAATGGC
TAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTGATCAAGTAACAAACGGGATTGTAAA
AGAGCGCTTAGCTGAGGATGATATCGCAGAAAAGGTTTTTACTTGTGATGGGTATCCACGTACTATTGAACAAGCACACGCCTTAGA
TGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATCATGTCTTATAGAGCGTTTGAGTGG
TCGTATTATCAATCGTAAAACCTGGTGAACTTTCCACAAAGTGTTCACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACG
TGAAGATGATAAGCCTGAAACTGTCAAACGTGCTTGGACGTTTATGCTCAAGGAGAACCATTCTTGAACACTATAGTAAGCT
TGGCCTTGTACAGATATTGAAGGTAATCAAGAAATAA

SEQ ID NO. 2104: SAG0079 FROM THE 18RS21 GBS TYPE II STRAIN (REVERSE COMPLEMENT)

AATCTTTTAACACCGGTTTCGCTGGTGTCTGGTAAAGGTACTCAAGCAGCTAAGATCGTTGAAGAATTTGGTGTGCTCACATCTCA
ACAGGGGATATGTTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTT
CCTGATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAGGTTTTTACTTGTGATGGATATCCA
CGTACTATTGAACAAGCACACGCCTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGAT
CCATCATGTCTTATAGAGCGTTTGAGTGGTGTGATTATCAATCGTAAAACCTGGTGAACTTTCCACAAAGTGTTCACCCACCAGTA
GATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGA
GAACCTATTCTTGAACACTATCGTAAGCTTGGTCTTGTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTTGCAGATGTT
GAAAAAGCGTTGCTAGAA

SEQ ID NO. 2105: SAG0079 FROM THE 2603V/R GBS TYPE V STRAIN (REVERSE COMPLEMENT)

AATCTTTTAATTATGGGTTTGCCTGGTGTCTGGTAAAGGTACTCAAGCAGCTAAGATCGTTGAAGAATTTGGTGTGCTCACATCTCA
ACAGGGGATATGTTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTT
CCTGATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAGGTTTTTACTTGTGATGGATATCCA
CGTACTATTGAACAAGCACACGCCTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGAT
CCATCATGTCTTATAGAGCGTTTGAGTGGTGTGATTATCAATCGTAAAACCTGGTGAACTTTCCACAAAGTGTTCACCCACCAGTA
GATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGA
GAACCTATTCTTGAACACTATCGTAAGCTTGGTCTTGTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTTGCAGATGTT
GAAAAAGCGTTG

SEQ ID NO. 2106: SAG0079 FROM THE A909 GBS TYPE Ia STRAIN (REVERSE COMPLEMENT)

AATCTTTTAATTATGGGTTTGCCTGGTGTCTGGTAAAGGTACTCAAGCAGCTAAGATCGTTGAAGAATTTGGTGTGCTCACATCTCA
ACAGGGGATATGTTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTT
CCTGATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAGGTTTTTACTTGTGATGGATATCCA
CGTACTATTGAACAAGCACACGCCTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGAT
CCATCATGTCTTATAGAGCGTTTGAGTGGTGTGATTATCAATCGTAAAACCTGGTGAACTTTCCACAAAGTGTTCACCCACCAGTA
GATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGA
GAATCTATTCTTGAACACTATCGAAAGCTTGGTCTTGTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTTGCAGATGTT

SEQ ID NO. 2107: SAG0079 FROM THE CJB110 GBS NONTYPEABLE STRAIN (REVERSE COMPLEMENT)

AATCTTTTAACACCGGTTTGCCTGGTGTCTGGTAAAGGTACTCAAGCAGCTAAGATCGTTGAAGAATTTGGTGTGCTCACATCTCA
ACAGGGGATATGTTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTT
CCTGATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAGGTTTTTACTTGTGATGGATATCCA
CGTACTATTGAACAAGCACACGCCTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGAT
CCATCATGTCTTATAGAGCGTTTGAGTGGTGTGATTATCAATCGTAAAACCTGGTGAACTTTCCACAAAGTGTTCACCCACCAGTA
GATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGA
GAACCTATTCTTGAACACTATAG

Table 21: Comparative Sequences relating to SAG0079 (adenylate kinase)

SEQ ID NO. 2108: SAG0079 FROM THE COH1 GBS TYPE III STRAIN (REVERSE COMPLEMENT)
 ATCTTTTAAATTATGGGTTTGCCTGGTGTGCTAAAGGTACTCAAGCAGCTAAGATTGTTGAAGAATTTGGTGTGCTCACATCTCAA
 CAGGGGATATGTTCCGCGCCGCAATGGCTAATCAAACCCAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTC
 CTGATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGTTTTTTACTTGTGATGGATATCCAC
 GTACTATTGAGCAAGCACACGCTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTATTATATATTAAAGTGGATC
 CAACATGCCTTATAGAGCGTTTGAGTGGCCGTATTATCAATCGTAAAACTGGTGAAACTTTCCACAAAGTGTTCACCCACCAGTAG
 ATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCTGAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAG
 AACCTATTCTTGAACACTATCGTAAGCTTGGTCTTGTTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTTGCAGATGTTG
 AAAAGCGTTGCTAG

SEQ ID NO. 2109: SAG0079 FROM THE H36b GBS TRYP Ib STRAIN (REVERSE COMPLEMENT)
 CAGGGGATATGTTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTC
 CTGATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGTTTTTTACTTGTGATGGATATCCAC
 GTACTATTGAACAAGCACACGCTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTATTATATATTAAAGTGGATC
 CATCATGTGCTTATAGAGCGTTTGAGTGGTGTGATTTATCAATCGTAAAACTGGTGAAACTTTCCACAAAGTGTTCACCCACCAGTAG
 ATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCTGAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAG
 AATCTATTCTTGAACACTATCGTAAGCTTGGTCTTGTTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTTGCAGATGTTG
 AAAAGCGTTGCT

SEQ ID NO. 2110: SAG0079 FROM THE JM9130013 GBS TYPE VIII STRAIN (REVERSE COMPLEMENT)
 AATCTTTTAAATTATGGGTTTGCCTGGTGTGCTAAAGGTACTCAAGCAGCTAAGATCGTTGAAGAATTTGGTGTGCTCACATCTCA
 ACAGGGGATATGTTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTC
 CCTGATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGTTTTTTACTTGTGATGGATATCCAC
 CGTACTATTGAACAAGCACACGCTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTATTATATATTAAAGTGGAT
 CCATCATGTCTTATAGAGCGTTTGAGTGGTGTGATTTATCAATCGTAAAACTGGTGAAACTTTCCACAAAGTGTTCACCCACCAGTA
 GATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCTGAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGA
 GAACCTATTCTTGAACACTATAAAAAGCTTGGTCTTGTTACAGATATTGAAGGTAATCA

SEQ ID NO. 2111: SAG0079 FROM THE M732 GBS TYPE III STRAIN (REVERSE COMPLEMENT)
 CTTTAAATTATGGGTTTGCCTGGTGTGCTAAAGGTACTCAAGCAGCTAAGATTGTTGAAGAATTTGGTGTGCTCACATCTCAACA
 GGGGATATGTTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCT
 GATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGTTTTTTACTTGTGATGGATATCCACGT
 ACTATTGAGCAAGCACACGCTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTATTATATATTAAAGTGGATCCA
 ACATGCCCTTATAGAGCGTTTGAGTGGCCGTATTATCAATCGTAAAACTGGTGAAACTTTCCACAAAGTGTTCACCCACCAGTAGAT
 TATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCTGAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAGAA
 CCTATTCTTGAACACTATCGTAAGCTTGGTCTTGTTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTTGCAGATGTTGAA
 AAGCGTTGCTAGAACTCAA

SEQ ID NO. 2112: SAG0079 FROM THE M781 GBS TYPE III STRAIN (REVERSE COMPLEMENT)
 AATCTTTTAAATTATGGGTTTGCCTGGTGTGCTAAAGGTACTCAAGCAGCTAAGATTGTTGAAGAATTTGGTGTGCTCACATCTCA
 ACAGGGGATATGTTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTC
 CCTGATGAAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGTTTTTTACTTGTGATGGATATCCA
 CGTACTATTGAGCAAGCACACGCTTAGATGCTACGCTTGAAGAACTAGGACTACGCTTAGATGGTGTATTATATATTAAAGTGGAT
 CCAACATGCCTTATAGAGCGTTTGAGTGGCCGTATTATCAATCGTAAAACTGGTGAAACTTTCCACAAAGTGTTCACCCACCAGTAGA
 GATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCTGAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAA

SEQ2101 ATCTTTTAAATTATGGGTTTGCCTGGTGTGCTAAAGGTACTCAAGCAGCTAAGATCGTT
 SEQ2102 ATCTTTTAAATTATGGGTTTGCCTGGTGTGCTAAAGGTACTCAAGCAGCTAAGATCGTT
 SEQ2103 -----TGGTAAAGGGACTCAAGCAGCTAAGATTGTT
 SEQ2104 ATCTTTTAAACCACGGGTTTCGCTGGTGTGCTAAAGGTACTCAAGCAGCTAAGATCGTT
 SEQ2105 ATCTTTTAAATTATGGGTTTGCCTGGTGTGCTAAAGGTACTCAAGCAGCTAAGATCGTT
 SEQ2106 ATCTTTTAAATTATGGGTTTGCCTGGTGTGCTAAAGGTACTCAAGCAGCTAAGATCGTT
 SEQ2107 ATCTTTTAAACCACGGGTTTGCCTGGTGTGCTAAAGGTACTCAAGCAGCTAAGATCGTT
 SEQ2108 ATCTTTTAAATTATGGGTTTGCCTGGTGTGCTAAAGGTACTCAAGCAGCTAAGATTGTT
 SEQ2109 -----
 SEQ2110 ATCTTTTAAATTATGGGTTTGCCTGGTGTGCTAAAGGTACTCAAGCAGCTAAGATCGTT
 SEQ2111 --CTTTTAAATTATGGGTTTGCCTGGTGTGCTAAAGGTACTCAAGCAGCTAAGATTGTT
 SEQ2112 ATCTTTTAAATTACGGGTTTGCCTGGTGTGCTAAAGGTACTCAAGCAGCTAAGATTGTT

SEQ2101 AAGAATTTGGTGTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTAAT
 SEQ2102 AAGAATTTGGTGTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTAAT
 SEQ2103 AAGAATTTGGTGTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTAAT
 SEQ2104 AAGAATTTGGTGTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTAAT
 SEQ2105 AAGAATTTGGTGTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTAAT
 SEQ2106 AAGAATTTGGTGTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTAAT
 SEQ2107 AAGAATTTGGTGTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTAAT
 SEQ2108 AAGAATTTGGTGTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTAAT

Table 21: Comparative Sequences relating to SAG0079 (adenylate kinase)

SEQ2109	-----CAGGGGATATGTTCCGCGCCGCAATGGCTAAT
SEQ2110	AAGAATTTGGTGTGTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTAAT
SEQ2111	AAGAATTTGGTGTGTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTAAT
SEQ2112	AAGAATTTGGTGTGTGCTCACATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTAAT
SEQ2101	CAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTGAT
SEQ2102	CAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTGAT
SEQ2103	CAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTGAT
SEQ2104	CAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTGAT
SEQ2105	CAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTGAT
SEQ2106	CAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTGAT
SEQ2107	CAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTGAT
SEQ2108	CAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTGAT
SEQ2109	CAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTGAT
SEQ2110	CAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTGAT
SEQ2111	CAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTGAT
SEQ2112	CAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTGAT
SEQ2101	AAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGT
SEQ2102	AAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGT
SEQ2103	AAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGT
SEQ2104	AAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGT
SEQ2105	AAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGT
SEQ2106	AAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGT
SEQ2107	AAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGT
SEQ2108	AAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGT
SEQ2109	AAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGT
SEQ2110	AAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGT
SEQ2111	AAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGT
SEQ2112	AAGTAACAAACGGGATTGTAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGT
SEQ2101	TTTTTACTTGATGGATATCCACGTACTATTGAACAAGCACACGCCTTAGATGCTACGCTT
SEQ2102	TTTTTACTTGATGGATATCCACGTACTATTGAACAAGCACACGCCTTAGATGCTACGCTT
SEQ2103	TTTTTACTTGATGGATATCCACGTACTATTGAACAAGCACACGCCTTAGATGCTACGCTT
SEQ2104	TTTTTACTTGATGGATATCCACGTACTATTGAACAAGCACACGCCTTAGATGCTACGCTT
SEQ2105	TTTTTACTTGATGGATATCCACGTACTATTGAACAAGCACACGCCTTAGATGCTACGCTT
SEQ2106	TTTTTACTTGATGGATATCCACGTACTATTGAACAAGCACACGCCTTAGATGCTACGCTT
SEQ2107	TTTTTACTTGATGGATATCCACGTACTATTGAACAAGCACACGCCTTAGATGCTACGCTT
SEQ2108	TTTTTACTTGATGGATATCCACGTACTATTGAACAAGCACACGCCTTAGATGCTACGCTT
SEQ2109	TTTTTACTTGATGGATATCCACGTACTATTGAACAAGCACACGCCTTAGATGCTACGCTT
SEQ2110	TTTTTACTTGATGGATATCCACGTACTATTGAACAAGCACACGCCTTAGATGCTACGCTT
SEQ2111	TTTTTACTTGATGGATATCCACGTACTATTGAACAAGCACACGCCTTAGATGCTACGCTT
SEQ2112	TTTTTACTTGATGGATATCCACGTACTATTGAACAAGCACACGCCTTAGATGCTACGCTT
SEQ2101	GAAGAAGTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATCATGTCTT
SEQ2102	GAAGAAGTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATCATGTCTT
SEQ2103	GAAGAAGTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATCATGTCTT
SEQ2104	GAAGAAGTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATCATGTCTT
SEQ2105	GAAGAAGTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATCATGTCTT
SEQ2106	GAAGAAGTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATCATGTCTT
SEQ2107	GAAGAAGTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATCATGTCTT
SEQ2108	GAAGAAGTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATCATGTCTT
SEQ2109	GAAGAAGTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATCATGTCTT
SEQ2110	GAAGAAGTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATCATGTCTT
SEQ2111	GAAGAAGTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATCATGTCTT
SEQ2112	GAAGAAGTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATCATGTCTT
SEQ2101	ATAGAGCGTTTGAGTGGTCGTATTATCAATCGTAAAACTGGTGAAACTTTCCACAAAAGTG
SEQ2102	ATAGAGCGTTTGAGTGGTCGTATTATCAATCGTAAAACTGGTGAAACTTTCCACAAAAGTG
SEQ2103	ATAGAGCGTTTGAGTGGTCGTATTATCAATCGTAAAACTGGTGAAACTTTCCACAAAAGTG
SEQ2104	ATAGAGCGTTTGAGTGGTCGTATTATCAATCGTAAAACTGGTGAAACTTTCCACAAAAGTG
SEQ2105	ATAGAGCGTTTGAGTGGTCGTATTATCAATCGTAAAACTGGTGAAACTTTCCACAAAAGTG
SEQ2106	ATAGAGCGTTTGAGTGGTCGTATTATCAATCGTAAAACTGGTGAAACTTTCCACAAAAGTG
SEQ2107	ATAGAGCGTTTGAGTGGTCGTATTATCAATCGTAAAACTGGTGAAACTTTCCACAAAAGTG
SEQ2108	ATAGAGCGTTTGAGTGGTCGTATTATCAATCGTAAAACTGGTGAAACTTTCCACAAAAGTG
SEQ2109	ATAGAGCGTTTGAGTGGTCGTATTATCAATCGTAAAACTGGTGAAACTTTCCACAAAAGTG
SEQ2110	ATAGAGCGTTTGAGTGGTCGTATTATCAATCGTAAAACTGGTGAAACTTTCCACAAAAGTG
SEQ2111	ATAGAGCGTTTGAGTGGTCGTATTATCAATCGTAAAACTGGTGAAACTTTCCACAAAAGTG
SEQ2112	ATAGAGCGTTTGAGTGGTCGTATTATCAATCGTAAAACTGGTGAAACTTTCCACAAAAGTG

Table 21: Comparative Sequences relating to SAG0079 (adenylate kinase)

SEQ2101	TTCAACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCT
SEQ2102	TTCAACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCT
SEQ2103	TTCAACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCT
SEQ2104	TTCAACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCT
SEQ2105	TTCAACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCT
SEQ2106	TTCAACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCT
SEQ2107	TTCAACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCT
SEQ2108	TTCAACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCT
SEQ2109	TTCAACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCT
SEQ2110	TTCAACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCT
SEQ2111	TTCAACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCT
SEQ2112	TTCAACCCACCAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCT
SEQ2101	GAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCTTGAACAC
SEQ2102	GAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCTTGAACAC
SEQ2103	GAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCTTGAACAC
SEQ2104	GAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCTTGAACAC
SEQ2105	GAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCTTGAACAC
SEQ2106	GAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAGAATCTATTCTTGAACAC
SEQ2107	GAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCTTGAACAC
SEQ2108	GAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCTTGAACAC
SEQ2109	GAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAGAATCTATTCTTGAACAC
SEQ2110	GAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCTTGAACAC
SEQ2111	GAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCTTGAACAC
SEQ2112	GAAACTGTCAAACGTCGCTTGGACGTTAATATTGCTCAATABCMARATVSTNCSR--AT
SEQ2101	ATCGTAAGCTTGGTCTTGTTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTT
SEQ2102	ATCGTAAGCTTGGTCTTGTTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTT
SEQ2103	ATAGTAAGCTTGGCCTTGTTACAGATATTGAAGGTAATCAAGAAATAA-----
SEQ2104	ATCGTAAGCTTGGTCTTGTTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTT
SEQ2105	ATCGTAAGCTTGGTCTTGTTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTT
SEQ2106	ATCGAAAGCTTGGTCTTGTTACAGATATTGAAGGTAA-----
SEQ2107	ATAG-----
SEQ2108	ATCGTAAGCTTGGTCTTGTTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTT
SEQ2109	ATCGTAAGCTTGGTCTTGTTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTT
SEQ2110	ATAAAAAGCTTGGTCTTGTTACAGATATTGAAGGTAATCA-----
SEQ2111	ATCGTAAGCTTGGTCTTGTTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTT
SEQ2112	GTSAGADNYATKNAS-----
SEQ2101	CAGATGTTGAAAAAGCGTTG-----
SEQ2102	CAGATGTTGAAAAAGCGTTGCTAGAACTCAAA
SEQ2103	-----
SEQ2104	CAGATGTTGAAAAAGCGTTGCTAGAA-----
SEQ2105	CAGATGTTGAAAAAGCGTTG-----
SEQ2106	-----
SEQ2107	-----
SEQ2108	CAGATGTTGAAAAAGCGTTGCTAG-----
SEQ2109	CAGATGTTGAAAAAGCGTTGCT-----
SEQ2110	-----
SEQ2111	CAGATGTTGAAAAAGCGTTGCTAGAACTCAAA
SEQ2112	-----

Table 21: Comparative Sequences relating to SAG0079 (adenylate kinase)

>SEQ ID NO 2150:090 frame: 1
 NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGR LAKSYIDKGELVPD
 EVTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINIKVDP SCL
 IERLSGRIINRKTGETFHKVFNP PVDYKEEDYYQREDDKPETVKRRLDVNIAQGEP ILEH
 YRKLGLVTDIEGNQEITEVFADVEKALLEK

>SEQ ID NO 2151:114_1169NT frame: 2
 GKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGR LAKSYIDKGELVPDQVTNGIVKER
 LAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINIKVDP SCLIERLSGRIIN
 RKTGETFHKVFNP PVDYKEEDYYQREDDKPETVKRRLDVHIAQGEP ILEHYSKLGLVTDI
 EGNQEI

>SEQ ID NO 2152: 114_18RS21 frame: 1
 NLLTTGSPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGR LAKSYIDKGELVPD
 EVTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINIKVDP SCL
 IERLSGRIINRKTGETFHKVFNP PVDYKEEDYYQREDDKPETVKRRLDVNIAQGEP ILEH
 YRKLGLVTDIEGNQEITEVFADVEKALLE

>SEQ ID NO 2153: 114_2603 frame: 1
 NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGR LAKSYIDKGELVPD
 EVTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINIKVDP SCL
 IERLSGRIINRKTGETFHKVFNP PVDYKEEDYYQREDDKPETVKRRLDVNIAQGEP ILEH
 YRKLGLVTDIEGNQEITEVFADVEKAL

>SEQ ID NO 2154: 114_A909 frame: 1
 NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGR LAKSYIDKGELVPD
 EVTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINIKVDP SCL
 IERLSGRIINRKTGETFHKVFNP PVDYKEEDYYQREDDKPETVKRRLDVNIAQGES ILEH
 YRKLGLVTDIEG

>SEQ ID NO 2155:114_A909 frame: 1
 NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGR LAKSYIDKGELVPD
 EVTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINIKVDP SCL
 IERLSGRIINRKTGETFHKVFNP PVDYKEEDYYQREDDKPETVKRRLDVNIAQGES ILEH
 YRKLGLVTDIEG

>SEQ ID NO 2156: 114_CJB110 frame: 1
 NLLITGLLGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGR LAKSYIDKGELVPD
 EVTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINIKVDP SCL
 IERLSGRIINRKTGETFHKVFNP PVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPI LEH
 Y

>SEQ ID NO 2157: 114_COH1 frame: 3
 LLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTOMGR LAKSYIDKGELVPDE
 VTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINIKVDPTCLI
 ERLSGRIINRKTGETFHKVFNP PVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPI LEHY
 RKLGLVTDIEGNQEITEVFADVEKALL

>SEQ ID NO 2158: 114_H36B frame: 3
 GDMFRAAMANQTEMGR LAKSYIDKGELVPDEV TNGIVKERLAEDDIAEKGFLLDGYPR TI
 EQAHALDATLEELGLRLDGVINIKVDP SCLIERLSGRIINRKTGETFHKVFNP PVDYKEE
 DYYQREDDKPETVKRRLDVNIAQGES ILEHYRKLGLVTDIEGNQEITEVFADVEKAL

>SEQ ID NO 2159: 114_JM9130013 frame: 1
 NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGR LAKSYIDKGELVPD
 EVTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINIKVDP SCL
 IERLSGRIINRKTGETFHKVFNP PVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPI LEH
 YKKLGLVTDIEGN

>SEQ ID NO 2160:114_M732 frame: 1
 LLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTOMGR LAKSYIDKGELVPDE
 VTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINIKVDPTCLI
 ERLSGRIINRKTGETFHKVFNP PVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPI LEHY
 RKLGLVTDIEGNQEITEVFADVEKALLEK

>SEQ ID NO 2161: 114_M781 frame: 1
 NLLITGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTOMGR LAKSYIDKGELVPD
 EVTNGIVKERLAEDDIAEKGFLLDGYPR TIEQAHALDATLEELGLRLDGVINIKVDPTCL
 IERLSGRIINRKTGETFHKVFNP PVDYKEEDYYQREDDKPETVKRRLDVNIAQ

Table 21: Comparative Sequences relating to SAG0079 (adenylate kinase)

SEQ2150	LLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAKSYIDKGELVPD
SEQ2151	-----GKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAKSYIDKGELVPD
SEQ2152	LLTTGSPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAKSYIDKGELVPD
SEQ2153	LLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAKSYIDKGELVPD
SEQ2154	LLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAKSYIDKGELVPD
SEQ2155	LLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAKSYIDKGELVPD
SEQ2156	LLTTGLLGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAKSYIDKGELVPD
SEQ2157	LLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTOMGRLAKSYIDKGELVPD
SEQ2158	-----GDMFRAAMANQTEMGRLAKSYIDKGELVPD
SEQ2159	LLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRLAKSYIDKGELVPD
SEQ2160	LLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTOMGRLAKSYIDKGELVPD
SEQ2161	LLITGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTOMGRLAKSYIDKGELVPD
SEQ2150	EVTNGIVKERLAEDDIAEKGFLLDGYPRTIEQAHALDATLEELGLRLDGVINIKVDPSC
SEQ2151	QVTNGIVKERLAEDDIAEKGFLLDGYPRTIEQAHALDATLEELGLRLDGVINIKVDPSC
SEQ2152	EVTNGIVKERLAEDDIAEKGFLLDGYPRTIEQAHALDATLEELGLRLDGVINIKVDPSC
SEQ2153	EVTNGIVKERLAEDDIAEKGFLLDGYPRTIEQAHALDATLEELGLRLDGVINIKVDPSC
SEQ2154	EVTNGIVKERLAEDDIAEKGFLLDGYPRTIEQAHALDATLEELGLRLDGVINIKVDPSC
SEQ2155	EVTNGIVKERLAEDDIAEKGFLLDGYPRTIEQAHALDATLEELGLRLDGVINIKVDPSC
SEQ2156	EVTNGIVKERLAEDDIAEKGFLLDGYPRTIEQAHALDATLEELGLRLDGVINIKVDPSC
SEQ2157	EVTNGIVKERLAEDDIAEKGFLLDGYPRTIEQAHALDATLEELGLRLDGVINIKVDPSC
SEQ2158	EVTNGIVKERLAEDDIAEKGFLLDGYPRTIEQAHALDATLEELGLRLDGVINIKVDPSC
SEQ2159	EVTNGIVKERLAEDDIAEKGFLLDGYPRTIEQAHALDATLEELGLRLDGVINIKVDPSC
SEQ2160	EVTNGIVKERLAEDDIAEKGFLLDGYPRTIEQAHALDATLEELGLRLDGVINIKVDPSC
SEQ2161	EVTNGIVKERLAEDDIAEKGFLLDGYPRTIEQAHALDATLEELGLRLDGVINIKVDPSC
SEQ2150	IERLSGRIINRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPIL
SEQ2151	IERLSGRIINRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPIL
SEQ2152	IERLSGRIINRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPIL
SEQ2153	IERLSGRIINRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPIL
SEQ2154	IERLSGRIINRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPIL
SEQ2155	IERLSGRIINRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPIL
SEQ2156	IERLSGRIINRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPIL
SEQ2157	IERLSGRIINRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPIL
SEQ2158	IERLSGRIINRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPIL
SEQ2159	IERLSGRIINRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPIL
SEQ2160	IERLSGRIINRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVNIAQGEPIL
SEQ2161	IERLSGRIINRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVNIAQ-----
SEQ2150	RKLGLVTDIEGNQEITEVFADVEKALLELK
SEQ2151	SKLGLVTDIEGNQEITEVFADVEKALLELK
SEQ2152	RKLGLVTDIEGNQEITEVFADVEKALLELK
SEQ2153	RKLGLVTDIEGNQEITEVFADVEKALLELK
SEQ2154	RKLGLVTDIEGNQEITEVFADVEKALLELK
SEQ2155	RKLGLVTDIEGNQEITEVFADVEKALLELK
SEQ2156	RKLGLVTDIEGNQEITEVFADVEKALLELK
SEQ2157	RKLGLVTDIEGNQEITEVFADVEKALLELK
SEQ2158	RKLGLVTDIEGNQEITEVFADVEKALLELK
SEQ2159	RKLGLVTDIEGNQEITEVFADVEKALLELK
SEQ2160	RKLGLVTDIEGNQEITEVFADVEKALLELK
SEQ2161	-----

**Table 22: Comparative Sequences relating to SAG0093
(D-alanyl-D-alanine carboxypeptidase family protein)**

SEQ ID NO. 2201: SAG0093 FROM THE 090 GBS TYPE Ia STRAIN (REVERSE COMPLEMENT)
AAGCCTAACAGTCAACAATCATCATCTCAAAAGTTGAGGAATGAGGATATAAAAAAGATATCCTCTCAAAAAAGAAATAAGAAATTA
CAATTACCAGCTGTATCATCAAAAGATTGGAACCTTGATTGTTGGTCAATCGTGACCATAAACATGAAGAATTAAGTCCAGATGTGGTT
CCTGTTGAAAATATTTATTTGGATAAACGTTATTACGAAGCAAGCTACTCAGTTTTTAGAGGCTGCTAGAGCAATTGATTACAGAGAA
CATTTAATTTCCGGTTATCGTAGTGTTCCTATCAGGAGAAGTTGTTCAATTCTTATGTTACTCAAGAGATGACTAGTAACCCCTAAT
TTGACGAGGGGACAAGCAGAAAAGTTGGTAAAAAATTACTCTCAGCCTGCAGGTGCTAGTGAACACCAGACTGGATTAGCGATGGAT
ATGAGTACTGTAGATTCTTTGAATGAGAGCGATCCTAGAGTAGTCAGTCAGTTGAAAAAGATAGCTCCACAATATGGTTTTGTCTTA
CGGTTTCCGGATGGTAAAACAGCAGAAACAGGGGTAGGTTATGAAGATTGGCATTACCGCTATGTTGGGGTAGAGTCTGCAAAATAT
ATGGCCAAACATCATTTAATATTAGAAGATAACATACTTTATTAAAGGAGAATAACCAA

SEQ ID NO. 2202: SAG0093 FROM THE 1169NT1 GBS TYPE V STRAIN (REVERSE COMPLEMENT)
AAGCCTAACAGTCAACAATCATCACTCAAAAGTTGAGGAATGAGGATATAAAAAAGATATCCTCTCAAAAAAGAAATAAGAAATTA
CGATTACCAGCTGTATCATCAAAAGATTGGAACCTTGATTGTTGGTCAATCGTGACCATAAACATGAAGAATTAAGTCCAGATGTGGTT
CCTGTTGAAAATATTTATTTGGATAAACGTTATTACGAAGCAAGCTACTCAGTTTTTAGAGGCTGCTAGAGCAATTGATTACAGAGAA
CATTTAATTTCCGGTTATCGTAGTGTTCCTATCAGGAGAAGTTGTTCAATTCTTATGTTACTCAAGAGATGACTAGTAACCCCTAAT
TTGACGAGGGGACAAGCAGAAAAGTTGGTAAAAAATTACTCTCAGCCTGCAGGTGCTAGTGAACACCAGACTGGATTAGCGATGGAT
ATGAGTACTGTAGATTCTTTGAATGAGAGCGATCCTAGAGTAGTCAGTCAGTTGAAAAAGATAGCTCCACAATATGGTTTTGTCTTA
CGGTTTCCGGATGGTAAAACAGCAGAAACAGGGGTAGGTTATGAAGATTGGCATTACCGCTATGTTGGGGTAGAGTCTGCAAAATAT
ATGGCCGAACATCGTTTAACTATTAGAAGATAACATACTTTATTAAAGGAGAATAACCAA

SEQ ID NO. 2203: SAG0093 FROM THE 18RS21 GBS TYPE II STRAIN
AAGCCTAACAGTCAACAATCATCATCTCAAAAGTTGAGGAATGAGGATATAAAAAAGATATCCTCTCAAAAAAGAAATAAGAAATTA
CAATTACCAGCTGTATCATCAAAAGATTGGAACCTTGATTGTTGGTCAATCGTGACCATAAACATGAAGAATTAAGTCCAGATGTGGTT
CCTGTTGAAAATATTTATTTGGATAAACGTTATTACGAAGCAAGCTACTCAGTTTTTAGAGGCTGCTAGAGCAATTGATTACAGAGAA
CATTTAATTTCCGGTTATCGTAGTGTTCCTATCAGGAGAAGTTGTTCAATTCTTATGTTACTCAAGAGATGACTAGTAACCCCTAAT
TTGACGAGGGGACAAGCAGAAAAGTTGGTAAAAAATTACTCTCAGCCTGCAGGTGCTAGTGAACACCAGACTGGATTAGCGATGGAT
ATGAGTACTGTAGATTCTTTGAATGAGAGCGATCCTAGAGTAGTCAGTCAGTTGAAAAAGATAGCTCCACAATATGGTTTTGTCTTA
CGGTTTCCGGATGGTAAAACAGCAGAAACAGGGGTAGGTTATGAAGATTGGCATTACCGCTATGTTGGGGTAGAGTCTGCAAAATAT
ATGGCCAAACATCATTTAATATTAGAAGATAACATACTTTATTAAAGGAGAATAACCAA

SEQ ID NO. 2204: SAG0093 FROM THE 2603V/R GBS TYPE V STRAIN
ACAGTCAACAATCATCATCTCAAAAGTTGAGGAATGAGGATATAAAAAAGATATCCTCTCAAAAAAGAAATAAGAAATTACAAATTAC
CAGCTGTATCATCAAAAGATTGGAACCTTGATTGTTGGTCAATCGTGACCATAAACATGAAGAATTAAGTCCAGATGTGGTTCTGTG
AAAATATTTATTTGGATAAACGTTATTACGAAGCAAGCTACTCAGTTTTTAGAGGCTGCTAGAGCAATTGATTACAGAGAACTTTAA
TTTCCGGTTATCGTAGTGTTCCTATCAGGAGAAGTTGTTCAATTCTTATGTTACTCAAGAGATGACTAGTAACCCCTAATTGACGA
GGGGACAAGCAGAAAAGTTGGTAAAAAATTACTCTCAGCCTGCAGGTGCTAGTGAACACCAGACTGGATTAGCGATGGATATGAGTA
CTGTAGATTCTTTGAATGAGAGCGATCCTAGAGTAGTCAGTCAGTTGAAAAAGATAGCTCCACAATATGGTTTTGTCTTA
CGGATGGTAAAACAGCAGAAACAGGGGTAGGTTATGAAGATTGGCATTACCGCTATGTTGGGGTAGAGTCTGCAAAATATATGGCCA
AACATCATTTAATATTAGAAGATAACATACTTTATTAAAGGAGAATAACCAAACCCAGCTTTCTTGTACAA

SEQ ID NO. 2205: SAG0093 FROM THE A909 GBS TYPE Ia STRAIN
AAGCCTAACAGTCAACAATCATCATCTCAAAAGTTGAGGAATGAGGATATAAAAAAGATATCCTCTCAAAAAAGAAATAAGAAATTA
CGATTACCAGCTGTATCATCAAAAGATTGGAACCTTGATTGTTGGTCAATCGTGACCATAAACATGAAGAATTAAGTCCAGATGTGGTT
CCTGTTGAAAATATTTATTTGGATAAACGTTATTACGAAGCAAGCTACTCAGTTTTTAGAGGCTGCTAGAGCAATTGATTACAGAGAA
CATTTAATTTCCGGTTATCGTAGTGTTCCTATCAGGAGAAGTTGTTCAATTCTTATGTTACTCAAGAAATGACTAGTAACCCCTAAT
TTGACGAAGGAACAAGCAGAAAAGTTGGTAAAAAATTACTCTCAGCCTGCAGGTGCTAGTGAACACCAGACTGGATTAGCGATGGAT
ATGAGTACTGTAGATTCTTTGAATGAGAGCGATCCTAGAGTAGTCAGTCAGTTGAAAAAGATAGCTCCACAATATGGTTTTGTCTTA
CGGTTTCCGGATGGTAAAACAGCAGAAACAGGGGTAGGTTATGAAGATTGGCATTACCGCTATGTTGGGGTAGAGTCTGCAAAATAT
ATGGCCAAACATCATTTAATATTAGAAGATAACATACTTTATTAAAGGAGAATAACCAA

SEQ ID NO. 2206: SAG0093 FROM THE CJB110 GBS NONTYPEABLE STRAIN
AAGCCTAACAGTCAACAATCATCATCTCAAAAGTTGAGGAATGAGGATATAAAAAAGATATCCTCTCAAAAAAGAAATAAGAAATTT
ACAATTACCAGCTGTATCATCAAAAGATTGGAACCTTGATTGTTGGTCAATCGTGACCATAAACATGAAGAATTAAGTCCAGATGTGGTT
TCCGTTGAAAATATTTATTTGGATAAACGTTATTACGAAGCAAGCTACTCAGTTTTTAGAGGCTGCTAGAGCAATTGATTACAGAGAA
ACATTTAATTTCCGGTTATCGTAGTGTTCCTATCAGGAGAAGTTGTTCAATTCTTATGTTACTCAAGAGATGACTAGTAACCCCTAA
TTTGACGAGGGGACAAGCAGAAAAGTTGGTAAAAAATTACTCTCAGCCTGCAGGTGCTAGTGAACACCAGACTGGATTAGCGATGGAT
TATGAGTACTGTAGATTCTTTGAATGAGAGCGATCCTAGAGTAGTCAGTCAGTTGAAAAAGATAGCTCCACAATATGGTTTTGTCTTA
ACGGTTTCCGGATGGTAAAACAGCAGAAACAGGGGTAGGTTATGAAGATTGGCATTACCGCTATGTTGGGGTAGAGTCTGCAAAATAT
TATGGCCAAACATCATTTAATATTAGAAGATAACATACTTTATTAAAGGAGAATAACCAA

**Table 22: Comparative Sequences relating to SAG0093
(D-alanyl-D-alanine carboxypeptidase family protein)**

SEQ ID NO. 2207: SAG0093 FROM THE COH1 GBS TYPE III STRAIN

CCTAACAGTCAACAATCATCATCTCTCAAAAGTTGAGGAATGAGGATATAAAAAAGACATCCTCTCAAAAAAGAAATTAAGAAATTACG
ATTACCAGCTGTATCATCAAAAGATTGGAACCTTGATTTTGGTCAATCGTGACCATAAACATGAAGAATTAAGTCCAGATGTGGTGCC
TGTTGAAAATATTTATTTGGATAAACGTATTACGAAGCAAGCTACTCAGTTTTTAGAGGCTGCTAGAGCAATTGATTCACGAGAAC
TTTAATTTTCGGGTATCGTAGTGTTCCTATCAGGAGAAGTTGTTCAATTCTTATGTTACTCAAGAGATGACTAGTAACCTAATTT
GACGAGGGGACAAGCAGAAAAGTTGGTAAAACTTACTCTCAGCCTGCAGGTGCTAGTGAACACCAGACTGGATTAGCGATGGATAT
GAGTACTGTAGATTCTTTGAATGAGAGCGATCCTAGAGTAGTCAGTCAGTTGAAAAAGATAGCTCCACAATATGGTTTTGTCTTACG
GTTTCCGGATGGTAAACAGCAGAAACAGGGGTAGGTTATGAAGATTGGCATTACCGCTATGTTGGGGTAGAGTCTGCAAAATATAT
GGTCAAACATCATTTAAACATTAGAAGAATACATAACTTTATTAAAGGAGAATAACCAAAACCCAGCTTTCTTGTACAA

SEQ ID NO. 2208: SAG0093 FROM THE H36b GBS TYPE Ib STRAIN

AAGCCTAACAGTCAACAATCATCATCTCAAAAGTTGAGGAATGAGGATATAAAAAAGACATCCTCTCAAAAAAGAAATTAAGAAATTA
CGATTACCAGCTGTATCATCAAAAGATTGGAACCTTGATTTTGGTCAATCGTGACCATAAACATGAAGAATTAAGTCCAGATGTGGTG
CCTGTTGAAAATATTTATTTGGATAAACGTATTACGAAGCAAGCTACTCAGTTTTTAGAGGCTGCTAGAGCAATTGATTCACGAGAA
CATTAAATTTTCGGGTATCGTAGTGTTCCTATCAGGAGAAGTTGTTCAATTCTTATGTTACTCAwGAAATGACTAGTAACCTAAT
TTGACGAAGGAACAAGCAGAAAAGTTGGTAAAACTTACTCTCAGCCTGCAGGTGCTAGTGAACACCAGACTGGATTAGCGATGGAT
ATGAGTACTGTAGATTCTTTGAATGAGAGCGATCCTAGAGTAGTCAGTCAGTTGAAAAAGATAGCTCCACAATATGGTTTTGTCTTA
CGTTTTCCGGATGGTAAACAGCAGAAACAGGGGTAGGTTATGAAGATTGGCATTACCGCTATGTTGGGGTAGAGTCTGCAAAATAT
ATGGCCAAACATCATTTAAACATTAGAAGAATACATAACTTTATTAAAGGAGAATAACCAA

SEQ ID NO. 2209: SAG0093 FROM THE JM9130013 GBS TYPE VIII STRAIN

AAGCCTAACAGTCAACAATCATCATCTCAAAAGTTGAGGAATGAGGATATAAAAAAGATATCCTCTCAAAAAAGAAATTAAGAAATTA
CAATTACCAGCTGTATCATCAAAAGATTGGAACCTTGATTTTGGTCAATCGTGACCATAAACATGAAGAATTAAGTCCAGATGTGGTT
CCTGTTGAAAATATTTATTTGGATAAACGTATTACGAAGCAAGCTACTCAGTTTTTAGAGGCTGCTAGAGCAATTGATTCACGAGAA
CATTAAATTTTCGGGTATCGTAGTGTTCCTATCAGGAGAAGTTGTTCAATTCTTATGTTACTCAAGAGATGACTAGTAACCTAAT
TTGACGAGGGGACAAGCAGAAAAGTTGGTAAAACTTACTCTCAGCCTGCAGGTGCTAGTGAACACCAGACTGGATTAGCGATGGAT
ATGAGTACTGTAGATTCTTTGAATGAGAGCGATCCTAGAGTAGTCAGTCAGTTGAAAAAGATAGCTCCACAATATGGTTTTGTCTTA
CGTTTTCCGGATGGTAAACAGCAGAAACAGGGGTAGGTTATGAAGATTGGCATTACCGCTATGTTGGGGTAGAGTCTGCAAAATAT
ATGGCCAAACATCATTTAAACATTAGAAGAATACATAACTTTATTAAAGGAGAATAACCAA

SEQ ID NO. 2210: SAG0093 FROM THE M732 GBS TYPE III STRAIN

AGCCTAACAGTCAACAATCATCATCTCAAAAGTTGAGGAATGAGGATATAAAAAAGACATCCTCTCAAAAAAGAAATTAAGAAATTAC
GATTACCAGCTGTATCATCAAAAGATTGGAACCTTGATTTTGGTCAATCGTGACCATAAACATGAAGAATTAAGTCCAGATGTGGTG
CTGTTGAAAATATTTATTTGGATAAACGTATTACGAAGCAAGCTACTCAGTTTTTAGAGGCTGCTAGAGCAATTGATTCACGAGAA
ATTAAATTTTCGGGTATCGTAGTGTTCCTATCAGGAGAAGTTGTTCAATTCTTATGTTACTCAAGAGATGACTAGTAACCTAAT
TGACGAGGGGACAAGCAGAAAAGTTGGTAAAACTTACTCTCAGCCTGCAGGTGCTAGTGAACACCAGACTGGATTAGCGATGGAT
TGAGTACTGTAGATTCTTTGAATGAGAGCGATCCTAGAGTAGTCAGTCAGTTGAAAAAGATAGCTCCACAATATGGTTTTGTCTTA
GGTTTTCCGGATGGTAAACAGCAGAAACAGGGGTAGGTTATGAAGATTGGCATTACCGCTATGTTGGGGTAGAGTCTGCAAAATAT
TGGTCAAACATCATTTAAACATTAGAAGAATACATAACTTTATTAAAGGAGAATAACCAAAACCCAGCTTTCTT

SEQ ID NO. 2211: SAG0093 FROM THE M781 GBS TYPE III STRAIN

AAGCCTAACAGTCAACAATCATCATCTCAAAAGTTGAGGAATGAGGATATAAAAAAGACATCCTCTCAAAAAAGAAATTAAGAAATTA
CGATTACCAGCTGTATCATCAAAAGATTGGAACCTTGATTTTGGTCAATCGTGACCATAAACATGAAGAATTAAGTCCAGATGTGGTG
CCTGTTGAAAATATTTATTTGGATAAACGTATTACGAAGCAAGCTACTCAGTTTTTAGAGGCTGCTAGAGCAATTGATTCACGAGAA
CATTAAATTTTCGGGTATCGTAGTGTTCCTATCAGGAGAAGTTGTTCAATTCTTATGTTACTCAAGAGATGACTAGTAACCTAAT
TTGACGAGGGGACAAGCAGAAAAGTTGGTAAAACTTACTCTCAGCCTGCAGGTGCTAGTGAACACCAGACTGGATTAGCGATGGAT
ATGAGTACTGTAGATTCTTTGAATGAGAGCGATCCTAGAGTAGTCAGTCAGTTGAAAAAGATAGCTCCACAATATGGTTTTGTCTTA
CGTTTTCCGGATGGTAAACAGCAGAAACAGGGGTAGGTTATGAAGATTGGCATTACCGCTATGTTGGGGTAGAGTCTGCAAAATAT
ATGGTCAAACATCATTTAAACATTAGAAGAATACATAACTTTATTAAAGGAGAATAACCAA

SEQ2201	AGCCTAACAGTCAACAATCATCATCTCAAAAGTTGAGGAATGAGGATATAAAAAAGATA
SEQ2202	AGCCTAACAGTCAACAATCATCACTCAAAAGTTGAGGAATGAGGATATAAAAAAGATA
SEQ2203	AGCCTAACAGTCAACAATCATCATCTCAAAAGTTGAGGAATGAGGATATAAAAAAGATA
SEQ2204	-----ACAGTCAACAATCATCATCTCAAAAGTTGAGGAATGAGGATATAAAAAAGATA
SEQ2205	AGCCTAACAGTCAACAATCATCATCTCAAAAGTTGAGGAATGAGGATATAAAAAAGATA
SEQ2206	AGCCTAACAGTCAACAATCATCATCTCAAAAGTTGAGGAATGAGGATATAAAAAAGATA
SEQ2207	--CCTAACAGTCAACAATCATCATCTCAAAAGTTGAGGAATGAGGATATAAAAAAGATA
SEQ2208	AGCCTAACAGTCAACAATCATCATCTCAAAAGTTGAGGAATGAGGATATAAAAAAGATA
SEQ2209	AGCCTAACAGTCAACAATCATCATCTCAAAAGTTGAGGAATGAGGATATAAAAAAGATA
SEQ2210	AGCCTAACAGTCAACAATCATCATCTCAAAAGTTGAGGAATGAGGATATAAAAAAGATA
SEQ2211	AGCCTAACAGTCAACAATCATCATCTCAAAAGTTGAGGAATGAGGATATAAAAAAGATA

**Table 22: Comparative Sequences relating to SAG0093
(D-alanyl-D-alanine carboxypeptidase family protein)**

SEQ2201	TCCTCTCAAAAAAGAAAT-AAGAAATT-ACAATTACCAGCTGTATCATCAAAAGATTGGA
SEQ2202	TCCTCTCAAAAAAGAAAT-AAGAAATT-ACGATTACCAGCTGTATCATCAAAAGATTGGA
SEQ2203	TCCTCTCAAAAAAGAAAT-AAGAAATT-ACAATTACCAGCTGTATCATCAAAAGATTGGA
SEQ2204	TCCTCTCAAAAAAGAAAT-AAGAAATT-ACAATTACCAGCTGTATCATCAAAAGATTGGA
SEQ2205	TCCTCTCAAAAAAGAAAT-AAGAAATT-ACGATTACCAGCTGTATCATCAAAAGATTGGA
SEQ2206	TCCTCTCAAAAAAGAAAT-AAGAAATTTACAATTACCAGCTGTATCATCAAAAGATTGGA
SEQ2207	TCCTCTCAAAAAAGAAATTAAGAAATT-ACGATTACCAGCTGTATCATCAAAAGATTGGA
SEQ2208	TCCTCTCAAAAAAGAAAT-AAGAAATT-ACGATTACCAGCTGTATCATCAAAAGATTGGA
SEQ2209	TCCTCTCAAAAAAGAAAT-AAGAAATT-ACAATTACCAGCTGTATCATCAAAAGATTGGA
SEQ2210	TCCTCTCAAAAAAGAAAT-AAGAAATT-ACGATTACCAGCTGTATCATCAAAAGATTGGA
SEQ2211	TCCTCTCAAAAAAGAAAT-AAGAAATT-ACGATTACCAGCTGTATCATCAAAAGATTGGA
SEQ2201	ACTTGATTTTGGTCAATCGTGACCATAAACATGAAGAATTAAGTCCAGATGTGGTTCCTG
SEQ2202	ACTTGATTTTGGTCAATCGTGACCATAAACATGAAGAATTAAGTCCAGATGTGGTTCCTG
SEQ2203	ACTTGATTTTGGTCAATCGTGACCATAAACATGAAGAATTAAGTCCAGATGTGGTTCCTG
SEQ2204	ACTTGATTTTGGTCAATCGTGACCATAAACATGAAGAATTAAGTCCAGATGTGGTTCCTG
SEQ2205	ACTTGATTTTGGTCAATCGTGACCATAAACATGAAGAATTAAGTCCAGATGTGGTTCCTG
SEQ2206	ACTTGATTTTGGTCAATCGTGACCATAAACATGAAGAATTAAGTCCAGATGTGGTTCCTG
SEQ2207	ACTTGATTTTGGTCAATCGTGACCATAAACATGAAGAATTAAGTCCAGATGTGGTTCCTG
SEQ2208	ACTTGATTTTGGTCAATCGTGACCATAAACATGAAGAATTAAGTCCAGATGTGGTTCCTG
SEQ2209	ACTTGATTTTGGTCAATCGTGACCATAAACATGAAGAATTAAGTCCAGATGTGGTTCCTG
SEQ2210	ACTTGATTTTGGTCAATCGTGACCATAAACATGAAGAATTAAGTCCAGATGTGGTTCCTG
SEQ2211	ACTTGATTTTGGTCAATCGTGACCATAAACATGAAGAATTAAGTCCAGATGTGGTTCCTG
SEQ2201	TTGAAAATATTTATTTGGATAAACGTTATACGAAGCAAGCTACTCAGTTTTTAGAGGCTG
SEQ2202	TTGAAAATATTTATTTGGATAAACGTTATACGAAGCAAGCTACTCAGTTTTTAGAGGCTG
SEQ2203	TTGAAAATATTTATTTGGATAAACGTTATACGAAGCAAGCTACTCAGTTTTTAGAGGCTG
SEQ2204	TTGAAAATATTTATTTGGATAAACGTTATACGAAGCAAGCTACTCAGTTTTTAGAGGCTG
SEQ2205	TTGAAAATATTTATTTGGATAAACGTTATACGAAGCAAGCTACTCAGTTTTTAGAGGCTG
SEQ2206	TTGAAAATATTTATTTGGATAAACGTTATACGAAGCAAGCTACTCAGTTTTTAGAGGCTG
SEQ2207	TTGAAAATATTTATTTGGATAAACGTTATACGAAGCAAGCTACTCAGTTTTTAGAGGCTG
SEQ2208	TTGAAAATATTTATTTGGATAAACGTTATACGAAGCAAGCTACTCAGTTTTTAGAGGCTG
SEQ2209	TTGAAAATATTTATTTGGATAAACGTTATACGAAGCAAGCTACTCAGTTTTTAGAGGCTG
SEQ2210	TTGAAAATATTTATTTGGATAAACGTTATACGAAGCAAGCTACTCAGTTTTTAGAGGCTG
SEQ2211	TTGAAAATATTTATTTGGATAAACGTTATACGAAGCAAGCTACTCAGTTTTTAGAGGCTG
SEQ2201	CTAGAGCAATTGATTACGAGAACATTAAATTCGGGTTATCGTAGTGTGCCTATCAGG
SEQ2202	CTAGAGCAATTGATTACGAGAACATTAAATTCGGGTTATCGTAGTGTGCCTATCAGG
SEQ2203	CTAGAGCAATTGATTACGAGAACATTAAATTCGGGTTATCGTAGTGTGCCTATCAGG
SEQ2204	CTAGAGCAATTGATTACGAGAACATTAAATTCGGGTTATCGTAGTGTGCCTATCAGG
SEQ2205	CTAGAGCAATTGATTACGAGAACATTAAATTCGGGTTATCGTAGTGTGCCTATCAGG
SEQ2206	CTAGAGCAATTGATTACGAGAACATTAAATTCGGGTTATCGTAGTGTGCCTATCAGG
SEQ2207	CTAGAGCAATTGATTACGAGAACATTAAATTCGGGTTATCGTAGTGTGCCTATCAGG
SEQ2208	CTAGAGCAATTGATTACGAGAACATTAAATTCGGGTTATCGTAGTGTGCCTATCAGG
SEQ2209	CTAGAGCAATTGATTACGAGAACATTAAATTCGGGTTATCGTAGTGTGCCTATCAGG
SEQ2210	CTAGAGCAATTGATTACGAGAACATTAAATTCGGGTTATCGTAGTGTGCCTATCAGG
SEQ2211	CTAGAGCAATTGATTACGAGAACATTAAATTCGGGTTATCGTAGTGTGCCTATCAGG
SEQ2201	AGAAGTTGTTCAATTCTTATGTTACTCAAGAGATGACTAGTAACCCTAATTTGACGAGGG
SEQ2202	AGAAGTTGTTCAATTCTTATGTTACTCAAGAGATGACTAGTAACCCTAATTTGACGAGGG
SEQ2203	AGAAGTTGTTCAATTCTTATGTTACTCAAGAGATGACTAGTAACCCTAATTTGACGAGGG
SEQ2204	AGAAGTTGTTCAATTCTTATGTTACTCAAGAGATGACTAGTAACCCTAATTTGACGAGGG
SEQ2205	AGAAGTTGTTCAATTCTTATGTTACTCAAGAAATGACTAGTAACCCTAATTTGACGAGGG
SEQ2206	AGAAGTTGTTCAATTCTTATGTTACTCAAGAGATGACTAGTAACCCTAATTTGACGAGGG
SEQ2207	AGAAGTTGTTCAATTCTTATGTTACTCAAGAGATGACTAGTAACCCTAATTTGACGAGGG
SEQ2208	AGAAGTTGTTCAATTCTTATGTTACTCAWGAATGACTAGTAACCCTAATTTGACGAGGG
SEQ2209	AGAAGTTGTTCAATTCTTATGTTACTCAAGAGATGACTAGTAACCCTAATTTGACGAGGG
SEQ2210	AGAAGTTGTTCAATTCTTATGTTACTCAAGAGATGACTAGTAACCCTAATTTGACGAGGG
SEQ2211	AGAAGTTGTTCAATTCTTATGTTACTCAAGAGATGACTAGTAACCCTAATTTGACGAGGG

**Table 22: Comparative Sequences relating to SAG0093
(D-alanyl-D-alanine carboxypeptidase family protein)**

SEQ2201	ACAAGCAGAAAAGTTGGTAAAAAATTACTCTCAGCCTGCAGGTGCTAGTGAACACCAGA
SEQ2202	ACAAGCAGAAAAGTTGGTAAAAAATTACTCTCAGCCTGCAGGTGCTAGTGAACACCAGA
SEQ2203	ACAAGCAGAAAAGTTGGTAAAAAATTACTCTCAGCCTGCAGGTGCTAGTGAACACCAGA
SEQ2204	ACAAGCAGAAAAGTTGGTAAAAAATTACTCTCAGCCTGCAGGTGCTAGTGAACACCAGA
SEQ2205	ACAAGCAGAAAAGTTGGTAAAAAATTACTCTCAGCCTGCAGGTGCTAGTGAACACCAGA
SEQ2206	ACAAGCAGAAAAGTTGGTAAAAAATTACTCTCAGCCTGCAGGTGCTAGTGAACACCAGA
SEQ2207	ACAAGCAGAAAAGTTGGTAAAAAATTACTCTCAGCCTGCAGGTGCTAGTGAACACCAGA
SEQ2208	ACAAGCAGAAAAGTTGGTAAAAAATTACTCTCAGCCTGCAGGTGCTAGTGAACACCAGA
SEQ2209	ACAAGCAGAAAAGTTGGTAAAAAATTACTCTCAGCCTGCAGGTGCTAGTGAACACCAGA
SEQ2210	ACAAGCAGAAAAGTTGGTAAAAAATTACTCTCAGCCTGCAGGTGCTAGTGAACACCAGA
SEQ2211	ACAAGCAGAAAAGTTGGTAAAAAATTACTCTCAGCCTGCAGGTGCTAGTGAACACCAGA
SEQ2201	CTGGATTAGCGATGGATATGAGTACTGTAGATTCTTTGAATGAGAGCGATCCTAGAGTAG
SEQ2202	CTGGATTAGCGATGGATATGAGTACTGTAGATTCTTTGAATGAGAGCGATCCTAGAGTAG
SEQ2203	CTGGATTAGCGATGGATATGAGTACTGTAGATTCTTTGAATGAGAGCGATCCTAGAGTAG
SEQ2204	CTGGATTAGCGATGGATATGAGTACTGTAGATTCTTTGAATGAGAGCGATCCTAGAGTAG
SEQ2205	CTGGATTAGCGATGGATATGAGTACTGTAGATTCTTTGAATGAGAGCGATCCTAGAGTAG
SEQ2206	CTGGATTAGCGATGGATATGAGTACTGTAGATTCTTTGAATGAGAGCGATCCTAGAGTAG
SEQ2207	CTGGATTAGCGATGGATATGAGTACTGTAGATTCTTTGAATGAGAGCGATCCTAGAGTAG
SEQ2208	CTGGATTAGCGATGGATATGAGTACTGTAGATTCTTTGAATGAGAGCGATCCTAGAGTAG
SEQ2209	CTGGATTAGCGATGGATATGAGTACTGTAGATTCTTTGAATGAGAGCGATCCTAGAGTAG
SEQ2210	CTGGATTAGCGATGGATATGAGTACTGTAGATTCTTTGAATGAGAGCGATCCTAGAGTAG
SEQ2211	CTGGATTAGCGATGGATATGAGTACTGTAGATTCTTTGAATGAGAGCGATCCTAGAGTAG
SEQ2201	TCAGTCAGTTGAAAAAGATAGCTCCACAATATGGTTTTGTCTTACGGTTTCCGGATGGTA
SEQ2202	TCAGTCAGTTGAAAAAGATAGCTCCACAATATGGTTTTGTCTTACGGTTTCCGGATGGTA
SEQ2203	TCAGTCAGTTGAAAAAGATAGCTCCACAATATGGTTTTGTCTTACGGTTTCCGGATGGTA
SEQ2204	TCAGTCAGTTGAAAAAGATAGCTCCACAATATGGTTTTGTCTTACGGTTTCCGGATGGTA
SEQ2205	TCAGTCAGTTGAAAAAGATAGCTCCACAATATGGTTTTGTCTTACGGTTTCCGGATGGTA
SEQ2206	TCAGTCAGTTGAAAAAGATAGCTCCACAATATGGTTTTGTCTTACGGTTTCCGGATGGTA
SEQ2207	TCAGTCAGTTGAAAAAGATAGCTCCACAATATGGTTTTGTCTTACGGTTTCCGGATGGTA
SEQ2208	TCAGTCAGTTGAAAAAGATAGCTCCACAATATGGTTTTGTCTTACGGTTTCCGGATGGTA
SEQ2209	TCAGTCAGTTGAAAAAGATAGCTCCACAATATGGTTTTGTCTTACGGTTTCCGGATGGTA
SEQ2210	TCAGTCAGTTGAAAAAGATAGCTCCACAATATGGTTTTGTCTTACGGTTTCCGGATGGTA
SEQ2211	TCAGTCAGTTGAAAAAGATAGCTCCACAATATGGTTTTGTCTTACGGTTTCCGGATGGTA
SEQ2201	AAACAGCAGAAACAGGGGTAGGTTATGAAGATTGGCATTACCGCTATGTTGGGGTAGAGT
SEQ2202	AAACAGCAGAAACAGGGGTAGGTTATGAAGATTGGCATTACCGCTATGTTGGGGTAGAGT
SEQ2203	AAACAGCAGAAACAGGGGTAGGTTATGAAGATTGGCATTACCGCTATGTTGGGGTAGAGT
SEQ2204	AAACAGCAGAAACAGGGGTAGGTTATGAAGATTGGCATTACCGCTATGTTGGGGTAGAGT
SEQ2205	AAACAGCAGAAACAGGGGTAGGTTATGAAGATTGGCATTACCGCTATGTTGGGGTAGAGT
SEQ2206	AAACAGCAGAAACAGGGGTAGGTTATGAAGATTGGCATTACCGCTATGTTGGGGTAGAGT
SEQ2207	AAACAGCAGAAACAGGGGTAGGTTATGAAGATTGGCATTACCGCTATGTTGGGGTAGAGT
SEQ2208	AAACAGCAGAAACAGGGGTAGGTTATGAAGATTGGCATTACCGCTATGTTGGGGTAGAGT
SEQ2209	AAACAGCAGAAACAGGGGTAGGTTATGAAGATTGGCATTACCGCTATGTTGGGGTAGAGT
SEQ2210	AAACAGCAGAAACAGGGGTAGGTTATGAAGATTGGCATTACCGCTATGTTGGGGTAGAGT
SEQ2211	AAACAGCAGAAACAGGGGTAGGTTATGAAGATTGGCATTACCGCTATGTTGGGGTAGAGT
SEQ2201	CTGCAAAATATATGGCCAAACATCATTTAACATTAGAAGAATACATAACTTTATTAAAGG
SEQ2202	CTGCAAAATATATGGCCAAACATCATTTAACATTAGAAGAATACATAACTTTATTAAAGG
SEQ2203	CTGCAAAATATATGGCCAAACATCATTTAACATTAGAAGAATACATAACTTTATTAAAGG
SEQ2204	CTGCAAAATATATGGCCAAACATCATTTAACATTAGAAGAATACATAACTTTATTAAAGG
SEQ2205	CTGCAAAATATATGGCCAAACATCATTTAACATTAGAAGAATACATAACTTTATTAAAGG
SEQ2206	CTGCAAAATATATGGCCAAACATCATTTAACATTAGAAGAATACATAACTTTATTAAAGG
SEQ2207	CTGCAAAATATATGGTCAAACATCATTTAACATTAGAAGAATACATAACTTTATTAAAGG
SEQ2208	CTGCAAAATATATGGCCAAACATCATTTAACATTAGAAGAATACATAACTTTATTAAAGG
SEQ2209	CTGCAAAATATATGGCCAAACATCATTTAACATTAGAAGAATACATAACTTTATTAAAGG
SEQ2210	CTGCAAAATATATGGTCAAACATCATTTAACATTAGAAGAATACATAACTTTATTAAAGG
SEQ2211	CTGCAAAATATATGGTCAAACATCATTTAACATTAGAAGAATACATAACTTTATTAAAGG

**Table 22: Comparative Sequences relating to SAG0093
(D-alanyl-D-alanine carboxypeptidase family protein)**

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SEQ2201      AGAATAACCAA-----
SEQ2202      AGAATAACCAA-----
SEQ2203      AGAATAACCAA-----
SEQ2204      AGAATAACCAAAACCCAGCTTTCTTGACAA-----
SEQ2205      AGAATAACCAA-----
SEQ2206      AGAATAACCAA-----
SEQ2207      AGAATAACCAAAACCCAGCTTTCTTGACAA-----
SEQ2208      AGAATAACCAA-----
SEQ2209      AGAATAACCAA-----
SEQ2210      AGAATAACCAAAACCCAGCTTTCTT-----
SEQ2211      AGAATAACCAATABCMARATVSTNCSRATNGTSAGDAANYDAANNCARXYTASAMYRT

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>SEQ ID NO 2250: 18_090 frame: 1

```

KPNSQQSSSQKLARNEDIKKISSQKRNNKQLPAVSSKDWNLILVNRDHKHEELSPDVVPV
ENIYLDKRITKQATQFLEAARAIIDSREHLISGYRSVAYQEKLFNSYVTQEMTSNPNLTRG
QAEKLVKTYSQPAGASEHQTLAMDMS TVDSLNESDPRVVSQKKIAPQYGFVLRFPDGK
TAETGVGYEDWHYRYVGVESAKYMAKHHLTLEEYITLLKENNQ

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>SEQ ID NO 2251: 18_1169NT frame: 1

```

KPNSQQSSSQKLARNEDIKKISSQKRNNKRLPAVSSKDWNLILVNRDHKHEELSPDVVPV
ENIYLDKRITKQATQFLEAARAIIDSREHLISGYRSVAYQEKLFNSYVTQEMTSNPNLTRG
QAEKLVKTYSQPAGASEHQTLAMDMS TVDSLNESDPRVVSQKKIAPQYGFVLRFPDGK
TAETGVGYEDWHYRYVGVESAKYMAEHRLTLEEYITLLKENNQ

```

>SEQ ID NO 2252: 18_18RS21 frame: 1

```

KPNSQQSSSQKLARNEDIKKISSQKRNNKQLPAVSSKDWNLILVNRDHKHEELSPDVVPV
ENIYLDKRITKQATQFLEAARAIIDSREHLISGYRSVAYQEKLFNSYVTQEMTSNPNLTRG
QAEKLVKTYSQPAGASEHQTLAMDMS TVDSLNESDPRVVSQKKIAPQYGFVLRFPDGK
TAETGVGYEDWHYRYVGVESAKYMAKHHLTLEEYITLLKENNQ

```

>SEQ ID NO 2253: 18_2603 frame: 3

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SQSSSQKLARNEDIKKISSQKRNNKQLPAVSSKDWNLILVNRDHKHEELSPDVVPVENI
YLDKRITKQATQFLEAARAIIDSREHLISGYRSVAYQEKLFNSYVTQEMTSNPNLTRGQAE
KLVKTYSQPAGASEHQTLAMDMS TVDSLNESDPRVVSQKKIAPQYGFVLRFPDGKTAE
TGVGYEDWHYRYVGVESAKYMAKHHLTLEEYITLLKENNQNPALY

```

>SEQ ID NO 2254: 18_A909 frame: 1

```

KPNSQQSSSQKLARNEDIKKTSSQKRNNKRLPAVSSKDWNLILVNRDHKHEELSPDVVPV
ENIYLDKRITKQATQFLEAARAIIDSREHLISGYRSVAYQEKLFNSYVTQEMTSNPNLTKE
QAEKLVKTYSQPAGASEHQTLAMDMS TVDSLNESDPRVVSQKKIAPQYGFVLRFPDGK
TAETGVGYEDWHYRYVGVESAKYMAKHHLTLEEYITLLKENNQ

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>SEQ ID NO 2255: 18_CJB110 frame: 1

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KPNSQQSSSQKLARNEDIKKISSQKRNNKFTITSCIIRLELDFGQS

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>SEQ ID NO 2256: 18_COH1 frame: 1

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PNSQQSSSQKLARNEDIKKTSSQKRNN

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>SEQ ID NO 2257: 18_H36B frame: 1

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KPNSQQSSSQKLARNEDIKKTSSQKRNNKRLPAVSSKDWNLILVNRDHKHEELSPDVVPV
ENIYLDKRITKQATQFLEAARAIIDSREHLISGYRSVAYQEKLFNSYVTXEMTSNPNLTKE
QAEKLVKTYSQPAGASEHQTLAMDMS TVDSLNESDPRVVSQKKIAPQYGFVLRFPDGK
TAETGVGYEDWHYRYVGVESAKYMAKHHLTLEEYITLLKENNQ

```

>SEQ ID NO 2258: 18_JM9130013 frame: 1

```

KPNSQQSSSQKLARNEDIKKISSQKRNNKQLPAVSSKDWNLILVNRDHKHEELSPDVVPV
ENIYLDKRITKQATQFLEAARAIIDSREHLISGYRSVAYQEKLFNSYVTQEMTSNPNLTRG
QAEKLVKTYSQPAGASEHQTLAMDMS TVDSLNESDPRVVSQKKIAPQYGFVLRFPDGK
TAETGVGYEDWHYRYVGVESAKYMAKHHLTLEEYITLLKENNQ

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>SEQ ID NO 2259: 18_M732 frame: 3

```

PNSQQSSSQKLARNEDIKKTSSQKRNNKRLPAVSSKDWNLILVNRDHKHEELSPDVVPVE
NIYLDKRITKQATQFLEAARAIIDSREHLISGYRSVAYQEKLFNSYVTQEMTSNPNLTRGQ
AEKLVKTYSQPAGASEHQTLAMDMS TVDSLNESDPRVVSQKKIAPQYGFVLRFPDGKT
AETGVGYEDWHYRYVGVESAKYMKHHLTLEEYITLLKENNQNPAP

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**Table 22: Comparative Sequences relating to SAG0093
(D-alanyl-D-alanine carboxypeptidase family protein)**

>SEQ ID NO 2260: 18 M781 frame: 1

KPNSQQSSSQKL RNEDIKKTSSQKRNNKLR LPAVSSKDWNLILVNRDHKHEELSPDVVPV
ENIYLDKRITKQATQFLEAARAIDSREHLISGYRSVAYQEKLFNSYVTQEMTSNPNLTRG
QAEKLVKTYSPAGASEHQTGLAMDMS TVDSL NESDPRVVSQ LKKIAPQYGFVLRFPD GK
TAETGVGYEDWHYRYVGVESAKYMKHHLTLEEYITLLKENNQ

SEQ2250	PNSQQSSSQKL RNEDIKKTSSQKRNNKLR LPAVSSKDWNLILVNRDHKHEELSPDVVPV
SEQ2251	PNSQQSSSQKL RNEDIKKTSSQKRNNKLR LPAVSSKDWNLILVNRDHKHEELSPDVVPV
SEQ2252	PNSQQSSSQKL RNEDIKKTSSQKRNNKLR LPAVSSKDWNLILVNRDHKHEELSPDVVPV
SEQ2253	--SQSSSQKL RNEDIKKTSSQKRNNKLR LPAVSSKDWNLILVNRDHKHEELSPDVVPV
SEQ2254	PNSQQSSSQKL RNEDIKKTSSQKRNNKLR LPAVSSKDWNLILVNRDHKHEELSPDVVPV
SEQ2255	PNSQQSSSQKL RNEDIKKTSSQKRNNKLR LPAVSSKDWNLILVNRDHKHEELSPDVVPV
SEQ2256	PNSQQSSSQKL RNEDIKKTSSQKRNNKLR LPAVSSKDWNLILVNRDHKHEELSPDVVPV
SEQ2257	PNSQQSSSQKL RNEDIKKTSSQKRNNKLR LPAVSSKDWNLILVNRDHKHEELSPDVVPV
SEQ2258	PNSQQSSSQKL RNEDIKKTSSQKRNNKLR LPAVSSKDWNLILVNRDHKHEELSPDVVPV
SEQ2259	PNSQQSSSQKL RNEDIKKTSSQKRNNKLR LPAVSSKDWNLILVNRDHKHEELSPDVVPV
SEQ2260	PNSQQSSSQKL RNEDIKKTSSQKRNNKLR LPAVSSKDWNLILVNRDHKHEELSPDVVPV
SEQ2250	NIYLDKRITKQATQFLEAARAIDSREHLISGYRSVAYQEKLFNSYVTQEMTSNPNLTRG
SEQ2251	NIYLDKRITKQATQFLEAARAIDSREHLISGYRSVAYQEKLFNSYVTQEMTSNPNLTRG
SEQ2252	NIYLDKRITKQATQFLEAARAIDSREHLISGYRSVAYQEKLFNSYVTQEMTSNPNLTRG
SEQ2253	NIYLDKRITKQATQFLEAARAIDSREHLISGYRSVAYQEKLFNSYVTQEMTSNPNLTRG
SEQ2254	NIYLDKRITKQATQFLEAARAIDSREHLISGYRSVAYQEKLFNSYVTQEMTSNPNLTRG
SEQ2255	-----
SEQ2256	-----
SEQ2257	NIYLDKRITKQATQFLEAARAIDSREHLISGYRSVAYQEKLFNSYVTQEMTSNPNLTRG
SEQ2258	NIYLDKRITKQATQFLEAARAIDSREHLISGYRSVAYQEKLFNSYVTQEMTSNPNLTRG
SEQ2259	NIYLDKRITKQATQFLEAARAIDSREHLISGYRSVAYQEKLFNSYVTQEMTSNPNLTRG
SEQ2260	NIYLDKRITKQATQFLEAARAIDSREHLISGYRSVAYQEKLFNSYVTQEMTSNPNLTRG
SEQ2250	AEKLVKTYSPAGASEHQTGLAMDMS TVDSL NESDPRVVSQ LKKIAPQYGFVLRFPD GK
SEQ2251	AEKLVKTYSPAGASEHQTGLAMDMS TVDSL NESDPRVVSQ LKKIAPQYGFVLRFPD GK
SEQ2252	AEKLVKTYSPAGASEHQTGLAMDMS TVDSL NESDPRVVSQ LKKIAPQYGFVLRFPD GK
SEQ2253	AEKLVKTYSPAGASEHQTGLAMDMS TVDSL NESDPRVVSQ LKKIAPQYGFVLRFPD GK
SEQ2254	AEKLVKTYSPAGASEHQTGLAMDMS TVDSL NESDPRVVSQ LKKIAPQYGFVLRFPD GK
SEQ2255	-----
SEQ2256	-----
SEQ2257	AEKLVKTYSPAGASEHQTGLAMDMS TVDSL NESDPRVVSQ LKKIAPQYGFVLRFPD GK
SEQ2258	AEKLVKTYSPAGASEHQTGLAMDMS TVDSL NESDPRVVSQ LKKIAPQYGFVLRFPD GK
SEQ2259	AEKLVKTYSPAGASEHQTGLAMDMS TVDSL NESDPRVVSQ LKKIAPQYGFVLRFPD GK
SEQ2260	AEKLVKTYSPAGASEHQTGLAMDMS TVDSL NESDPRVVSQ LKKIAPQYGFVLRFPD GK
SEQ2250	AETGVGYEDWHYRYVGVESAKYMAKHHLTLEEYITLLKENNQ-----
SEQ2251	AETGVGYEDWHYRYVGVESAKYMAKHHLTLEEYITLLKENNQ-----
SEQ2252	AETGVGYEDWHYRYVGVESAKYMAKHHLTLEEYITLLKENNQ-----
SEQ2253	AETGVGYEDWHYRYVGVESAKYMAKHHLTLEEYITLLKENNQNPFLY-----
SEQ2254	AETGVGYEDWHYRYVGVESAKYMAKHHLTLEEYITLLKENNQ-----
SEQ2255	-----
SEQ2256	-----
SEQ2257	AETGVGYEDWHYRYVGVESAKYMAKHHLTLEEYITLLKENNQ-----
SEQ2258	AETGVGYEDWHYRYVGVESAKYMAKHHLTLEEYITLLKENNQ-----
SEQ2259	AETGVGYEDWHYRYVGVESAKYMAKHHLTLEEYITLLKENNQNPFLY-----
SEQ2260	AETGVGYEDWHYRYVGVESAKYMAKHHLTLEEYITLLKENNQTABLECMPARATIVESE
SEQ2250	-----
SEQ2251	-----
SEQ2252	-----
SEQ2253	-----
SEQ2254	-----
SEQ2255	-----
SEQ2256	-----
SEQ2257	-----
SEQ2258	-----
SEQ2259	-----
SEQ2260	ENCESRELATINGTSAGDALANYLDALANINECARBXYPEPTIDASEFAMILYPRTEIN

**Table 23: Comparative Sequences relating to SAG0163
(competence protein Cg1A)**

SEQ ID NO. 2301: SAG0163 FROM THE 090 GBS TYPE III STRAIN (REVERSE COMPLEMENT)
 GGCAGTAGAAGTAAATGCTCAAGATATTTATATCATTTCCCAAAGGTGATTGTTATGAACTCTATATGCGTATTGATGATGAAAGGCG
 GTTTATTGATGTTTTTTGAGTTTAAATAGGATGGCTAGTCTTATTAGTCACTTTAAATTTGTGGCAGGCATGAACGTTGGAGAAAAAG
 ACGAAGTCAATTAGGTTCTTGTGACTATGAACTGTCAGAGGGAAGACTGGTTTCATTACGACTATCGAGTGTGGGAGATTATCGTGG
 TCAAGAATCTTTAGTTATTCGTATTTTGTATTTCAGGTCATCAGGACTTAAATATTTGGTTTGATAATATAAAGCAAATGAAGGAAGT
 ACTGGGTACAAGAGGGCTATATCTTTTTCCGGCCCTGTGGGGAGTGGTAAACAACCTCTCATGTATCAATTAGCTTCAGAAGTATT
 TAAAAATAAGCAAATTATCACGATTGAAGATCCGGTAGAAATCAAGAATGACAAGATGTTACAACCTCCAATTGAATGAGGATATTGG
 AATGACTTATGATGCTTTAATCAAACGTCTTTACGGCATCGTCCAGATATTTTAATTATCGGAGAGATTAGAGATCAAGCGACGGC
 CCGTGCTGTTATTCGTGCAAGTTTAAACGGGAGTGATGGTTTTTCTACTATTTCATGCTAAAAGTATTTCCGGAGTCTATGATAGGCT
 TATAGAATTAGGGTTAACTATCAAGAGTTAGAAAAATAGTCTAAAATTAATAGCATATCAACGTTTAAATTGGAGGAGGAAGCCTAAT
 TGACTTTGAGACAGGTAACCTTAAAAACAACCTCATCAGACAAGTGAATAGACAAGTGGATATCTTGGCTGAAGAAGGACATATCAG
 TAAGAAACAGGCACAAGTCGAAAAAATTATCCCTCAAGAAACAACGGAAAGTAGTCCAACTTTT

SEQ ID NO. 2302: SAG0163 FROM THE 1169NT1 GBS TYPE V STRAIN (REVERSE COMPLEMENT)
 GGTGATTGTTATGAAACCTCTACTATTGCGTATTGATGATGAAAGGCGGTTTTATGATGTTTTTGTAGTTTAAATAGGATGGCTAGTC
 TTATTAGTCACTTTAAATTTGTGGCAGGCATGAACGTTGGAGAAAAAGACGAAGTCAATTAGGTTCTTGTGACTATGAACTGTGAG
 AGGGAAGACTGGTTTCATTACGACTATCGAGTGTGGGAGATTATCGTGGTCAAGAATCTTTAGTTATTTCGTATTTTGTATTGAGGTC
 ATCAGGACTTAAAAATTGGTTTGATAATATAAAGCAAATGAAGGAAGTACTGGGTACAAGAGGCTATATCTTTTTTCCGGCCCTG
 TGGGGAGTGGTAAAAACAACCTCTCATGTATCAATTAGCTTCAGAAAGTATTTAAAAATAAGCAAATATCACGATTGAAGATCCGGTAG
 AAATCAAGAATGACAAGATGTTTACAACCTCAAATGGAATGAGGATTTGGAATGACTTATGATGCTTTAATCAAACGTCTTTACGGC
 ATCGTCCAGATATTTTAATTATCGGAGAGATTAGAGATCAAGCGACGGCTCGTGTCTGTTATTTCGTGCAAGTTTAAACGGGAGTGATGG
 TTTTTTCTACTATTTCATGCTAAAAGTATTTCCCGGAGTCTATGATAGGCTTATAGAATTAGGGGTTAACTATCAAGAGTTAGAAAAATA
 GTCTAAAATTAATAGCATATCAACGTTTAAATTGGAGGAGGAAGCCTAATTGACTTTGAGACAAGTAACTTTAAAAACAACCTCATCAG
 ACAAGTGAATAGACAAGTGGATATCTTGGCTGAAGAAGGATATCAGTAAGAAACAGGCACAAGTCGAAAAAATTATCCCTCAAG
 AAACAACGGAAGTAGTCCAACTTTT

SEQ ID NO. 2303: SAG0163 FROM THE 18RS21 GBS TYPE II STRAIN (REVERSE COMPLEMENT)
 GTTCAATCATTAGCAAAGCAAGTCATTTCATCAGGCAGTAGAAGTAAATGCTCAAGATATTTATATCATTTCCCAAAGGTGATTGTTAT
 GAACTCTATATGCGTATTGATGATGAAAGGCGGTTTTATGATGTTTTTGTAGTTTAAATAGGATGGCTAGTCTTATTAGTCACTTTAAA
 TTTGTGGCAGGCATGAACGTTTGAGAAAAAAGACGAAGTCAATTAGGTTCTTGTGACTATGAACTGTGAGAGGGAAGACTGGTTTCA
 TTACGACTATCGAGTGTGGGAGATTATCGTGGTCAAGAATCTTTAGTTATTTCGTATTTTGTATTTCAGGTCATCAGGACTTAAAAAT
 TGGTTTGATAATATAAAGCAAATGAAGGAAGTACTGGGTATAAGAGGGCTATATCTTTTTTCCGGCCCTGTGGGGAGTGGTAAACA
 ACTCTCATGTATCAATTAGCTTCAGAAAGTATTTAAAAATAAGCAAATATCACGATTGAAGATCCGGTAGAAATCAAGAATGACAAG
 ATGTTTACAACCTCCAATTGAATGAGGATATTGGAATGACTTATGATGCTTTAATCAAACGTCTTTACGGCATCGTCCAGATATTTTA
 ATTATCGGAGAGATTAGAGATCAAGCGACGGCCCGTGTCTGTTATTCGTGCAAGTTTAAACGGGAGTGATGGTTTTTCTACTATTTCAT
 GCTAAAAGTATTTCCCGGAGTCTATGATAGGCTTATAGAATTAGGGGTTAACTATCAAGAGTTAGAAAAATAGTCTAAAATTAATAGCA
 TATCAACGTTTTAATTGGAGGAGGAAGCCTAATTGACTTTGAGACAGGTAATTTTAAAAACAACCTCATCAGACAAGTGGAAATAGACAA
 GTGGATATCTTGGCTGAAGAAGGACATATCAGTAAGAAACAGGCACAAGTCGAAAAAATTATCCCTCAAGAAACAACGGAAAGTAGT
 CCAACTTTT

SEQ ID NO. 2304: SAG0163 FROM THE 2603 V/R GBS TYPE V STRAIN (REVERSE COMPLEMENT)
 GATATTTATATCATTTCCCAAAGGTGATTGTTATGAACTCTATATGCGTATTGATGATGAAAGGCGGTTTTATGATGTTTTTGTAGTTT
 AATAGGATGGCTAGTCTTATTAGTCACTTTAAATTTGTGGCAGGCATGAACGTTGGAGAAAAAAGACGAAGTCAATTAGGTTCTTGT
 GACTATGAACTGTCAGAGGGAAGACTGGTTTCATTACGACTATCGAGTGTGGGAGATTATCGTGGTCAAGAATCTTTAGTTATTTCGT
 ATTTTGTATTTCAGGTCATCAGGACTTAAATATTTGGTTTGATAATATAAAGCAAATGAAGGAAGTACTGGGTATAAGAGGGCTATAT
 CTTTTTCCGGCCCTGTGGGGAGTGGTAAACAACCTCTCATGTATCAATTAGCTTCAGAAGTATTTAAAAATAAGCAAATATCACG
 ATTGAAGATCCGGTAGAAATCAAGAATGACAAGATGTTTCAACTCCAATTGAATGAGGATATTGGAATGACTTATGATGCTTTAATC
 AAACGTCTTTACGGCATCGTCCAGATATTTTAATTATCGGAGAGATTAGAGATCAAGCGACGGCCCGTGTCTGTTATTTCGTGCAAGT
 TTAACGGGAGTGATGGTTTTTCTACTATTTCATGCTAAAAGTATTTCCCGGAGTCTATGATAGGCTTATAGAATTAGGGGTTAACTAT
 CAAGAGTTAGAAAAATAGTCTAAAATTAATAGCATATCAACGTTTAAATTGGAGGAGGAAGCCTAATTGACTTTGAGACAGGTAATTTT
 AAAAAACAACCTCATCAGACAAGTGAATAGACAAGTGGATATCTTGGCTGAAGAAGGACATATCAGTAAGAAACAGGCACAAGTGGCGA
 AAAAAATTATCCCTCAAGAAACAACGGAAAGTAGTCCAACTTTT

**Table 23: Comparative Sequences relating to SAG0163
(competence protein Cg1A)**

SEQ ID NO. 2305: SAG0163 FROM THE A909 GBS TYPE Ia STRAIN (REVERSE COMPLEMENT)
 GTTCAATCATAGCAAAGCAAGTCATTTCATCAGGCAGTAGAAGTAAATGCTCAAGATATTTATATCATTTCCCAAAGGTGATTGTTAT
 GAACTCTATATGCGTATTGATGATGAAAGGCGGTTTATTGATGTTTTGAGTTTAAATAGGATGGCTAGTCTTATTAGTCACTTTAAA
 TTTGTGGCAGGCATGAACGTTGGAGAAAAAGACGAAGTCAATTAGGTTCTTGTGACTATGAACTGTCAGAGGGAAGACTGGTTTCA
 TTACGACTATCGAGTGTGGGAGATTATCGTGGTCAAGAATCTTTAGTTATTTCGTATTTTGTATTTCAGGTTCATCAGGACTTAAATAT
 TGGTTTGATAATATAAAGCAAATGAAGGAAGTACTGGGTATAAGAGGGCTATATCTTTTTCCGGCCCTGTGGGGAGTGGTAAACAA
 ACTCTCATGTATCAATTAGCTTCAGAAAGTATTTAAAAATAAGCAAATATACGATTGAAGATCCGGTAGAAATCAAGAATGACAAG
 ATGTTACAACCTCAAATTGAATGAGGATATTGGAATGACTTATGATGCTTTAATCAAACCTGCTTTACGGCATCGTCCAGATATTTTA
 ATTATCGGAGAGATTAGAGATCAAGCGACGGCCCGTCTGTTATTTCGTGCAAGTTTAAACGGGAGTGATGGTTTTTCTACTATTTCAT
 GCTAAAAGTATTTCCCGAGTCTATGATAGGCTTATAGAATTAGGGGTTAACTATCAAGAGTTAGAAAATAGTCTAAAATTAATAGCA
 TATCAACGTTTAATTGGAGGAGGAAGCCTAATTGACTTTGAGACAGGTAATTTAAAAAACACTCATCAGACAAGTGGAAATAGACAA
 GTGGATATCTTGGCTGAAGAAGGACATATCAGTAAGAAAACAGGCACAAGTCGAAAAAATTATCCCTCAAGAAACAACGGAAGTAGT
 CCAACTTTT

SEQ ID NO. 2306: SAG0163 FROM THE CJB110 GBS NONTYPEABLE STRAIN (REVERSE COMPLEMENT)
 GTTCAATCATAGCAAAGCAAGTCATTTCATCAGGCAGTAGAAGTAAATGCTCAAGATATTTATATCATTTCCCAAAGGTGATTGTTAT
 GAACTCTATATGCGTATTGATGATGAAAGGCGGTTTATTGATGTTTTGAGTTTAAATAGGATGGCTAGTCTTATTAGTCACTTTAAA
 TTTGTGGCAGGCATGAACGTTGGAGAAAAAGACGAAGTCAATTAGGTTCTTGTGACTATGAACTGTCAGAGGGAAGACTGGTTTCA
 TTACGACTATCGAGTGTGGGAGATTATCGTGGTCAAGAATCTTTAGTTATTTCGTATTTTGTATTTCAGGTTCATCAGGACTTAAATAT
 TGGTTTGATAATATAAAGCAAATGAAGGAAGTACTGGGTACAAGAGGGCTATATCTTTTTCCGGCCCTGTGGGGAGTGGTAAACAA
 ACTCTCATGTATCAATTAGCTTCAGAAAGTATTTAAAAATAAGCAAATATACGATTGAAGATCCGGTAGAAATCAAGAATGACAAG
 ATGTTACAACCTCAAATTGAATGAGGATATTGGAATGACTTATGATGCTTTAATCAAACCTGCTTTACGGCATCGTCCAGATATTTTA
 ATTATCGGAGAGATTAGAGATCAAGCGACGGCCCGTCTGTTATTTCGTGCAAGTTTAAACGGGAGTGATGGTTTTTCTACTATTTCAT
 GCTAAAAGTATTTCCCGAGTCTATGATAGGCTTATAGAATTAGGGGTTAACTATCAAGAGTTAGAAAATAGTCTAAAATTAATAGCA
 TATCAACGTTTAATTGGAGGAGGAAGCCTAATTGACTTTGAGACAGGTAACTTAAAAAACACTCATCAGACAAGTGGAAATAGACAA
 GTGGATATCTTGGCTGAAGAAGGACATATCAGTAAGAAAACAGGCACAAGTCGAAAAAATTATCCCTCAAGAAACAACGGAAGTAGT
 CCAACTTTT

SEQ ID NO. 2307: SAG0163 FROM THE COH1 GBS TYPE III STRAIN (REVERSE COMPLEMENT)
 AGGTGATTGTTATGAAATTCATATATGCGTATTGATGATGAAAGGCGGTTTATTGATGTTTTGAGTTTAAATAGGATGGCTAGTCTTA
 TTAGTCACTTTAAATTTGTGGCAGGCATGAACGTTGGAGAAAAAGACGAAGTCAATTAGGTTCTTGTGACTATGAACTGTCAGAGG
 GAAGACTGGTTTCATTACGACTATCAAGTGTGGGAGATTATCGTGGTCAAGAATCTTTAGTTATTTCGTACTTTTGTATTTCAGGTATC
 AGGACTTAAATATTTGGTTTGATAATATAAAGTAAATGAAGGAAGTACTGTGTGCAAGAGGGCTATATCTTTTTCCGGCCCTGTGG
 GGAGTGGTAAAACAACTCTCATGTATCAATTAGCTTCAGAAAGTATTTAAAAATAAGCAAATATACGATTGAAGATCCGGTAGAAA
 TCAAGAATGACAAGATGTTACAACCTCAATTGAATGAGGATATTGGAATGACTTATGATGCTTTAATCAAACCTGCTTTACGGCATC
 GTCCAGATATTTTAATTATCGGAGAGATTAGAGATCAAGCGACGGCCCGTCTGTTATTTCGTGCAAGTTTAAACGGGAGTAAATGGTTT
 TTTCTACTATTTCATGCTAAAAGTATTTCCCGAGTCTATGATAGGCTTATAGAATTAGGGGTTAACTATCAAGAGTTAGAAAATAGTC
 TAAAATTAATAGCATATCAACGTTTAAATTGGAGGAGGAAGCCTAATTGACTTTGAGACAAGTAACTTTAAAAAACACTCATCAGACA
 AGTGGAAATAGACAAGTGGATATCTTGGCTGAAGAAGGACATATCAGTAAGAAAACAGGCACAAGTCGAAAAAATTATCCCTCAAGAAA
 CAACGGAAAGTAGTCCAACCTTT

SEQ ID NO. 2308: SAG0163 FROM THE H36b GBS TYPE Ib STRAIN (REVERSE COMPLEMENT)
 TCATTAGCAAAGCAAGTCATTTCATCAGGCAGTAGAAGTAAATGCTCAAGATATTTATATCATTTCCCAAAGGTGATTGTTATGAACTC
 TATATGCGTATTGATGATGAAAGGCGGTTTATTGATGTTTTGAGTTTAAATAGGATGGCTAGTCTTATTAGTCACTTTAAATTTGTG
 GCAGGCATGAACGTTGGAGAAAAAGACGAAGTCAATTAGGTTCTTGTGACTATGAACTGTCAGAGGGAAGACTGGTTTCATTACGA
 CTATCGAGTGTGGGAGATTATCGTGGTCAAGAATCTTTAGTTATTTCGTATTTTGTATTTCAGGTTCATCAGGACTTAAATATTGGTTT
 GATAATATAAAGCAAATGAAGGAAGTACTGGGTATAAGAGGGCTATATCTTTTTCCGGCCCTGTGGGGAGTGGTAAACAACTCTC
 ATGTATCAATTAGCTTCAGAAAGTATTTAAAAATAAGCAAATATACGATTGAAGATCCGGTAGAAATCAAGAATGACAAGATGTTA
 CAACCTCAAATTGAATGAGGATATTGGAATGACTTATGATGCTTTAATCAAACCTGCTTTACGGCATCGTCCAGATATTTTAATTATC
 GGAGAGAAATAGAGATCAAGCGACGGCCCGTCTGTTATTTCGTGCAAGTTTAAACGGGAGTGATGTTTTTCTACTATTTCATGCTAA
 AAGTATTTCCCGAGTCTATGATAGGCTTATAGAATTAGGGGTTAACTATCAAGAGTTAGAAAATAGTCTAAAATTAATAGCATATCA
 ACGTTTAATTGGAGGAGGAAGCCTAATTGACTTTGAGACAGGTAATTTAAAAAACACTCATCAGACAAGTGGAAATAGACAAGTGGAA
 TATCTTGGCTGAAGAAGGACATATCAGTAAGAAAACAGGCACAAGTCGAAAAAATTATCCCTCAAGAAACAACGGAAGTAGTCCAAC
 TTTT

**Table 23: Comparative Sequences relating to SAG0163
(competence protein Cg1A)**

SEQ ID NO. 2309: SAG0163 FROM THE JM9130013 GBS TYPE VIII STRAIN (REVERSE COMPLEMENT)
 GTTCAATCATTAGCAAAGCAAGTCATTCATCAGGCAGTAGAAGTAAATGCTCAAGATATTTATATCATTCCTCCAAAGGTGATTGTTAT
 GAACCTCTATATGCGTATTGATGATGAAAGGCGGTTTATTGATGTTTTTGAGTTAATAGGATGGCTAGTCTTATTAGTCACTTTAAA
 TTTGTGGCAGGCATGAACGTTGGAGAAAAAGACGGAAGTCAATTAGGTTCTTGTGACTATGAACTGTGAGAGGAAGACTGGTTTCA
 TTACGACTATCGAGTGTGGGAGATTATCGTGGTCAAGAATCTTTAGTTATTCTGATTTTGTATTTCAGGTCATCAGGACTTAAAAAT
 TGGTTTGATAATATAAAGCAAATGAAGGAAGTACTGGGTATAAGAGGGCTATATCTTTTTCCGGCCCTGTGGGGAGTGGTAAAAACA
 ACTCTCATGTATCAATTAGCTTCAGAAGTATTTAAAAATAAGCAAATTATCACGATTGAAGATCCGGTAGAAATCAAGAATGACAAG
 ATGTTACAACCTCCAATTGAATGAGGATATTGGAATGACTTATGATGCTTTAATCAAACGTCTTTACGGCATCGTCCAGATATTTTA
 ATTATCGGAGAGATTAGAGATCAAGCGACGGCCCGTGTCTTTATTCGTGCAAGTTTAAACGGGAGTGATGGTTTTTTCTACTATTCAT
 GCTAAAAGTATTCCTGGAGTCTATGATAGGCTTATAGAATTAGGGGTTAACTATCAAGAGTTAGAAAATAGTCTAAAAATTAATAGCA
 TATCAACGTTTAAATTGGAGGAGGAAGCCTAATTGACTTTGAGACAGGTAATTTTAAAAACACTCATCAGACAAGTGGAAATAGACAA
 GTGGATATCTTGGCTGAAGAAGGACATATCAGTAAGAAACAGGCACAAGTCGAAAAAATTATCCCTCAAGAAACAACGGAAAGTAGT
 CCAACTTTT

SEQ ID NO. 2310: SAG0163 FROM THE M732 GBS TYPE III STRAIN (REVERSE COMPLEMENT)
 TGACTTGTATGAAACTCTATATGCGTATTGATGATGAAAAGGCGGTTTATTGATGTTTTTGAGTTAATAGGATGGCTAGTCTTA
 TTAGTCACTTTAAATTTGTGGCAGGCATGAACGTTGGAGAAAAAGACGGAAGTCAATTAGGTTCTTGTGACTATGAACTGTGAGAGG
 GAAGACTGGTTTCATTACGACTATCAAGTGTGGGAGATTATCGTGGTCAAGAATCTTTAGTTATTCTGACTTTGTATTTCAGGTCATC
 AGGACTTAAAAATATTGGTTTGATAATATAAAGTAAATGAAGGAAGTACTGTGTGCAAGAGGGCTATATCTTTTTCCGGCCCTGTGG
 GGAGTGGTAAAAACAACCTCTCATGTATCAATTAGCTTCAGAAGTATTTAAAAATAAGCAAATTATCACGATTGAAGATCCGGTAGAAA
 TCAAGAATGACAAGATGTTACAACCTCCAATTGAATGAGGATATTGGAATGACTTATGATGCTTTAATCAAACGTCTTTACGGCATC
 GTCCAGATATTTTAAATTCGGAGAGATTAGAGATCAAGCGACGGCCCGTGTCTGTTATTCTGCAAGTTTAAACGGGAGTAATGGTTTT
 TTTCTACTATTTCATGCTAAAAGTATTCCTGGAGTCTATGATAGGCTTATAGAATTAGGGGTTAACTATCAAGAGTTAGAAAATAGTC
 TAAAAATTAATAGCATATCAACGTTTAAATTGGAGGAGGAAGCCTAATTGACTTTGAGACAAGTAACTTTAAAAAACACTCATCAGACA
 AGTGGAAATAGACAAGTGGATATCTTGGCTGAAGAAGGACATATCAGTAAGAAACAGGCACAAGTCGAAAAAATTATCCCTCAAGAAA
 CAACGGAAAGTAGTCCAACCTTTT

SEQ ID NO. 2311: SAG0163 FROM THE M781 GBS TYPE III STRAIN (REVERSE COMPLEMENT)
 CAGTAGAAGTAAATGCTCAAGATATTTATATCATTCCCAAAGGTGATTGTTATGAATTCATATGCGTATTGATGATGAAAAGGCGGT
 TTATTGATGTTTTTGAGTTAATAGGATGGCTAGTCTTATTAGTCACTTTAAATTTGTGGCAGGCATGAACGTTGGAGAAAAAGAC
 GAAGTCAATTAGGTTCTTGTGACTATGAACTGTGAGAGGAAGACTGGTTTCATTACGACTATCAAGTGTGGGAGATTATCGTGGTC
 AAGAATCTTTAGTTATTCTGACTTTGTATTTCAGGTCATCAGGACTTAAATATTGGTTTGATAATATAAAGCAAATGAAGGAAGTAC
 TGTGTGCAAGAGGGCTATATCTTTTTCCGGCCCTGTGGGGAGTGGTAAAACAACTCTCATGTATCAATTAGCTTCAGAAGTATTTA
 AAAATAAGCAAATTATCACGATTGAAGATCCGGTAGAAATCAAGAATGACAAGATGTTACAACCTCAATTGAATGAGGATATTGGAA
 TGACTTATGATGCTTTAATCAAACGTCTTTACGGCATCGTCCAGATATTTAATTATCGGAGAGATTAGAGATCAAGCGACGGCCC
 GTGCTGTTATTCTGTCAGGTTTAAACGGGAGTAATGGTTTTTTCTACTATTTCATGCTAAAAGTATTCCTGGAGTCTATGATAGGCTTA
 TAGAATTAGGGGTTAACTATCAAGAGTTAGAAAATAGTCTAAAAATTAATAGCATATCAACGTTTAAATTGGAGGAGGAAGCCTAATTG
 ACTTTGAGACAAGTAACTTTAAAAACACTCATCAGACAAGTGGAAATAGACAAGTGGATATCTTGGCTGAAGAAGGACATATCAGTA
 AGAAACAGGCACAAGTCGAAAAAATTATCCCTCAAGAAACAACGGAAGTAGTCCAACCTTTT

**Table 23: Comparative Sequences relating to SAG0163
(competence protein Cg1A)**

SEQ2301	-----GGCAGTAGAAGTAAATGCTCAAGATATT
SEQ2302	-----
SEQ2303	TTCAATCATTAGCAAAGCAAGTCATTCATCAGGCAGTAGAAGTAAATGCTCAAGATATT
SEQ2304	-----GATATT
SEQ2305	TTCAATCATTAGCAAAGCAAGTCATTCATCAGGCAGTAGAAGTAAATGCTCAAGATATT
SEQ2306	TTCAATCATTAGCAAAGCAAGTCATTCATCAGGCAGTAGAAGTAAATGCTCAAGATATT
SEQ2307	-----
SEQ2308	-----TCATTAGCAAAGCAAGTCATTCATCAGGCAGTAGAAGTAAATGCTCAAGATATT
SEQ2309	TTCAATCATTAGCAAAGCAAGTCATTCATCAGGCAGTAGAAGTAAATGCTCAAGATATT
SEQ2310	-----
SEQ2311	-----CAGTAGAAGTAAATGCTCAAGATATT
SEQ2301	ATATCATTCCTCCAAAGGTGA-TTGTTATGAA-CTCTATA----TGCGTATT-GATGATGA
SEQ2302	-----GGTGA-TTGTTATGAA-ACCTCTACTATTGCGTATTTGATGATGA
SEQ2303	ATATCATTCCTCCAAAGGTGA-TTGTTATGAA-CTCTATA----TGCGTATT-GATGATGA
SEQ2304	ATATCATTCCTCCAAAGGTGA-TTGTTATGAA-CTCTATA----TGCGTATT-GATGATGA
SEQ2305	ATATCATTCCTCCAAAGGTGA-TTGTTATGAA-CTCTATA----TGCGTATT-GATGATGA
SEQ2306	ATATCATTCCTCCAAAGGTGA-TTGTTATGAA-CTCTATA----TGCGTATT-GATGATGA
SEQ2307	-----AGGTGA-TTGTTATGAAATCTCTATA----TGCGTATT-GATGATGA
SEQ2308	ATATCATTCCTCCAAAGGTGA-TTGTTATGAA-CTCTATA----TGCGTATT-GATGATGA
SEQ2309	ATATCATTCCTCCAAAGGTGA-TTGTTATGAA-CTCTATA----TGCGTATT-GATGATGA
SEQ2310	-----TGACTTGTTATGAACTCTATA----TGCGTATTTGATGATGA
SEQ2311	ATATCATTCCTCCAAAGGTGA-TTGTTATGAA-TTCTATA----TGCGTATT-GATGATGA
SEQ2301	AA-GGCGGTTTATTGATGTTTTTGAGTTTAAATAGGATGGCTAGTCTTATTAGTCACCTTA
SEQ2302	AA-GGCGGTTTATTGATGTTTTTGAGTTTAAATAGGATGGCTAGTCTTATTAGTCACCTTA
SEQ2303	AA-GGCGGTTTATTGATGTTTTTGAGTTTAAATAGGATGGCTAGTCTTATTAGTCACCTTA
SEQ2304	AA-GGCGGTTTATTGATGTTTTTGAGTTTAAATAGGATGGCTAGTCTTATTAGTCACCTTA
SEQ2305	AA-GGCGGTTTATTGATGTTTTTGAGTTTAAATAGGATGGCTAGTCTTATTAGTCACCTTA
SEQ2306	AA-GGCGGTTTATTGATGTTTTTGAGTTTAAATAGGATGGCTAGTCTTATTAGTCACCTTA
SEQ2307	AA-GGCGGTTTATTGATGTTTTTGAGTTTAAATAGGATGGCTAGTCTTATTAGTCACCTTA
SEQ2308	AA-GGCGGTTTATTGATGTTTTTGAGTTTAAATAGGATGGCTAGTCTTATTAGTCACCTTA
SEQ2309	AA-GGCGGTTTATTGATGTTTTTGAGTTTAAATAGGATGGCTAGTCTTATTAGTCACCTTA
SEQ2310	AAAGGCGGTTTATTGATGTTTTTGAGTTTAAATAGGATGGCTAGTCTTATTAGTCACCTTA
SEQ2311	AA-GGCGGTTTATTGATGTTTTTGAGTTTAAATAGGATGGCTAGTCTTATTAGTCACCTTA
SEQ2301	AATTTGTGGCAGGCATGAACGTTGGAGAAAAAAGACGAAGTCAATTAGGTTCTTGTGACT
SEQ2302	AATTTGTGGCAGGCATGAACGTTGGAGAAAAAAGACGAAGTCAATTAGGTTCTTGTGACT
SEQ2303	AATTTGTGGCAGGCATGAACGTTGGAGAAAAAAGACGAAGTCAATTAGGTTCTTGTGACT
SEQ2304	AATTTGTGGCAGGCATGAACGTTGGAGAAAAAAGACGAAGTCAATTAGGTTCTTGTGACT
SEQ2305	AATTTGTGGCAGGCATGAACGTTGGAGAAAAAAGACGAAGTCAATTAGGTTCTTGTGACT
SEQ2306	AATTTGTGGCAGGCATGAACGTTGGAGAAAAAAGACGAAGTCAATTAGGTTCTTGTGACT
SEQ2307	AATTTGTGGCAGGCATGAACGTTGGAGAAAAAAGACGAAGTCAATTAGGTTCTTGTGACT
SEQ2308	AATTTGTGGCAGGCATGAACGTTGGAGAAAAAAGACGAAGTCAATTAGGTTCTTGTGACT
SEQ2309	AATTTGTGGCAGGCATGAACGTTGGAGAAAAAAGACGAAGTCAATTAGGTTCTTGTGACT
SEQ2310	AATTTGTGGCAGGCATGAACGTTGGAGAAAAAAGACGAAGTCAATTAGGTTCTTGTGACT
SEQ2311	AATTTGTGGCAGGCATGAACGTTGGAGAAAAAAGACGAAGTCAATTAGGTTCTTGTGACT

**Table 23: Comparative Sequences relating to SAG0163
(competence protein Cg1A)**

SEQ2301	ATGAACGTGTAGAGGGAAGACTGGTTTCATTACGACTATCGAGTGTGGGAGATTATCGTG
SEQ2302	ATGAACGTGTAGAGGGAAGACTGGTTTCATTACGACTATCGAGTGTGGGAGATTATCGTG
SEQ2303	ATGAACGTGTAGAGGGAAGACTGGTTTCATTACGACTATCGAGTGTGGGAGATTATCGTG
SEQ2304	ATGAACGTGTAGAGGGAAGACTGGTTTCATTACGACTATCGAGTGTGGGAGATTATCGTG
SEQ2305	ATGAACGTGTAGAGGGAAGACTGGTTTCATTACGACTATCGAGTGTGGGAGATTATCGTG
SEQ2306	ATGAACGTGTAGAGGGAAGACTGGTTTCATTACGACTATCGAGTGTGGGAGATTATCGTG
SEQ2307	ATGAACGTGTAGAGGGAAGACTGGTTTCATTACGACTATCAAGTGTGGGAGATTATCGTG
SEQ2308	ATGAACGTGTAGAGGGAAGACTGGTTTCATTACGACTATCGAGTGTGGGAGATTATCGTG
SEQ2309	ATGAACGTGTAGAGGGAAGACTGGTTTCATTACGACTATCGAGTGTGGGAGATTATCGTG
SEQ2310	ATGAACGTGTAGAGGGAAGACTGGTTTCATTACGACTATCAAGTGTGGGAGATTATCGTG
SEQ2311	ATGAACGTGTAGAGGGAAGACTGGTTTCATTACGACTATCAAGTGTGGGAGATTATCGTG
SEQ2301	GTCAAGAATCTTTAGTTATTCGTATTTTGTATTTCAGGTCATCAGGACTTAAAATATTGGT
SEQ2302	GTCAAGAATCTTTAGTTATTCGTATTTTGTATTTCAGGTCATCAGGACTTAAAATATTGGT
SEQ2303	GTCAAGAATCTTTAGTTATTCGTATTTTGTATTTCAGGTCATCAGGACTTAAAATATTGGT
SEQ2304	GTCAAGAATCTTTAGTTATTCGTATTTTGTATTTCAGGTCATCAGGACTTAAAATATTGGT
SEQ2305	GTCAAGAATCTTTAGTTATTCGTATTTTGTATTTCAGGTCATCAGGACTTAAAATATTGGT
SEQ2306	GTCAAGAATCTTTAGTTATTCGTATTTTGTATTTCAGGTCATCAGGACTTAAAATATTGGT
SEQ2307	GTCAAGAATCTTTAGTTATTCGTATTTTGTATTTCAGGTCATCAGGACTTAAAATATTGGT
SEQ2308	GTCAAGAATCTTTAGTTATTCGTATTTTGTATTTCAGGTCATCAGGACTTAAAATATTGGT
SEQ2309	GTCAAGAATCTTTAGTTATTCGTATTTTGTATTTCAGGTCATCAGGACTTAAAATATTGGT
SEQ2310	GTCAAGAATCTTTAGTTATTCGTATTTTGTATTTCAGGTCATCAGGACTTAAAATATTGGT
SEQ2311	GTCAAGAATCTTTAGTTATTCGTATTTTGTATTTCAGGTCATCAGGACTTAAAATATTGGT
SEQ2301	TTGATAATATAAAGCAAATGAAGGAAGTACTGGGTACAAGAGGGCTATATCTTTTTTCCG
SEQ2302	TTGATAATATAAAGCAAATGAAGGAAGTACTGGGTACAAGAGGGCTATATCTTTTTTCCG
SEQ2303	TTGATAATATAAAGCAAATGAAGGAAGTACTGGGTACAAGAGGGCTATATCTTTTTTCCG
SEQ2304	TTGATAATATAAAGCAAATGAAGGAAGTACTGGGTACAAGAGGGCTATATCTTTTTTCCG
SEQ2305	TTGATAATATAAAGCAAATGAAGGAAGTACTGGGTACAAGAGGGCTATATCTTTTTTCCG
SEQ2306	TTGATAATATAAAGCAAATGAAGGAAGTACTGGGTACAAGAGGGCTATATCTTTTTTCCG
SEQ2307	TTGATAATATAAAGTAAATGAAGGAAGTACTGTGTGCAAGAGGGCTATATCTTTTTTCCG
SEQ2308	TTGATAATATAAAGCAAATGAAGGAAGTACTGGGTACAAGAGGGCTATATCTTTTTTCCG
SEQ2309	TTGATAATATAAAGCAAATGAAGGAAGTACTGGGTACAAGAGGGCTATATCTTTTTTCCG
SEQ2310	TTGATAATATAAAGTAAATGAAGGAAGTACTGTGTGCAAGAGGGCTATATCTTTTTTCCG
SEQ2311	TTGATAATATAAAGCAAATGAAGGAAGTACTGTGTGCAAGAGGGCTATATCTTTTTTCCG
SEQ2301	GCCCTGTGGGGAGTGGTAAAACAACCTCTCATGTATCAATTAGCTTCAGAAGTATTTAAAA
SEQ2302	GCCCTGTGGGGAGTGGTAAAACAACCTCTCATGTATCAATTAGCTTCAGAAGTATTTAAAA
SEQ2303	GCCCTGTGGGGAGTGGTAAAACAACCTCTCATGTATCAATTAGCTTCAGAAGTATTTAAAA
SEQ2304	GCCCTGTGGGGAGTGGTAAAACAACCTCTCATGTATCAATTAGCTTCAGAAGTATTTAAAA
SEQ2305	GCCCTGTGGGGAGTGGTAAAACAACCTCTCATGTATCAATTAGCTTCAGAAGTATTTAAAA
SEQ2306	GCCCTGTGGGGAGTGGTAAAACAACCTCTCATGTATCAATTAGCTTCAGAAGTATTTAAAA
SEQ2307	GCCCTGTGGGGAGTGGTAAAACAACCTCTCATGTATCAATTAGCTTCAGAAGTATTTAAAA
SEQ2308	GCCCTGTGGGGAGTGGTAAAACAACCTCTCATGTATCAATTAGCTTCAGAAGTATTTAAAA
SEQ2309	GCCCTGTGGGGAGTGGTAAAACAACCTCTCATGTATCAATTAGCTTCAGAAGTATTTAAAA
SEQ2310	GCCCTGTGGGGAGTGGTAAAACAACCTCTCATGTATCAATTAGCTTCAGAAGTATTTAAAA
SEQ2311	GCCCTGTGGGGAGTGGTAAAACAACCTCTCATGTATCAATTAGCTTCAGAAGTATTTAAAA

**Table 23: Comparative Sequences relating to SAG0163
(competence protein Cg1A)**

SEQ2301	ATAAGCAAATTATCACGATTGAAGATCCGGTAGAAATCAAGAATGACAAGATGTTTACAAC
SEQ2302	ATAAGCAAATTATCACGATTGAAGATCCGGTAGAAATCAAGAATGACAAGATGTTTACAAC
SEQ2303	ATAAGCAAATTATCACGATTGAAGATCCGGTAGAAATCAAGAATGACAAGATGTTTACAAC
SEQ2304	ATAAGCAAATTATCACGATTGAAGATCCGGTAGAAATCAAGAATGACAAGATGTTTACAAC
SEQ2305	ATAAGCAAATTATCACGATTGAAGATCCGGTAGAAATCAAGAATGACAAGATGTTTACAAC
SEQ2306	ATAAGCAAATTATCACGATTGAAGATCCGGTAGAAATCAAGAATGACAAGATGTTTACAAC
SEQ2307	ATAAGCAAATTATCACGATTGAAGATCCGGTAGAAATCAAGAATGACAAGATGTTTACAAC
SEQ2308	ATAAGCAAATTATCACGATTGAAGATCCGGTAGAAATCAAGAATGACAAGATGTTTACAAC
SEQ2309	ATAAGCAAATTATCACGATTGAAGATCCGGTAGAAATCAAGAATGACAAGATGTTTACAAC
SEQ2310	ATAAGCAAATTATCACGATTGAAGATCCGGTAGAAATCAAGAATGACAAGATGTTTACAAC
SEQ2311	ATAAGCAAATTATCACGATTGAAGATCCGGTAGAAATCAAGAATGACAAGATGTTTACAAC
SEQ2301	TCCAATTGAATGAGGATATTGGAATGACTTATGATGCTTTAATCAAACGTCTTTACGGC
SEQ2302	TCCAATTGAATGAGGATATTGGAATGACTTATGATGCTTTAATCAAACGTCTTTACGGC
SEQ2303	TCCAATTGAATGAGGATATTGGAATGACTTATGATGCTTTAATCAAACGTCTTTACGGC
SEQ2304	TCCAATTGAATGAGGATATTGGAATGACTTATGATGCTTTAATCAAACGTCTTTACGGC
SEQ2305	TCCAATTGAATGAGGATATTGGAATGACTTATGATGCTTTAATCAAACGTCTTTACGGC
SEQ2306	TCCAATTGAATGAGGATATTGGAATGACTTATGATGCTTTAATCAAACGTCTTTACGGC
SEQ2307	TCCAATTGAATGAGGATATTGGAATGACTTATGATGCTTTAATCAAACGTCTTTACGGC
SEQ2308	TCCAATTGAATGAGGATATTGGAATGACTTATGATGCTTTAATCAAACGTCTTTACGGC
SEQ2309	TCCAATTGAATGAGGATATTGGAATGACTTATGATGCTTTAATCAAACGTCTTTACGGC
SEQ2310	TCCAATTGAATGAGGATATTGGAATGACTTATGATGCTTTAATCAAACGTCTTTACGGC
SEQ2311	TCCAATTGAATGAGGATATTGGAATGACTTATGATGCTTTAATCAAACGTCTTTACGGC
SEQ2301	ATCGTCCAGATATTTTAATTATCGGAGAGAT-TAGAGATCAAGCGACGGCCCGTGCTGTT
SEQ2302	ATCGTCCAGATATTTTAATTATCGGAGAGAT-TAGAGATCAAGCGACGGCCCGTGCTGTT
SEQ2303	ATCGTCCAGATATTTTAATTATCGGAGAGAT-TAGAGATCAAGCGACGGCCCGTGCTGTT
SEQ2304	ATCGTCCAGATATTTTAATTATCGGAGAGAT-TAGAGATCAAGCGACGGCCCGTGCTGTT
SEQ2305	ATCGTCCAGATATTTTAATTATCGGAGAGAT-TAGAGATCAAGCGACGGCCCGTGCTGTT
SEQ2306	ATCGTCCAGATATTTTAATTATCGGAGAGAT-TAGAGATCAAGCGACGGCCCGTGCTGTT
SEQ2307	ATCGTCCAGATATTTTAATTATCGGAGAGAT-TAGAGATCAAGCGACGGCCCGTGCTGTT
SEQ2308	ATCGTCCAGATATTTTAATTATCGGAGAGAT-TAGAGATCAAGCGACGGCCCGTGCTGTT
SEQ2309	ATCGTCCAGATATTTTAATTATCGGAGAGAT-TAGAGATCAAGCGACGGCCCGTGCTGTT
SEQ2310	ATCGTCCAGATATTTTAATTATCGGAGAGAT-TAGAGATCAAGCGACGGCCCGTGCTGTT
SEQ2311	ATCGTCCAGATATTTTAATTATCGGAGAGAT-TAGAGATCAAGCGACGGCCCGTGCTGTT
SEQ2301	ATTCGTGCAAGTTTAAACGGGAGTGATGGTTTTTTTCTACTATTTCATGCTAAAAGTATTCCC
SEQ2302	ATTCGTGCAAGTTTAAACGGGAGTGATGGTTTTTTTCTACTATTTCATGCTAAAAGTATTCCC
SEQ2303	ATTCGTGCAAGTTTAAACGGGAGTGATGGTTTTTTTCTACTATTTCATGCTAAAAGTATTCCC
SEQ2304	ATTCGTGCAAGTTTAAACGGGAGTGATGGTTTTTTTCTACTATTTCATGCTAAAAGTATTCCC
SEQ2305	ATTCGTGCAAGTTTAAACGGGAGTGATGGTTTTTTTCTACTATTTCATGCTAAAAGTATTCCC
SEQ2306	ATTCGTGCAAGTTTAAACGGGAGTGATGGTTTTTTTCTACTATTTCATGCTAAAAGTATTCCC
SEQ2307	ATTCGTGCAAGTTTAAACGGGAGTGATGGTTTTTTTCTACTATTTCATGCTAAAAGTATTCCC
SEQ2308	ATTCGTGCAAGTTTAAACGGGAGTGATGGTTTTTTTCTACTATTTCATGCTAAAAGTATTCCC
SEQ2309	ATTCGTGCAAGTTTAAACGGGAGTGATGGTTTTTTTCTACTATTTCATGCTAAAAGTATTCCC
SEQ2310	ATTCGTGCAAGTTTAAACGGGAGTGATGGTTTTTTTCTACTATTTCATGCTAAAAGTATTCCC
SEQ2311	ATTCGTGCAAGTTTAAACGGGAGTGATGGTTTTTTTCTACTATTTCATGCTAAAAGTATTCCC
SEQ2301	GGAGTCTATGATAGGCTTATAGAATTAGGGGTTAACTATCAAGAGTTAGAAAATAGTCTA
SEQ2302	GGAGTCTATGATAGGCTTATAGAATTAGGGGTTAACTATCAAGAGTTAGAAAATAGTCTA
SEQ2303	GGAGTCTATGATAGGCTTATAGAATTAGGGGTTAACTATCAAGAGTTAGAAAATAGTCTA
SEQ2304	GGAGTCTATGATAGGCTTATAGAATTAGGGGTTAACTATCAAGAGTTAGAAAATAGTCTA
SEQ2305	GGAGTCTATGATAGGCTTATAGAATTAGGGGTTAACTATCAAGAGTTAGAAAATAGTCTA
SEQ2306	GGAGTCTATGATAGGCTTATAGAATTAGGGGTTAACTATCAAGAGTTAGAAAATAGTCTA
SEQ2307	GGAGTCTATGATAGGCTTATAGAATTAGGGGTTAACTATCAAGAGTTAGAAAATAGTCTA
SEQ2308	GGAGTCTATGATAGGCTTATAGAATTAGGGGTTAACTATCAAGAGTTAGAAAATAGTCTA
SEQ2309	GGAGTCTATGATAGGCTTATAGAATTAGGGGTTAACTATCAAGAGTTAGAAAATAGTCTA
SEQ2310	GGAGTCTATGATAGGCTTATAGAATTAGGGGTTAACTATCAAGAGTTAGAAAATAGTCTA
SEQ2311	GGAGTCTATGATAGGCTTATAGAATTAGGGGTTAACTATCAAGAGTTAGAAAATAGTCTA
SEQ2301	AAATTAATAGCATATCAACGTTTAAATTGGAGGAGGAAGCCTAATTGACTTTGAGACAGGT
SEQ2302	AAATTAATAGCATATCAACGTTTAAATTGGAGGAGGAAGCCTAATTGACTTTGAGACAGGT
SEQ2303	AAATTAATAGCATATCAACGTTTAAATTGGAGGAGGAAGCCTAATTGACTTTGAGACAGGT
SEQ2304	AAATTAATAGCATATCAACGTTTAAATTGGAGGAGGAAGCCTAATTGACTTTGAGACAGGT
SEQ2305	AAATTAATAGCATATCAACGTTTAAATTGGAGGAGGAAGCCTAATTGACTTTGAGACAGGT
SEQ2306	AAATTAATAGCATATCAACGTTTAAATTGGAGGAGGAAGCCTAATTGACTTTGAGACAGGT
SEQ2307	AAATTAATAGCATATCAACGTTTAAATTGGAGGAGGAAGCCTAATTGACTTTGAGACAGGT

**Table 23: Comparative Sequences relating to SAG0163
(competence protein Cg1A)**

SEQ2308	AAATTAATAGCATATCAACGTTTAAATTGGAGGAGGAAGCCTAATTGACTTTGAGACAGGT
SEQ2309	AAATTAATAGCATATCAACGTTTAAATTGGAGGAGGAAGCCTAATTGACTTTGAGACAGGT
SEQ2310	AAATTAATAGCATATCAACGTTTAAATTGGAGGAGGAAGCCTAATTGACTTTGAGACAAGT
SEQ2311	AAATTAATAGCATATCAACGTTTAAATTGGAGGAGGAAGCCTAATTGACTTTGAGACAAGT
SEQ2301	AACTTTAAAAAACACTCATCAGACAAGTGGAAATAGACAAGTGGATATCTTGGCTGAAGAA
SEQ2302	AACTTTAAAAAACACTCATCAGACAAGTGGAAATAGACAAGTGGATATCTTGGCTGAAGAA
SEQ2303	AATTTTAAAAAACACTCATCAGACAAGTGGAAATAGACAAGTGGATATCTTGGCTGAAGAA
SEQ2304	AATTTTAAAAAACACTCATCAGACAAGTGGAAATAGACAAGTGGATATCTTGGCTGAAGAA
SEQ2305	AATTTTAAAAAACACTCATCAGACAAGTGGAAATAGACAAGTGGATATCTTGGCTGAAGAA
SEQ2306	AACTTTAAAAAACACTCATCAGACAAGTGGAAATAGACAAGTGGATATCTTGGCTGAAGAA
SEQ2307	AACTTTAAAAAACACTCATCAGACAAGTGGAAATAGACAAGTGGATATCTTGGCTGAAGAA
SEQ2308	AATTTTAAAAAACACTCATCAGACAAGTGGAAATAGACAAGTGGATATCTTGGCTGAAGAA
SEQ2309	AATTTTAAAAAACACTCATCAGACAAGTGGAAATAGACAAGTGGATATCTTGGCTGAAGAA
SEQ2310	AACTTTAAAAAACACTCATCAGACAAGTGGAAATAGACAAGTGGATATCTTGGCTGAAGAA
SEQ2311	AACTTTAAAAAACACTCATCAGACAAGTGGAAATAGACAAGTGGATATCTTGGCTGAAGAA
SEQ2301	GGACATATCAGTAAGAAACAGGCACAAGT - CGAAAAAATTATCCCTCAAGAAACAAACGGA
SEQ2302	GGATATATCAGTAAGAAACAGGCACAAGT - CGAAAAAATTATCCCTCAAGAAACAAACGGA
SEQ2303	GGACATATCAGTAAGAAACAGGCACAAGT - CGAAAAAATTATCCCTCAAGAAACAAACGGA
SEQ2304	GGACATATCAGTAAGAAACAGGCACAAGT - CGAAAAAATTATCCCTCAAGAAACAAACGGA
SEQ2305	GGACATATCAGTAAGAAACAGGCACAAGT - CGAAAAAATTATCCCTCAAGAAACAAACGGA
SEQ2306	GGACATATCAGTAAGAAACAGGCACAAGT - CGAAAAAATTATCCCTCAAGAAACAAACGGA
SEQ2307	GGACATATCAGTAAGAAACAGGCACAAGT - CGAAAAAATTATCCCTCAAGAAACAAACGGA
SEQ2308	GGACATATCAGTAAGAAACAGGCACAAGT - CGAAAAAATTATCCCTCAAGAAACAAACGGA
SEQ2309	GGACATATCAGTAAGAAACAGGCACAAGT - CGAAAAAATTATCCCTCAAGAAACAAACGGA
SEQ2310	GGACATATCAGTAAGAAACAGGCACAAGT - CGAAAAAATTATCCCTCAAGAAACAAACGGA
SEQ2311	GGACATATCAGTAAGAAACAGGCACAAGT - CGAAAAAATTATCCCTCAAGAAACAAACGGA
SEQ2301	AAGTAGTCCAACCTTTT-----
SEQ2302	AAGTAGTCCAACCTTTT-----
SEQ2303	AAGTAGTCCAACCTTTT-----
SEQ2304	AAGTAGTCCAACCTTTT-----
SEQ2305	AAGTAGTCCAACCTTTT-----
SEQ2306	AAGTAGTCCAACCTTTT-----
SEQ2307	AAGTAGTCCAACCTTTT-----
SEQ2308	AAGTAGTCCAACCTTTT-----
SEQ2309	AAGTAGTCCAACCTTTT-----
SEQ2310	AAGTAGTCCAACCTTTT-----
SEQ2311	AAGTAGTCCAACCTTTT-----
>SEQ ID NO 2350:63_090 frame: 2	
AVEVNAQDIYIIPKGDCELYMRIDDERRFIDVFEFNRMASLISHFKFVAGMNVGEKRRS	
QLGSCDYELSEGRVSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDNIKQMKVGLGTR	
GLYLFSGPVGSGKTTLMYQLASEVFNKQIITIEDPVEIKNDKMLQLQLNEDIGMTYDAL	
IKLSLRHRPDILIGEIRDQATARAVIRASLTGVMVFSTIHAKSISGVYDRLELGVNYQ	
ELENSLKLIAIYQRLIGGSLIDFETGNFKHSSDKWNRQVDILAEEGHISKKAQVEKII	
PQETTESPTF	
>SEQ ID NO 2351:63_1169NT frame: 3	
.LL.NLYYCVFDDERRRFIDVFEFNRMASLISHFKFVAGMNVGEKRRSRLGSCDYELSEGR	
LVSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDNIKQMKVGLGTRGLYLFSGPVGSGK	
TTLMYQLASEVFNKQIITIEDPVEIKNDKMLQLQLNEDIGMTYDALIKLSLRHRPDILI	
IGEIRDQATARAVIRASLTGVMVFSTIHAKSIPGVYDRLELGVNYQELENLKLIAIYQR	
LIGGSLIDFETSNFKHSSDKWNRQVDILAEEGYISKKAQVEKIIPQETTESPTF	
>SEQ ID NO 2352:63_18RS21 frame: 1	
VQSLAKQVHQAVEVNAQDIYIIPKGDCELYMRIDDERRFIDVFEFNRMASLISHFKFV	
AGMNVGEKRRSRLGSCDYELSEGRVSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDN	
IKQMKVGLGIRGLYLFSGPVGSGKTTLMYQLASEVFNKQIITIEDPVEIKNDKMLQLQL	
NEDIGMTYDALIKLSLRHRPDILIGEIRDQATARAVIRASLTGVMVFSTIHAKSIPGVY	
DRLELGVNYQELENLKLIAIYQRLIGGSLIDFETGNFKHSSDKWNRQVDILAEEGHI	
SKKAQVEKIIPQETTESPTF	
>SEQ ID NO 2353: 63_2603 frame: 1	
DIYIIPKGDCELYMRIDDERRFIDVFEFNRMASLISHFKFVAGMNVGEKRRSRLGSCDY	
ELSEGRVSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDNIKQMKVGLGIRGLYLFSG	

**Table 23: Comparative Sequences relating to SAG0163
(competence protein Cg1A)**

PVSGSKTTLMYQLASEVFKNKQIITIEDPVEIKNDKMLQLQLNEDIGMTYDALIKLSLRH
RPDILIIIGEIRDQATARAVIRASLTGVMVFSTIHAKSIPGVYDRLIELGVNYQELENLKL
LIAYQRLIGGSLIDFETGNFKKHSSDKWNRQVDILAEEGHISKQAQVRKNYPSRNNKG
.SNF

>SEQ ID NO 2354:63_A909 frame: 1

VQSLAKQVIHQAVEVNAQDIYIIPKGDCELYMRIDDERRFIDVFEFNRMASLISHFKFV
AGMNVGEKRRSQLGSCDYELSEGRLVSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDN
IKQMKVEVLGIRGLYLFSGPVGSGKTTLMYQLASEVFKNKQIITIEDPVEIKNDKMLQLQL
NEDIGMTYDALIKLSLRHRPDILIIIGEIRDQATARAVIRASLTGVMVFSTIHAKSIPGVY
DRLIELGVNYQELENLKLIIAYQRLIGGSLIDFETGNFKKHSSDKWNRQVDILAEEGHI
SKKQAQVEKIIPQETTESPTF

>SEQ ID NO 2355:63_CJB110 frame: 1

VQSLAKQVIHQAVEVNAQDIYIIPKGDCELYMRIDDERRFIDVFEFNRMASLISHFKFV
AGMNVGEKRRSQLGSCDYELSEGRLVSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDN
IKQMKVEVLGTRGLYLFSGPVGSGKTTLMYQLASEVFKNKQIITIEDPVEIKNDKMLQLQL
NEDIGMTYDALIKLSLRHRPDILIIIGEIRDQATARAVIRASLTGVMVFSTIHAKSIPGVY
DRLIELGVNYQELENLKLIIAYQRLIGGSLIDFETGNFKKHSSDKWNRQVDILAEEGHI
SKKQAQVEKIIPQETTESPTF

>SEQ ID NO 2356:63_CJB110 frame: 1

VQSLAKQVIHQAVEVNAQDIYIIPKGDCELYMRIDDERRFIDVFEFNRMASLISHFKFV
AGMNVGEKRRSQLGSCDYELSEGRLVSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDN
IKQMKVEVLGTRGLYLFSGPVGSGKTTLMYQLASEVFKNKQIITIEDPVEIKNDKMLQLQL
NEDIGMTYDALIKLSLRHRPDILIIIGEIRDQATARAVIRASLTGVMVFSTIHAKSIPGVY
DRLIELGVNYQELENLKLIIAYQRLIGGSLIDFETGNFKKHSSDKWNRQVDILAEEGHI
SKKQAQVEKIIPQETTESPTF

>SEQ ID NO 2357: 63_H36B frame: 1

SLAKQVIHQAVEVNAQDIYIIPKGDCELYMRIDDERRFIDVFEFNRMASLISHFKFVAG
MNVGEKRRSQLGSCDYELSEGRLVSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDNIK
QMKEVLGIRGLYLFSGPVGSGKTTLMYQLASEVFKNKQIITIEDPVEIKNDKMLQLQLNE
DIGMTYDALIKLSLRHRPDILIIIGEIK

>SEQ ID NO 2358:63_JM9130013 frame: 1

VQSLAKQVIHQAVEVNAQDIYIIPKGDCELYMRIDDERRFIDVFEFNRMASLISHFKFV
AGMNVGEKRRSQLGSCDYELSEGRLVSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDN
IKQMKVEVLGIRGLYLFSGPVGSGKTTLMYQLASEVFKNKQIITIEDPVEIKNDKMLQLQL
NEDIGMTYDALIKLSLRHRPDILIIIGEIRDQATARAVIRASLTGVMVFSTIHAKSIPGVY
DRLIELGVNYQELENLKLIIAYQRLIGGSLIDFETGNFKKHSSDKWNRQVDILAEEGHI
SKKQAQVEKIIPQETTESPTF

>SEQ ID NO 2359:63_M732 frame: 3

TCYETLYAYLMMKRRFIDVFEFNRMASLISHFKFVAGMNVGEKRRSQLGSCDYELSEGRL
VSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDNIK.MKEVLCARGLYLFSGPVGSGKT
TLMYQLASEVFKNKQIITIEDPVEIKNDKMLQLQLNEDIGMTYDALIKLSLRHRPDILII
GEIRDQATARAVIRASLTGVMVFSTIHAKSIPGVYDRLIELGVNYQELENLKLIIAYQRL
IGGSLIDFETSNFKKHSSDKWNRQVDILAEEGHISKQAQVEKIIPQETTESPTF

>SEQ ID NO 2360:63_M781 frame: 3

VEVNAQDIYIIPKGDCELYFMRIDDERRFIDVFEFNRMASLISHFKFVAGMNVGEKRRSQ
LGSCDYELSEGRLVSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDNIKQMKEVLCARG
LYLFSGPVGSGKTTLMYQLASEVFKNKQIITIEDPVEIKNDKMLQLQLNEDIGMTYDALI
KLSLRHRPDILIIIGEIRDQATARAVIRASLTGVMVFSTIHAKSIPGVYDRLIELGVNYQE
LENSLKLIIAYQRLIGGSLIDFETSNFKKHSSDKWNRQVDILAEEGHISKQAQVEKIIP
QETTESPTF

>SEQ ID NO 2361:63_COH1 frame: 3

VIVMKFYMRIDDERRFIDVFEFNRMASLISHFKFVAGMNVGEKRRSQLGSCDYELSEGRL
VSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDNIK

**Table 23: Comparative Sequences relating to SAG0163
(competence protein Cg1A)**

SEQ2350	-----AVEVNAQDIYIIPKGDCELYMRIDDERRFIDVFEFNRMASLISHFKFV
SEQ2351	-----LLNLYYCVFDDERRFIDVFEFNRMASLISHFKFV
SEQ2352	QSLAKQVIHQAVEVNAQDIYIIPKGDCELYMRIDDERRFIDVFEFNRMASLISHFKFV
SEQ2353	-----DIYIIPKGDCELYMRIDDERRFIDVFEFNRMASLISHFKFV
SEQ2354	QSLAKQVIHQAVEVNAQDIYIIPKGDCELYMRIDDERRFIDVFEFNRMASLISHFKFV
SEQ2355	QSLAKQVIHQAVEVNAQDIYIIPKGDCELYMRIDDERRFIDVFEFNRMASLISHFKFV
SEQ2356	QSLAKQVIHQAVEVNAQDIYIIPKGDCELYMRIDDERRFIDVFEFNRMASLISHFKFV
SEQ2357	-SLAKQVIHQAVEVNAQDIYIIPKGDCELYMRIDDERRFIDVFEFNRMASLISHFKFV
SEQ2358	QSLAKQVIHQAVEVNAQDIYIIPKGDCELYMRIDDERRFIDVFEFNRMASLISHFKFV
SEQ2359	-----TCYETLYAYLMMKRRFIDVFEFNRMASLISHFKFV
SEQ2360	-----VEVNAQDIYIIPKGDCELYFMRIDDERRFIDVFEFNRMASLISHFKFV
SEQ2361	-----VIVMKFYMRIDDERRFIDVFEFNRMASLISHFKFV
SEQ2350	AGMNVGEKRRSQLGSCDYELSEGRLVSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDN
SEQ2351	AGMNVGEKRRSQLGSCDYELSEGRLVSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDN
SEQ2352	AGMNVGEKRRSQLGSCDYELSEGRLVSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDN
SEQ2353	AGMNVGEKRRSQLGSCDYELSEGRLVSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDN
SEQ2354	AGMNVGEKRRSQLGSCDYELSEGRLVSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDN
SEQ2355	AGMNVGEKRRSQLGSCDYELSEGRLVSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDN
SEQ2356	AGMNVGEKRRSQLGSCDYELSEGRLVSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDN
SEQ2357	AGMNVGEKRRSQLGSCDYELSEGRLVSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDN
SEQ2358	AGMNVGEKRRSQLGSCDYELSEGRLVSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDN
SEQ2359	AGMNVGEKRRSQLGSCDYELSEGRLVSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDN
SEQ2360	AGMNVGEKRRSQLGSCDYELSEGRLVSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDN
SEQ2361	AGMNVGEKRRSQLGSCDYELSEGRLVSLRLSSVGDYRGQESLVIRILYSGHQDLKYWFDN
SEQ2350	IKQMKEVLGTRGLYLFSGPVGSGKTTLMYQLASEVFKNKQIITIEDPVEIKNDKMLQLQL
SEQ2351	IKQMKEVLGTRGLYLFSGPVGSGKTTLMYQLASEVFKNKQIITIEDPVEIKNDKMLQLQL
SEQ2352	IKQMKEVLGIRGLYLFSGPVGSGKTTLMYQLASEVFKNKQIITIEDPVEIKNDKMLQLQL
SEQ2353	IKQMKEVLGIRGLYLFSGPVGSGKTTLMYQLASEVFKNKQIITIEDPVEIKNDKMLQLQL
SEQ2354	IKQMKEVLGIRGLYLFSGPVGSGKTTLMYQLASEVFKNKQIITIEDPVEIKNDKMLQLQL
SEQ2355	IKQMKEVLGTRGLYLFSGPVGSGKTTLMYQLASEVFKNKQIITIEDPVEIKNDKMLQLQL
SEQ2356	IKQMKEVLGTRGLYLFSGPVGSGKTTLMYQLASEVFKNKQIITIEDPVEIKNDKMLQLQL
SEQ2357	IKQMKEVLGIRGLYLFSGPVGSGKTTLMYQLASEVFKNKQIITIEDPVEIKNDKMLQLQL
SEQ2358	IKQMKEVLGIRGLYLFSGPVGSGKTTLMYQLASEVFKNKQIITIEDPVEIKNDKMLQLQL
SEQ2359	IK-MKEVLGIRGLYLFSGPVGSGKTTLMYQLASEVFKNKQIITIEDPVEIKNDKMLQLQL
SEQ2360	IKQMKEVLGIRGLYLFSGPVGSGKTTLMYQLASEVFKNKQIITIEDPVEIKNDKMLQLQL
SEQ2361	IK-----
SEQ2350	EDIGMTYDALIKLSLRHRPDILIGEIRDQATARAVIRASLTGVMVFSTIHAKSISGVY
SEQ2351	EDIGMTYDALIKLSLRHRPDILIGEIRDQATARAVIRASLTGVMVFSTIHAKSIPGVY
SEQ2352	EDIGMTYDALIKLSLRHRPDILIGEIRDQATARAVIRASLTGVMVFSTIHAKSIPGVY
SEQ2353	EDIGMTYDALIKLSLRHRPDILIGEIRDQATARAVIRASLTGVMVFSTIHAKSIPGVY
SEQ2354	EDIGMTYDALIKLSLRHRPDILIGEIRDQATARAVIRASLTGVMVFSTIHAKSIPGVY
SEQ2355	EDIGMTYDALIKLSLRHRPDILIGEIRDQATARAVIRASLTGVMVFSTIHAKSISGVY
SEQ2356	EDIGMTYDALIKLSLRHRPDILIGEIRDQATARAVIRASLTGVMVFSTIHAKSISGVY
SEQ2357	EDIGMTYDALIKLSLRHRPDILIGEIR-----
SEQ2358	EDIGMTYDALIKLSLRHRPDILIGEIRDQATARAVIRASLTGVMVFSTIHAKSIPGVY
SEQ2359	EDIGMTYDALIKLSLRHRPDILIGEIRDQATARAVIRASLTGVMVFSTIHAKSIPGVY
SEQ2360	EDIGMTYDALIKLSLRHRPDILIGEIRDQATARAVIRASLTGVMVFSTIHAKSIPGVY
SEQ2361	-----
SEQ2350	RLIELGVNYQELENLSKLIAYQRLIGGGSLLDFETGNFKKHSSDKWNRQVDILAEEGHI
SEQ2351	RLIELGVNYQELENLSKLIAYQRLIGGGSLLDFETSNFKKHSSDKWNRQVDILAEEGYI
SEQ2352	RLIELGVNYQELENLSKLIAYQRLIGGGSLLDFETGNFKKHSSDKWNRQVDILAEEGHI
SEQ2353	RLIELGVNYQELENLSKLIAYQRLIGGGSLLDFETGNFKKHSSDKWNRQVDILAEEGHI
SEQ2354	RLIELGVNYQELENLSKLIAYQRLIGGGSLLDFETGNFKKHSSDKWNRQVDILAEEGHI
SEQ2355	RLIELGVNYQELENLSKLIAYQRLIGGGSLLDFETGNFKKHSSDKWNRQVDILAEEGHI
SEQ2356	RLIELGVNYQELENLSKLIAYQRLIGGGSLLDFETGNFKKHSSDKWNRQVDILAEEGHI
SEQ2357	-----
SEQ2358	RLIELGVNYQELENLSKLIAYQRLIGGGSLLDFETGNFKKHSSDKWNRQVDILAEEGHI
SEQ2359	RLIELGVNYQELENLSKLIAYQRLIGGGSLLDFETSNFKKHSSDKWNRQVDILAEEGHI
SEQ2360	RLIELGVNYQELENLSKLIAYQRLIGGGSLLDFETSNFKKHSSDKWNRQVDILAEEGHI
SEQ2361	-----

**Table 23: Comparative Sequences relating to SAG0163
(competence protein Cg1A)**

SEQ2350	KKQAQVEKIIPQETTESSPTF
SEQ2351	KKQAQVEKIIPQETTESSPTF
SEQ2352	KKQAQVEKIIPQETTESSPTF
SEQ2353	KKQAQVRKNYPSRNGKSNF-
SEQ2354	KKQAQVEKIIPQETTESSPTF
SEQ2355	KKQAQVEKIIPQETTESSPTF
SEQ2356	KKQAQVEKIIPQETTESSPTF
SEQ2357	-----
SEQ2358	KKQAQVEKIIPQETTESSPTF
SEQ2359	KKQAQVEKIIPQETTESSPTF
SEQ2360	KKQAQVEKIIPQETTESSPTF
SEQ2361	-----

**Figure 24: Comparative Sequences relating to SAG0290
(ABC transporter, substrate-binding protein)**

SEQ ID NO. 2401: SAG0290 FROM THE 1169NT1 GBS TYPE V STRAIN (REVERSE COMPLEMENT)

GTATCAGTTCAGGCGTCAGAGAAAGTAGAACTTAAAGTAGCTACAGATTCTGACACGGCACCATTCTACTTA
TCAAAAAGACGGGAAATTCAAAGGTTATGATGTTGATGTTGTCAAAGCTGTTTTTAAAGGTAGTAAGTACA
AAGTAACCTTCAAGACAGTTCCTTTTGATACTATTTCAACAGGTATTGATGCAGGGAAATTTGATTTATCA
GCTAATGATTTTTTCATACAATAAAGAAAGAGCAGAAAAATATCTCTTCTCAGACCCTATATCCCGTTCAAA
TTATGCCGTAGTAGGGAAGAAGGGGAGCCATTACAAATCATTAAAGTGACCTCTCTGGAAAATCAACAGAAG
TTTTATCTGGCGTTAACTATGCACAGGTTCTAGAAAATTGGAATAAAAAATCATCCTAATAAAAAACCAATA
AAAATCAAATATGTTTTCTGGGACAACTGGTGTTACTAGCAGATTAAAAAATATTGAGAGTGGGAAAATTGA
CTTTATCCTATATGATGCCATTTTCATCTGACTATATTGTAAAAGATCAATCATTAACTTAAGCGTTTCTC
CTTTGAAAGGTAAAATTGGTAATAATAAGGATGGATTAGAATACCTCCTTTTACCAAAGATAAAAAAGGT
AAAACCTCTACAGAAATTTATAAATAAGCGTATTAAAGTTTTGAAAGAAGATGGTACTTTGGCAGGTTTAAG
TAAACAATATTTTCGGTGGAGATTACGTTTCAAACATTGATAAA

SEQ ID NO. 2402: SAG0290 FROM THE 18RS21 GBS TYPE II STRAIN (REVERSE COMPLEMENT)

GTATCAGTTCAGGCGTCAGAGAAAGTAGAACTTAAAGTAGCTACAGATTCTGACACGGCACCATTCTACTTA
TRAAAAAGACGGGAAATTCAAAGGTTATGATGTTGATGTTGTCAAAGCTGTTTTTAAAGGTAGTAAGTACA
AAGTAACCTTCAAGACAGTTCCTTTTGATACTATTTCAACAGGTATTGATGCAGGGAAATTTGATTTATCA
GCTAATGATTTTTTCATACAATAAAGAAAGAGCAGAAAAATATCTCTTCTCAGATCCTATATCCCGTTCAAA
TTATGCCGTAGTAGGGAAGAAGGGGAGCCATTACAAATCATTAAAGTGACCTCTCTGGAAAATCAACCGAAG
TTTTATCTGGCGTTAACTATGCACAGGTTCTAGAAAATTGGAATAAAAAATCATCCTAATAAAAAACCAATA
AAAATCAAATATGTTTTCTGGGACAACTGGTGTTACTAGCAGATTAAAAAATATTGAGAGTGGGAAAATTGA
CTTTATCCTATATGATGCCATTTTCATCCGACTATATTGTAAAAGACCAATCATTAACTTAAGCGTTTCTC
CTTTGAAAGGTAAAATTGGTAATAATAAGGATGGACTAGAATACCTCCTTTTACCAAAGATAAAAAAGGT
AAAACCTCTACAGAAATTTATAAATAAGCGTATTAAAGTTTTGAAAGAAGATGGTACTTTGGCAGGTTTAAG
TAAACAATATTTTCGGTGGAGATTACGTTTCAAACATTGATAAA

SEQ ID NO. 2403: SAG0290 FROM THE 2603 V/R GBS TYPE V STRAIN (REVERSE COMPLEMENT)

ATTCAAAGGTTATGATGTTGATGTTGTCAAAGCTGTTTTTAAAGGTAGTAAGTACAAAGTAACCTTCAAGA
CAGTTCCTTTTGATACTATTTCAACAGGTATTGATGCAGGGAAATTTGATTTATCAGCTAATGATTTTTCA
TACAATAAAGAAAGAGCAGAAAAATATCTCTTCTCAGATCCTATATCCCGTTCAAATTATGCCGTAGTAGG
GAAGAAGGGGAGCCATTACAAATCATTAAAGTGACCTCTCTGGAAAATCAACCGAAGTTTTATCTGGCGTTA
ACTATGCACAGGTTCTAGAAAATTGGAATAAAAAATCATCCTAATAAAAAACCAATAAAAAATCAAATATGTT
TCTGGGACAACTGGTGTTACTAGCAGATTAAAAAATATTGAGAGTGGGAAAATTGACTTTATCCTATATGA
TGCCATTTTCATCCGACTATATTGTAAAAGACCAATCATTAAACTTAAGCGTTTCTCCTTTGAAAGGTAAAA
TTGGTAATAATAAGGATGGACTAGAATACCTCCTTTTACCAAAGATAAAAAAG

SEQ ID NO. 2404: SAG0290 FROM THE 090 GBS TYPE Ia STRAIN (REVERSE COMPLEMENT)

GTATCAGTTCAGGCGTCAGAGAAAGTAGAACTTAAAGTAGCTACAGATTCTGACACGGCACCATTCTACTTA
TCAAAAAGACGGGAAATTCAAAGGTTATGATGTTGATGTTGTCAAAGCTGTTTTTAAAGGTAGTAAGTACA
AAGTAACCTTCAAGACAGTTCCTTTTGATACTATTTCAACAGGTATTGATGCAGGGAAATTTGATTTATCA
GCTAATGATTTTTTCATACAATAAAGAAAGAGCAGAAAAATATCTCTTCTCAGATCCTATATCCCGTTCAAA
TTATGCCGTAGTAGGGAAGAAGGGGAGCCATTACAAATCATTAAAGTGACCTCTCTGGAAAATCAACCGAAG
TTTTATCTGGCGTTAACTATGCACAGGTTCTAGAAAATTGGAATAAAAAATCATCCTAATAAAAAACCAATA
AAAATCAAATATGTTTTCTGGGACAACTGGTGTTACTAGCAGATTAAAAAATATTGAGAGTGGGAAAATTGA
CTTTATCCTATATGATGCCATTTTCATCCGACTATATTGTAAAAGACCAATCATTAACTTAAGCGTTTCTCCT
TTGAAAGGTAAAATTGGTAATAATAAGGATGGACTAGAATACCTCCTTTTACCAAAGATAAAAAAGGTAAACTCTA
CAGAAATTTATAAATAAGCGTATTAAAGTTTTGAAAGAAATGGTACTTTGGCAGGTTTAAGTAAACAATATTTTCGGT
GGAGATTACGTTTCAAACATTGATAAA

**Figure 24: Comparative Sequences relating to SAG0290
(ABC transporter, substrate-binding protein)**

SEQ ID NO. 2405: SAG0290 FROM THE A909 GBS TYPE Ia STRAIN (REVERSE COMPLEMENT)

GTATCAGTTTCAGGCGTCAGAGAAAGTAGAACTTAAAGTAGCTACAGATTCTGACACGGCACCATTTACTTTA
TCAAAAAGACGGGAAATTCAAAGGTTATGATGTTGATGTTGTCAAAGCTGTTTTTAAAGGTAGTAAGTACA
AAGTAACCTTCAAGACAGTTCCTTTTGATACTATTTCAACAGGTATTGATGCAGGGAAATTTGATTTATCA
GCTAATGATTTTTTCATACAATAAAGAAAGAGCAGAAAAATATCTCTTCTCAGATCCTATATCCCGTTCAAA
TTATGCCGTAGTAGGGAAGAAGGGGAGCCATTACAAATCATTAAAGTGACCTCTCTGGAAAATCAACCGAAG
TTTTATCTGGCGTTAACTATGCACAGGTTCTAGAAAAATTGGAATAAAAAATCATNNTAATAAAAAACCANTA
AAAAATNAAATATGTTTTCTGGGACAACCTGGTGTTACTAGCAGATTAAAAAATATTGAGAGTGGGAAAATTGA
CTTTATCCTATATGATGCCATTTTCATCCGACTATATTGTAAAAGACCAATCATTAACTTAAGCGTTTTCTC
CTTTGAAAGGTAAAATTGGTAATAATAAGGATGGACTAGAATACCTCCTTTTACCAAAAGATAAAAAAGGT
AAAACCTCTACAGAAATTTATAAATAAGCGT

SEQ ID NO. 2406: SAG0290 FROM THE CJB110 GBS NONTYPEABLE STRAIN (REVERSE COMPLEMENT)

GTATCAGTTTCAGGCGTCAGAGAAAGTAGAACTTAAAGTAGCTACAGATTCTGACACGGCACCATTTACTTTA
TCAAAAAGACGGGAAATTCAAAGGTTATGATGTTGATGTTGTCAAAGCTGTTTTTAAAGGTAGTAAGTACA
AAGTAACCTTCAAGACAGTTCCTTTTGATACTATTTCAACAGGTATTGATGCAGGGAAATTTGATTTATCA
GCTAATGATTTTTTCATACAATAAAGAAAGAGCAGAAAAATATCTCTTCTCAGATCCTATATCCCGTTCAAA
TTATGCCGTAGTAGGGAAGAAGGGGAGCCATTACAAATCATTAAAGTGACCTCTCTGGAAAATCAACCGAAG
TTTTATCTGGCGTTAACTATGCACAGGTTCTAGAAAAATTGGAATAAAAAATCATCCTAATAAAAAACCAATA
AAAATCAAATATGTTTTCTGGGACAACCTGGTGTTACTAGCAGATTAAAAAATATTGAGAGTGGGAAAATTGA
CTTTATCCTATATGATGCCATTTTCATCCGACTATATTGTAAAAGACCAATCATTAACTTAAGCGTTTTCTC
CTTTGAAAGGTAAAATTGGTAATAATAAGGATGGACTAGAATACCTCCTTTTACCAAAAGATAAAAAAGGT
AAAACCTCTACAGAAATTTATAAATAAGCGTATTAAAGTTTTGAAAGAAAATGGTACTTTGGCACGTTTAAG
TAAACAATATTTCCGTGGAGATTACGTTTCAAACATTGATAAA

SEQ ID NO. 2407: SAG0290 FROM THE COH1 GBS TYPE III STRAIN (REVERSE COMPLEMENT)

GTATCAGTTTCAGGCGTCAGAGAAAGTAGAACTTAAAGTAGCTACAGATTCTGACACGGCACCATTTACTTTA
TCAAAAAGACGGGAAATTCAAAGGTTATGACGTTGATGTTGTCAAAGCTGTTTTTAAAGGTAGTAAGTACA
AAGTAACCTTCAAGACAGTTCCTTTTGATACTATTTCAACAGGTATTGATGCAGGGAAATTTGATTTATCA
GCTAATGATTTTTTCATATAATAAAGAAAGAGCAGAAAAATATCTCTTCTCAGATCCTATATCCCGTTCAAA
TTATGCCGTAGTAGGGAAGAAGGGGAGCCATTACAAATCATTAAAGTGACCTCTCTGGAAAATCAACAGAAG
TTTTATCTGGCGTTAACTATGCACAGGTTCTAGAAAAATTGGAATAAAAAATCATCCTAATAAAAAACCAATA
AAAATCAAATATGTTTTCTGGGACAACCTGGTGTTACTAGCAGATTAAAAAATATTGAGAGTGGGAAAATTGA
CTTTATCCTATATGATGCCATTTTCATCTGACTATATTGTAAAAGATCAATCATTAACTTAAGCGTTTTCTC
CTTTGAAAGGTAAAATTGGTAATAATAAGGATGGATTAGAATACCTCCTTTTACCAAAAGATAAAAAAGGT
AAAACCTCTACAGAAATTTATAAATAAGCGTATTAAAGTTTTGAAAGAAGATGGTACTTTGGCACGTTTAAG
TAAACAATATTTCCGTGGAGATTACGTTTCAAACATTGATAAA

SEQ ID NO. 2408: SAG0290 FROM THE H36b GBS TYPE Ib STRAIN (REVERSE COMPLEMENT)

GTATCAGTTTCAGGCGTCAGAGAAAGTAGAACTTAAAGTAGCTACAGATTCTGACACGGCACCATTTACTTTA
TCAAAAAGACGGGAAATTCAAAGGTTATGATGTTGATGTTGTCAAAGCTGTTTTTAAAGGTAGTAAGTACA
AAGTAACCTTCAAGACAGTTCCTTTTGATACTATTTCAACAGGTATTGATGCAGGGAAATTTGATTTATCA
GCTAATGATTTTTTCATACAATAAAGAAAGAGCAGAAAAATATCTCTTCTCAGATCCTATATCCCGTTCAAA
TTATGCCGTAGTAGGGAAGAAGGGGAGCCATTACAAATCATTAAAGTGACCTCTCTGGAAAATCAACCGAAG
TTTTATCTGGCGTTAACTATGCACAGGTTCTAGAAAAATTGGAATAAAAAATCATCCTAATAAAAAACCAATA
AAAATCAAATATGTTTTCTGGGACAACCTGGTGTTACTAGCAGATTAAAAAATATTGAGAGTGGGAAAATTGA
CTTTATCCTATATGATGCCATTTTCATCCGACTATATTGTAAAAGACCAATCATTAACTTAAGCGTTTTCTC
CTTTGAAAGGTAAAATTGGTAATAATAAGGATGGACTAGAATACCTCCTTTTACCAAAAGATAAAAAAGGT
AAAACCTCTACAGAAATTTATAAATAAGCGTATTAAAGTTTTGAAAGAAAATGGTACTTTGGCACGTTTAAG
TAAACAATATTTCCGTGGAGATTACGTTTCAAACATTGATAAA

**Figure 24: Comparative Sequences relating to SAG0290
(ABC transporter, substrate-binding protein)**

SEQ ID NO. 2409: SAG0290 FROM THE JM9130013 GBS STRAIN VIII (REVERSE COMPLEMENT)

GTATCAGTTCAGGCGTCAGAGAAAGTAGAACTTAAAGTAGCTACAGATTCTGACACGGCACCATTCTACTTATCAAAAAGACGGGAAATTCAAAGGTTATGATGTTGATGTTGTCAAAGCTGTTTTTAAAGGTAGTAAGTACAAGTAACCTTCAAGACAGTTCCTTTTGATACTATTTCAACAGGTATTGATGCAGGGAAATTTGATTTATCAGCTAATGATTTTTCATACAATAAAGAAAGAGCAGAAAAATATCTCTTCTCAGATCCTATATCCCGTTCAAA TTATGCCGTAGTAGGGAAGAAGGGGAGCCATTACAAATCATTAAAGTGACCTCTCTGGAAAATCAACCGAAG TTTTATCTGGCGTTAACTATGCACAGGTTCTAGAAAATTGGAATAAAAATCATCCTAATAAAAAACCAATA AAAATCAAATATGTTTCTGGGACAACTGGTGTTACTAGCAGATTAAAAAATATTGAGAGTGGGAAAATTGA CTTTATCCTATATGATGCCATTTTCATCCGACTATATTGTAAAAGACCAATCATTAACTTAAGCGTTTCTC CTTTGAAAGGTAAAATTGGTAATAATAAGGATGGACTAGAATACCTCCTTTTACCAAAAGATAAAAAAGGT AAAACTCTACAGAAATTTATAAATAAGCGTAATAAAGTTTTTGAAAGAAAATGGTA

SEQ ID NO. 2410: SAG0290 FROM THE M732 GBS TYPE III STRAIN (REVERSE COMPLEMENT)

GTATCAGTTCAGGCGTCAGAGAAAGTAGAACTTAAAGTAGCTACAGATTCTGACACGGCACCATTCTACTTATCAAAAAGACGGGAAATTCAAAGGTTATGACGTTGATGTTGTCAAAGCTGTTTTTAAAGGTAGTAAGTACA AAGTAACCTTCAAGACAGTTCCTTTTGATACTATTTCAACAGGTATTGATGCAGGGAAATTTGATTTATCAGCTAATGATTTTTCATATAATAAAGAAAGAGCAGAAAAATATCTCTTCTCAGATCCTATATCCCGTTCAAA TTATGCCGTAGTAGGGAAGAAGGGGAGCCATTACAAATCATTAAAGTGACCTCTCTGGAAAATCAACAGAAG TTTTATCTGGCGTTAACTATGCACAGGTTCTAGAAAATTGGAATAAAAATCATCCTAATAAAAAACCAATA AAAATCAAATATGTTTCTGGGACAACTGGTGTTACTAGCAGATTAAAAAATATTGAGAGTGGGAAAATTGA CTTTATCCTATATGATGCCATTTTCATCTGACTATATTGTAAAAGATCAATCATTAACTTAAGCGTTTCTC CTTTGAAAGGTAAAATTGGTAATAATAAGGATGGATTAGAATACCTCCTTTTACCAAAAGATAAAAAAGGT AAAACTCTACAGAAATTTATAAATAAGCGTATTAAAGTTTTTGAAAGAAGATGGTACTTTGGCACGTTTAAG TAAACAATATTTTCGGTGGAGATTACGTTTCAAACATTGATAAA

SEQ ID NO. 2411: SAG0290 FROM THE M781 GBS TYPE III STRAIN (REVERSE COMPLEMENT)

GTATCAGTTCAGGCGTCAGAGAAAGTAGAACTTAAAGTAGCTACAGATTCTGACACGGCACCATTCTACTTATCAAAAAGACGGGAAATTCAAAGGTTATGACGTTGATGTTGTCAAAGCTGTTTTTAAAGGTAGTAAGTACA AAGTAACCTTCAAGACAGTTCCTTTTGATACTATTTCAACAGGTATTGATGCAGGGAAATTTGATTTATCAGCTAATGATTTTTCATATAATAAAGAAAGAGCAGAAAAATATCTCTTCTCAGATCCTATATCCCGTTCAAA TTATGCCGTAGTAGGGAAGAAGGGGAGCCATTACAAATCATTAAAGTGACCTCTCTGGAAAATCAACAGAAG TTTTATCTGGCGTTAACTATGCACAGGTTCTAGAAAATTGGAATAAAAATCATCCTAATAAAAAACCAATA AAAATCAAATATGTTTCTGGGACAACTGGTGTTACTAGCAGATTAAAAAATATTGAGAGTGGGAAAATTGA CTTTATCCTATATGATGCCATTTTCATCTGACTATATTGTAAAAGATCAATCATTAACTTAAGCGTTTCTC CTTTGAAAGGTAAAATTGGTAATAATAAGGATGGATTAGAATACCTCCTTTTACCAAAAGATAAAAAAGGT AAAACTCTACAGAAATTTATAAATAAGCGTATTAAAGTTTTTGAAAGAAGATGGTACTTTGGCACGTTTAAG TAAACAATATTTTCGGTGGAGATTACGTTTCAAACATTGATAAA

SEQ2401	TATCAGTTCAGGCGTCAGAGAAAGTAGAACTTAAAGTAGCTACAGATTCTGACACGGCA
SEQ2402	TATCAGTTCAGGCGTCAGAGAAAGTAGAACTTAAAGTAGCTACAGATTCTGACACGGCA
SEQ2403	-----
SEQ2404	TATCAGTTCAGGCGTCAGAGAAAGTAGAACTTAAAGTAGCTACAGATTCTGACACGGCA
SEQ2405	TATCAGTTCAGGCGTCAGAGAAAGTAGAACTTAAAGTAGCTACAGATTCTGACACGGCA
SEQ2406	TATCAGTTCAGGCGTCAGAGAAAGTAGAACTTAAAGTAGCTACAGATTCTGACACGGCA
SEQ2407	TATCAGTTCAGGCGTCAGAGAAAGTAGAACTTAAAGTAGCTACAGATTCTGACACGGCA
SEQ2408	TATCAGTTCAGGCGTCAGAGAAAGTAGAACTTAAAGTAGCTACAGATTCTGACACGGCA
SEQ2409	TATCAGTTCAGGCGTCAGAGAAAGTAGAACTTAAAGTAGCTACAGATTCTGACACGGCA
SEQ2410	TATCAGTTCAGGCGTCAGAGAAAGTAGAACTTAAAGTAGCTACAGATTCTGACACGGCA
SEQ2411	TATCAGTTCAGGCGTCAGAGAAAGTAGAACTTAAAGTAGCTACAGATTCTGACACGGCA

SEQ2401	CATTACTTATCAAAAAGACGGGAAATTCAAAGGTTATGATGTTGATGTTGTCAAAGCT
SEQ2402	CATTACTTATRAAAAAGACGGGAAATTCAAAGGTTATGATGTTGATGTTGTCAAAGCT
SEQ2403	-----ATTCAAAGGTTATGATGTTGATGTTGTCAAAGCT
SEQ2404	CATTACTTATCAAAAAGACGGGAAATTCAAAGGTTATGATGTTGATGTTGTCAAAGCT
SEQ2405	CATTACTTATCAAAAAGACGGGAAATTCAAAGGTTATGATGTTGATGTTGTCAAAGCT
SEQ2406	CATTACTTATCAAAAAGACGGGAAATTCAAAGGTTATGATGTTGATGTTGTCAAAGCT
SEQ2407	CATTACTTATCAAAAAGACGGGAAATTCAAAGGTTATGATGTTGATGTTGTCAAAGCT
SEQ2408	CATTACTTATCAAAAAGACGGGAAATTCAAAGGTTATGATGTTGATGTTGTCAAAGCT
SEQ2409	CATTACTTATCAAAAAGACGGGAAATTCAAAGGTTATGATGTTGATGTTGTCAAAGCT

**Figure 24: Comparative Sequences relating to SAG0290
(ABC transporter, substrate-binding protein)**

SEQ2410 CATTTACTTATCAAAAAGACGGGAAATTCAAAGGTTATGACGTTGATGTTGTCAAAGCT
SEQ2411 CATTTACTTATCAAAAAGACGGGAAATTCAAAGGTTATGACGTTGATGTTGTCAAAGCT

SEQ2401 GTTTTTAAAGGTAGTAAGTACAAAGTAACCTTCAAGACAGTTCCTTTTGATACTATTTTCA
SEQ2402 GTTTTTAAAGGTAGTAAGTACAAAGTAACCTTCAAGACAGTTCCTTTTGATACTATTTTCA
SEQ2403 GTTTTTAAAGGTAGTAAGTACAAAGTAACCTTCAAGACAGTTCCTTTTGATACTATTTTCA
SEQ2404 GTTTTTAAAGGTAGTAAGTACAAAGTAACCTTCAAGACAGTTCCTTTTGATACTATTTTCA
SEQ2405 GTTTTTAAAGGTAGTAAGTACAAAGTAACCTTCAAGACAGTTCCTTTTGATACTATTTTCA
SEQ2406 GTTTTTAAAGGTAGTAAGTACAAAGTAACCTTCAAGACAGTTCCTTTTGATACTATTTTCA
SEQ2407 GTTTTTAAAGGTAGTAAGTACAAAGTAACCTTCAAGACAGTTCCTTTTGATACTATTTTCA
SEQ2408 GTTTTTAAAGGTAGTAAGTACAAAGTAACCTTCAAGACAGTTCCTTTTGATACTATTTTCA
SEQ2409 GTTTTTAAAGGTAGTAAGTACAAAGTAACCTTCAAGACAGTTCCTTTTGATACTATTTTCA
SEQ2410 GTTTTTAAAGGTAGTAAGTACAAAGTAACCTTCAAGACAGTTCCTTTTGATACTATTTTCA
SEQ2411 GTTTTTAAAGGTAGTAAGTACAAAGTAACCTTCAAGACAGTTCCTTTTGATACTATTTTCA

SEQ2401 ACAGGTATTGATGCAGGGAAATTGATTATTCAGCTAATGATTTTTCATACAATAAAGAA
SEQ2402 ACAGGTATTGATGCAGGGAAATTGATTATTCAGCTAATGATTTTTCATACAATAAAGAA
SEQ2403 ACAGGTATTGATGCAGGGAAATTGATTATTCAGCTAATGATTTTTCATACAATAAAGAA
SEQ2404 ACAGGTATTGATGCAGGGAAATTGATTATTCAGCTAATGATTTTTCATACAATAAAGAA
SEQ2405 ACAGGTATTGATGCAGGGAAATTGATTATTCAGCTAATGATTTTTCATACAATAAAGAA
SEQ2406 ACAGGTATTGATGCAGGGAAATTGATTATTCAGCTAATGATTTTTCATACAATAAAGAA
SEQ2407 ACAGGTATTGATGCAGGGAAATTGATTATTCAGCTAATGATTTTTCATACAATAAAGAA
SEQ2408 ACAGGTATTGATGCAGGGAAATTGATTATTCAGCTAATGATTTTTCATACAATAAAGAA
SEQ2409 ACAGGTATTGATGCAGGGAAATTGATTATTCAGCTAATGATTTTTCATACAATAAAGAA
SEQ2410 ACAGGTATTGATGCAGGGAAATTGATTATTCAGCTAATGATTTTTCATACAATAAAGAA
SEQ2411 ACAGGTATTGATGCAGGGAAATTGATTATTCAGCTAATGATTTTTCATACAATAAAGAA

SEQ2401 AGAGCAGAAAAATATCTCTTCTCAGACCTATATCCCGTTCAAATTATGCCGTAGTAGGG
SEQ2402 AGAGCAGAAAAATATCTCTTCTCAGATCCTATATCCCGTTCAAATTATGCCGTAGTAGGG
SEQ2403 AGAGCAGAAAAATATCTCTTCTCAGATCCTATATCCCGTTCAAATTATGCCGTAGTAGGG
SEQ2404 AGAGCAGAAAAATATCTCTTCTCAGATCCTATATCCCGTTCAAATTATGCCGTAGTAGGG
SEQ2405 AGAGCAGAAAAATATCTCTTCTCAGATCCTATATCCCGTTCAAATTATGCCGTAGTAGGG
SEQ2406 AGAGCAGAAAAATATCTCTTCTCAGATCCTATATCCCGTTCAAATTATGCCGTAGTAGGG
SEQ2407 AGAGCAGAAAAATATCTCTTCTCAGATCCTATATCCCGTTCAAATTATGCCGTAGTAGGG
SEQ2408 AGAGCAGAAAAATATCTCTTCTCAGATCCTATATCCCGTTCAAATTATGCCGTAGTAGGG
SEQ2409 AGAGCAGAAAAATATCTCTTCTCAGATCCTATATCCCGTTCAAATTATGCCGTAGTAGGG
SEQ2410 AGAGCAGAAAAATATCTCTTCTCAGATCCTATATCCCGTTCAAATTATGCCGTAGTAGGG
SEQ2411 AGAGCAGAAAAATATCTCTTCTCAGATCCTATATCCCGTTCAAATTATGCCGTAGTAGGG

SEQ2401 AAGAAGGGGAGCCATTACAAATCATTAAGTGACCTCTCTGGAAAAATCAACAGAAGTTTTA
SEQ2402 AAGAAGGGGAGCCATTACAAATCATTAAGTGACCTCTCTGGAAAAATCAACCGAAGTTTTA
SEQ2403 AAGAAGGGGAGCCATTACAAATCATTAAGTGACCTCTCTGGAAAAATCAACCGAAGTTTTA
SEQ2404 AAGAAGGGGAGCCATTACAAATCATTAAGTGACCTCTCTGGAAAAATCAACCGAAGTTTTA
SEQ2405 AAGAAGGGGAGCCATTACAAATCATTAAGTGACCTCTCTGGAAAAATCAACCGAAGTTTTA
SEQ2406 AAGAAGGGGAGCCATTACAAATCATTAAGTGACCTCTCTGGAAAAATCAACCGAAGTTTTA
SEQ2407 AAGAAGGGGAGCCATTACAAATCATTAAGTGACCTCTCTGGAAAAATCAACCGAAGTTTTA
SEQ2408 AAGAAGGGGAGCCATTACAAATCATTAAGTGACCTCTCTGGAAAAATCAACCGAAGTTTTA
SEQ2409 AAGAAGGGGAGCCATTACAAATCATTAAGTGACCTCTCTGGAAAAATCAACCGAAGTTTTA
SEQ2410 AAGAAGGGGAGCCATTACAAATCATTAAGTGACCTCTCTGGAAAAATCAACAGAAGTTTTA
SEQ2411 AAGAAGGGGAGCCATTACAAATCATTAAGTGACCTCTCTGGAAAAATCAACAGAAGTTTTA

SEQ2401 TCTGGCGTTAACTATGCACAGGTTCTAGAAAAATGGAATAAAAAATCATCCTAATAAAAAA
SEQ2402 TCTGGCGTTAACTATGCACAGGTTCTAGAAAAATGGAATAAAAAATCATCCTAATAAAAAA
SEQ2403 TCTGGCGTTAACTATGCACAGGTTCTAGAAAAATGGAATAAAAAATCATCCTAATAAAAAA
SEQ2404 TCTGGCGTTAACTATGCACAGGTTCTAGAAAAATGGAATAAAAAATCATCCTAATAAAAAA
SEQ2405 TCTGGCGTTAACTATGCACAGGTTCTAGAAAAATGGAATAAAAAATCATCCTAATAAAAAA
SEQ2406 TCTGGCGTTAACTATGCACAGGTTCTAGAAAAATGGAATAAAAAATCATCCTAATAAAAAA
SEQ2407 TCTGGCGTTAACTATGCACAGGTTCTAGAAAAATGGAATAAAAAATCATCCTAATAAAAAA
SEQ2408 TCTGGCGTTAACTATGCACAGGTTCTAGAAAAATGGAATAAAAAATCATCCTAATAAAAAA
SEQ2409 TCTGGCGTTAACTATGCACAGGTTCTAGAAAAATGGAATAAAAAATCATCCTAATAAAAAA
SEQ2410 TCTGGCGTTAACTATGCACAGGTTCTAGAAAAATGGAATAAAAAATCATCCTAATAAAAAA
SEQ2411 TCTGGCGTTAACTATGCACAGGTTCTAGAAAAATGGAATAAAAAATCATCCTAATAAAAAA

SEQ2401 CCAATAAAAAATCAAATATGTTTCTGGGACAACCTGGTGTACTAGCAGATTAAAAAATATT
SEQ2402 CCAATAAAAAATCAAATATGTTTCTGGGACAACCTGGTGTACTAGCAGATTAAAAAATATT
SEQ2403 CCAATAAAAAATCAAATATGTTTCTGGGACAACCTGGTGTACTAGCAGATTAAAAAATATT
SEQ2404 CCAATAAAAAATCAAATATGTTTCTGGGACAACCTGGTGTACTAGCAGATTAAAAAATATT
SEQ2405 CCAATAAAAAATCAAATATGTTTCTGGGACAACCTGGTGTACTAGCAGATTAAAAAATATT
SEQ2406 CCAATAAAAAATCAAATATGTTTCTGGGACAACCTGGTGTACTAGCAGATTAAAAAATATT
SEQ2407 CCAATAAAAAATCAAATATGTTTCTGGGACAACCTGGTGTACTAGCAGATTAAAAAATATT
SEQ2408 CCAATAAAAAATCAAATATGTTTCTGGGACAACCTGGTGTACTAGCAGATTAAAAAATATT
SEQ2409 CCAATAAAAAATCAAATATGTTTCTGGGACAACCTGGTGTACTAGCAGATTAAAAAATATT

**Figure 24: Comparative Sequences relating to SAG0290
(ABC transporter, substrate-binding protein)**

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SEQ2410      CCAATAAAAAATCAAATATGTTTCTGGGACAACTGGTGTACTAGCAGATTAAAAAATATT
SEQ2411      CCAATAAAAAATCAAATATGTTTCTGGGACAACTGGTGTACTAGCAGATTAAAAAATATT

SEQ2401      GAGAGTGGGAAAAATTGACTTTATCCTATATGATGCCATTTTCATCTGACTATATTGTAAAA
SEQ2402      GAGAGTGGGAAAAATTGACTTTATCCTATATGATGCCATTTTCATCCGACTATATTGTAAAA
SEQ2403      GAGAGTGGGAAAAATTGACTTTATCCTATATGATGCCATTTTCATCCGACTATATTGTAAAA
SEQ2404      GAGAGTGGGAAAAATTGACTTTATCCTATATGATGCCATTTTCATCCGACTATATTGTAAAA
SEQ2405      GAGAGTGGGAAAAATTGACTTTATCCTATATGATGCCATTTTCATCCGACTATATTGTAAAA
SEQ2406      GAGAGTGGGAAAAATTGACTTTATCCTATATGATGCCATTTTCATCCGACTATATTGTAAAA
SEQ2407      GAGAGTGGGAAAAATTGACTTTATCCTATATGATGCCATTTTCATCTGACTATATTGTAAAA
SEQ2408      GAGAGTGGGAAAAATTGACTTTATCCTATATGATGCCATTTTCATCCGACTATATTGTAAAA
SEQ2409      GAGAGTGGGAAAAATTGACTTTATCCTATATGATGCCATTTTCATCCGACTATATTGTAAAA
SEQ2410      GAGAGTGGGAAAAATTGACTTTATCCTATATGATGCCATTTTCATCTGACTATATTGTAAAA
SEQ2411      GAGAGTGGGAAAAATTGACTTTATCCTATATGATGCCATTTTCATCTGACTATATTGTAAAA

SEQ2401      GATCAATCATTAAACTTAAGCGTTTCTCCTTTGAAAGGTAAAAATTGGTAATAATAAGGAT
SEQ2402      GACCAATCATTAAACTTAAGCGTTTCTCCTTTGAAAGGTAAAAATTGGTAATAATAAGGAT
SEQ2403      GACCAATCATTAAACTTAAGCGTTTCTCCTTTGAAAGGTAAAAATTGGTAATAATAAGGAT
SEQ2404      GACCAATCATTAAACTTAAGCGTTTCTCCTTTGAAAGGTAAAAATTGGTAATAATAAGGAT
SEQ2405      GACCAATCATTAAACTTAAGCGTTTCTCCTTTGAAAGGTAAAAATTGGTAATAATAAGGAT
SEQ2406      GACCAATCATTAAACTTAAGCGTTTCTCCTTTGAAAGGTAAAAATTGGTAATAATAAGGAT
SEQ2407      GATCAATCATTAAACTTAAGCGTTTCTCCTTTGAAAGGTAAAAATTGGTAATAATAAGGAT
SEQ2408      GACCAATCATTAAACTTAAGCGTTTCTCCTTTGAAAGGTAAAAATTGGTAATAATAAGGAT
SEQ2409      GACCAATCATTAAACTTAAGCGTTTCTCCTTTGAAAGGTAAAAATTGGTAATAATAAGGAT
SEQ2410      GATCAATCATTAAACTTAAGCGTTTCTCCTTTGAAAGGTAAAAATTGGTAATAATAAGGAT
SEQ2411      GATCAATCATTAAACTTAAGCGTTTCTCCTTTGAAAGGTAAAAATTGGTAATAATAAGGAT

SEQ2401      GGATTAGAATACCTCCTTTTACCAAAAGATAAAAAAGGTAAAACTCTACAGAAATTTATA
SEQ2402      GGACTAGAATACCTCCTTTTACCAAAAGATAAAAAAGGTAAAACTCTACAGAAATTTATA
SEQ2403      GGACTAGAATACCTCCTTTTACCAAAAGATAAAAAAGGTAAAACTCTACAGAAATTTATA
SEQ2404      GGACTAGAATACCTCCTTTTACCAAAAGATAAAAAAGGTAAAACTCTACAGAAATTTATA
SEQ2405      GGACTAGAATACCTCCTTTTACCAAAAGATAAAAAAGGTAAAACTCTACAGAAATTTATA
SEQ2406      GGACTAGAATACCTCCTTTTACCAAAAGATAAAAAAGGTAAAACTCTACAGAAATTTATA
SEQ2407      GGATTAGAATACCTCCTTTTACCAAAAGATAAAAAAGGTAAAACTCTACAGAAATTTATA
SEQ2408      GGACTAGAATACCTCCTTTTACCAAAAGATAAAAAAGGTAAAACTCTACAGAAATTTATA
SEQ2409      GGATTAGAATACCTCCTTTTACCAAAAGATAAAAAAGGTAAAACTCTACAGAAATTTATA
SEQ2410      GGATTAGAATACCTCCTTTTACCAAAAGATAAAAAAGGTAAAACTCTACAGAAATTTATA
SEQ2411      GGATTAGAATACCTCCTTTTACCAAAAGATAAAAAAGGTAAAACTCTACAGAAATTTATA

SEQ2401      ATAAGCGTATTAAAGTTTGAAGAAGATGGTACTTTGGCACGTTTAAGTAAACAATAT
SEQ2402      ATAAGCGTATTAAAGTTTGAAGAAGATGGTACTTTGGCACGTTTAAGTAAACAATAT
SEQ2403      -----
SEQ2404      ATAAGCGTATTAAAGTTTGAAGAAGATGGTACTTTGGCACGTTTAAGTAAACAATAT
SEQ2405      ATAAGCGT-----
SEQ2406      ATAAGCGTATTAAAGTTTGAAGAAGATGGTACTTTGGCACGTTTAAGTAAACAATAT
SEQ2407      ATAAGCGTATTAAAGTTTGAAGAAGATGGTACTTTGGCACGTTTAAGTAAACAATAT
SEQ2408      ATAAGCGTATTAAAGTTTGAAGAAGATGGTACTTTGGCACGTTTAAGTAAACAATAT
SEQ2409      ATAAGCGTAATAAAGTTTGAAGAAGATGGTA-----
SEQ2410      ATAAGCGTATTAAAGTTTGAAGAAGATGGTACTTTGGCACGTTTAAGTAAACAATAT
SEQ2411      ATAAGCGTATTAAAGTTTGAAGAAGATGGTACTTTGGCACGTTTAAGTAAACAATAT

SEQ2401      TCGGTGGAGATTACGTTTCAAACATTGATAAA-----
SEQ2402      TCGGTGGAGATTACGTTTCAAACATTGATAAA-----
SEQ2403      -----
SEQ2404      TCGGTGGAGATTACGTTTCAAACATTGATAAA-----
SEQ2405      -----
SEQ2406      TCGGTGGAGATTACGTTTCAAACATTGATAAA-----
SEQ2407      TCGGTGGAGATTACGTTTCAAACATTGATAAA-----
SEQ2408      TCGGTGGAGATTACGTTTCAAACATTGATAAA-----
SEQ2409      -----
SEQ2410      TCGGTGGAGATTACGTTTCAAACATTGATAAA-----
SEQ2411      TCGGTGGAGATTACGTTTCAAACATTGATAAAGTRCMARATVSTNCSRATNGTSAGABC

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**Figure 24: Comparative Sequences relating to SAG0290
(ABC transporter, substrate-binding protein)**

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SEQ2401      -----
SEQ2402      -----
SEQ2403      -----
SEQ2404      -----
SEQ2405      -----
SEQ2406      -----
SEQ2407      -----
SEQ2408      -----
SEQ2409      -----
SEQ2410      -----
SEQ2411      RANSRTRSTBSTRATBNDNGRTN

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>SEQ ID NO 2450: 8_1169NT frame: 1

VSVQASEKVELKVATDSDTAPFTYQKDGFKGVDVVDVVKAVFKGSKYKVTFTKTPPFDTIS
 TGIDAGKFDLSANDFSYNKERAEEKYLFSDPISRSNYAVVGKKGSHYKSLSDLGKSTEV
 SGVNYAQVLENWKNHNPKNKPIKIKYVSGTTGVTSLKKNIESGKIDFILYDAISSDYIVK
 DQSLNLSVSPKKGKIGNNKDGLEYLLLPKDKKGKTLQKFINKRIKVLKEDGTLARLSKQY
 FGGDYVSNIDK

>SEQ ID NO 2451: 8_18RS21 frame: 1

VSVQASEKVELKVATDSDTAPFTYQKDGFKGVDVVDVVKAVFKGSKYKVTFTKTPPFDTIS
 TGIDAGKFDLSANDFSYNKERAEEKYLFSDPISRSNYAVVGKKGSHYKSLSDLGKSTEV
 SGVNYAQVLENWKNHNPKNKPIKIKYVSGTTGVTSLKKNIESGKIDFILYDAISSDYIVK
 DQSLNLSVSPKKGKIGNNKDGLEYLLLPKDKKGKTLQKFINKRIKVLKENGTLARLSKQY
 FGGDYVSNIDK

>SEQ ID NO 2452: 8_2603 frame: 2

FKGYDVDVVKAVFKGSKYKVTFTKTPPFDTISTGIDAGKFDLSANDFSYNKERAEEKYLFSD
 PISRSNYAVVGKKGSHYKSLSDLGKSTEVLSGVNYAQVLENWKNHNPKNKPIKIKYVSG
 TTGVTSLKKNIESGKIDFILYDAISSDYIVKDQSLNLSVSPKKGKIGNNKDGLEYLLLPK
 DKK

>SEQ ID NO 2453: 8_090 frame: 1

VSVQASEKVELKVATDSDTAPFTYQKDGFKGVDVVDVVKAVFKGSKYKVTFTKTPPFDTIS
 TGIDAGKFDLSANDFSYNKERAEEKYLFSDPISRSNYAVVGKKGSHYKSLSDLGKSTEV
 SGVNYAQVLENWKNHNPKNKPIKIKYVSGTTGVTSLKKNIESGKIDFILYDAISSDYIVK
 DQSLNLSVSPKKGKIGNNKDGLEYLLLPKDKKGKTLQKFINKRIKVLKENGTLARLSKQY
 FGGDYVSNIDK

>SEQ ID NO 2454: 8_A909 frame: 1

VSVQASEKVELKVATDSDTAPFTYQKDGFKGVDVVDVVKAVFKGSKYKVTFTKTPPFDTIS
 TGIDAGKFDLSANDFSYNKERAEEKYLFSDPISRSNYAVVGKKGSHYKSLSDLGKSTEV
 SGVNYAQVLENWKNHNPKNKPIKIKYVSGTTGVTSLKKNIESGKIDFILYDAISSDYIVK
 DQSLNLSVSPKKGKIGNNKDGLEYLLLPKDKKGKTLQKFINKRIKVLKENGTLARLSKQY

>SEQ ID NO 2455: 8_CJB110 frame: 1

VSVQASEKVELKVATDSDTAPFTYQKDGFKGVDVVDVVKAVFKGSKYKVTFTKTPPFDTIS
 TGIDAGKFDLSANDFSYNKERAEEKYLFSDPISRSNYAVVGKKGSHYKSLSDLGKSTEV
 SGVNYAQVLENWKNHNPKNKPIKIKYVSGTTGVTSLKKNIESGKIDFILYDAISSDYIVK
 DQSLNLSVSPKKGKIGNNKDGLEYLLLPKDKKGKTLQKFINKRIKVLKENGTLARLSKQY
 FGGDYVSNIDK

>SEQ ID NO 2456: 8_COH1 frame: 1

VSVQASEKVELKVATDSDTAPFTYQKDGFKGVDVVDVVKAVFKGSKYKVTFTKTPPFDTIS
 TGIDAGKFDLSANDFSYNKERAEEKYLFSDPISRSNYAVVGKKGSHYKSLSDLGKSTEV
 SGVNYAQVLENWKNHNPKNKPIKIKYVSGTTGVTSLKKNIESGKIDFILYDAISSDYIVK
 DQSLNLSVSPKKGKIGNNKDGLEYLLLPKDKKGKTLQKFINKRIKVLKEDGTLARLSKQY
 FGGDYVSNIDK

>SEQ ID NO 2457: 8_H36B frame: 1

VSVQASEKVELKVATDSDTAPFTYQKDGFKGVDVVDVVKAVFKGSKYKVTFTKTPPFDTIS
 TGIDAGKFDLSANDFSYNKERAEEKYLFSDPISRSNYAVVGKKGSHYKSLSDLGKSTEV
 SGVNYAQVLENWKNHNPKNKPIKIKYVSGTTGVTSLKKNIESGKIDFILYDAISSDYIVK
 DQSLNLSVSPKKGKIGNNKDGLEYLLLPKDKKGKTLQKFINKRIKVLKENGTLARLSKQY
 FGGDYVSNIDK

**Figure 24: Comparative Sequences relating to SAG0290
(ABC transporter, substrate-binding protein)**

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>SEQ ID NO 2458:8_JM9130013 frame: 1
VSVQASEKVELKVATDSDTAPFTYQKDGKFKGYDVDVVKAVFKGSKYKVTFTKVPFDTIS
TGIDAGKFDLSANDFSYNKERAEEKYLFSDPISRSNYAVVGKKGSHYKSLSDLSGKSTEV
SGVNYAQVLENWKNHNPKNKKPIKIKYVSGTTGVTSLRNIESGKIDFILYDAISSDYIVK
DQSLNLSVSPKKGKIGNNKDGLEYLLLPKDKKGGKTLQKFINKRNKVLKENG

>SEQ ID NO 2459:8_M732 frame: 1
VSVQASEKVELKVATDSDTAPFTYQKDGKFKGYDVDVVKAVFKGSKYKVTFTKVPFDTIS
TGIDAGKFDLSANDFSYNKERAEEKYLFSDPISRSNYAVVGKKGSHYKSLSDLSGKSTEV
SGVNYAQVLENWKNHNPKNKKPIKIKYVSGTTGVTSLRNIESGKIDFILYDAISSDYIVK
DQSLNLSVSPKKGKIGNNKDGLEYLLLPKDKKGGKTLQKFINKRIKVLKEDGTLARLSKQY
FGGDYVSNIDK

>SEQ ID NO 2460:8_M781 frame: 1
VSVQASEKVELKVATDSDTAPFTYQKDGKFKGYDVDVVKAVFKGSKYKVTFTKVPFDTIS
TGIDAGKFDLSANDFSYNKERAEEKYLFSDPISRSNYAVVGKKGSHYKSLSDLSGKSTEV
SGVNYAQVLENWKNHNPKNKKPIKIKYVSGTTGVTSLRNIESGKIDFILYDAISSDYIVK
DQSLNLSVSPKKGKIGNNKDGLEYLLLPKDKKGGKTLQKFINKRIKVLKEDGTLARLSKQY
FGGDYVSNIDK

SEQ2450      SVQASEKVELKVATDSDTAPFTYQKDGKFKGYDVDVVKAVFKGSKYKVTFTKVPFDTIS
SEQ2451      SVQASEKVELKVATDSDTAPFTYQKDGKFKGYDVDVVKAVFKGSKYKVTFTKVPFDTIS
SEQ2452      -----FKGYDVDVVKAVFKGSKYKVTFTKVPFDTIS
SEQ2453      SVQASEKVELKVATDSDTAPFTYQKDGKFKGYDVDVVKAVFKGSKYKVTFTKVPFDTIS
SEQ2454      SVQASEKVELKVATDSDTAPFTYQKDGKFKGYDVDVVKAVFKGSKYKVTFTKVPFDTIS
SEQ2455      SVQASEKVELKVATDSDTAPFTYQKDGKFKGYDVDVVKAVFKGSKYKVTFTKVPFDTIS
SEQ2456      SVQASEKVELKVATDSDTAPFTYQKDGKFKGYDVDVVKAVFKGSKYKVTFTKVPFDTIS
SEQ2457      SVQASEKVELKVATDSDTAPFTYQKDGKFKGYDVDVVKAVFKGSKYKVTFTKVPFDTIS
SEQ2458      SVQASEKVELKVATDSDTAPFTYQKDGKFKGYDVDVVKAVFKGSKYKVTFTKVPFDTIS
SEQ2459      SVQASEKVELKVATDSDTAPFTYQKDGKFKGYDVDVVKAVFKGSKYKVTFTKVPFDTIS
SEQ2460      SVQASEKVELKVATDSDTAPFTYQKDGKFKGYDVDVVKAVFKGSKYKVTFTKVPFDTIS

SEQ2450      TGIDAGKFDLSANDFSYNKERAEEKYLFSDPISRSNYAVVGKKGSHYKSLSDLSGKSTEV
SEQ2451      TGIDAGKFDLSANDFSYNKERAEEKYLFSDPISRSNYAVVGKKGSHYKSLSDLSGKSTEV
SEQ2452      TGIDAGKFDLSANDFSYNKERAEEKYLFSDPISRSNYAVVGKKGSHYKSLSDLSGKSTEV
SEQ2453      TGIDAGKFDLSANDFSYNKERAEEKYLFSDPISRSNYAVVGKKGSHYKSLSDLSGKSTEV
SEQ2454      TGIDAGKFDLSANDFSYNKERAEEKYLFSDPISRSNYAVVGKKGSHYKSLSDLSGKSTEV
SEQ2455      TGIDAGKFDLSANDFSYNKERAEEKYLFSDPISRSNYAVVGKKGSHYKSLSDLSGKSTEV
SEQ2456      TGIDAGKFDLSANDFSYNKERAEEKYLFSDPISRSNYAVVGKKGSHYKSLSDLSGKSTEV
SEQ2457      TGIDAGKFDLSANDFSYNKERAEEKYLFSDPISRSNYAVVGKKGSHYKSLSDLSGKSTEV
SEQ2458      TGIDAGKFDLSANDFSYNKERAEEKYLFSDPISRSNYAVVGKKGSHYKSLSDLSGKSTEV
SEQ2459      TGIDAGKFDLSANDFSYNKERAEEKYLFSDPISRSNYAVVGKKGSHYKSLSDLSGKSTEV
SEQ2460      TGIDAGKFDLSANDFSYNKERAEEKYLFSDPISRSNYAVVGKKGSHYKSLSDLSGKSTEV

SEQ2450      SGVNYAQVLENWKNHNPKNKKPIKIKYVSGTTGVTSLRNIESGKIDFILYDAISSDYIVK
SEQ2451      SGVNYAQVLENWKNHNPKNKKPIKIKYVSGTTGVTSLRNIESGKIDFILYDAISSDYIVK
SEQ2452      SGVNYAQVLENWKNHNPKNKKPIKIKYVSGTTGVTSLRNIESGKIDFILYDAISSDYIVK
SEQ2453      SGVNYAQVLENWKNHNPKNKKPIKIKYVSGTTGVTSLRNIESGKIDFILYDAISSDYIVK
SEQ2454      SGVNYAQVLENWKNHNPKNKKPIKIKYVSGTTGVTSLRNIESGKIDFILYDAISSDYIVK
SEQ2455      SGVNYAQVLENWKNHNPKNKKPIKIKYVSGTTGVTSLRNIESGKIDFILYDAISSDYIVK
SEQ2456      SGVNYAQVLENWKNHNPKNKKPIKIKYVSGTTGVTSLRNIESGKIDFILYDAISSDYIVK
SEQ2457      SGVNYAQVLENWKNHNPKNKKPIKIKYVSGTTGVTSLRNIESGKIDFILYDAISSDYIVK
SEQ2458      SGVNYAQVLENWKNHNPKNKKPIKIKYVSGTTGVTSLRNIESGKIDFILYDAISSDYIVK
SEQ2459      SGVNYAQVLENWKNHNPKNKKPIKIKYVSGTTGVTSLRNIESGKIDFILYDAISSDYIVK
SEQ2460      SGVNYAQVLENWKNHNPKNKKPIKIKYVSGTTGVTSLRNIESGKIDFILYDAISSDYIVK

SEQ2450      DQSLNLSVSPKKGKIGNNKDGLEYLLLPKDKKGGKTLQKFINKRIKVLKEDGTLARLSKQY
SEQ2451      DQSLNLSVSPKKGKIGNNKDGLEYLLLPKDKKGGKTLQKFINKRIKVLKENGTLARLSKQY
SEQ2452      DQSLNLSVSPKKGKIGNNKDGLEYLLLPKDKK-----
SEQ2453      DQSLNLSVSPKKGKIGNNKDGLEYLLLPKDKKGGKTLQKFINKRIKVLKENGTLARLSKQY
SEQ2454      DQSLNLSVSPKKGKIGNNKDGLEYLLLPKDKKGGKTLQKFINKR-----
SEQ2455      DQSLNLSVSPKKGKIGNNKDGLEYLLLPKDKKGGKTLQKFINKRIKVLKENGTLARLSKQY
SEQ2456      DQSLNLSVSPKKGKIGNNKDGLEYLLLPKDKKGGKTLQKFINKRIKVLKEDGTLARLSKQY
SEQ2457      DQSLNLSVSPKKGKIGNNKDGLEYLLLPKDKKGGKTLQKFINKRIKVLKENGTLARLSKQY
SEQ2458      DQSLNLSVSPKKGKIGNNKDGLEYLLLPKDKKGGKTLQKFINKRNKVLKENG-----
SEQ2459      DQSLNLSVSPKKGKIGNNKDGLEYLLLPKDKKGGKTLQKFINKRIKVLKEDGTLARLSKQY
SEQ2460      DQSLNLSVSPKKGKIGNNKDGLEYLLLPKDKKGGKTLQKFINKRIKVLKEDGTLARLSKQY

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**Figure 24: Comparative Sequences relating to SAG0290
(ABC transporter, substrate-binding protein)**

SEQ2450	GGDYVSNIDK
SEQ2451	GGDYVSNIDK
SEQ2452	-----
SEQ2453	GGDYVSNIDK
SEQ2454	-----
SEQ2455	GGDYVSNIDK
SEQ2456	GGDYVSNIDK
SEQ2457	GGDYVSNIDK
SEQ2458	-----
SEQ2459	GGDYVSNIDK
SEQ2460	GGDYVSNIDK

**Table 25: Comparative Sequences relating to SAG0368
(protein of unknown function)**

SEQ ID NO. 2501: SAG0368 FROM THE 090 GBS TYPE Ia STRAIN

TATAATTTTTCGACTAATGAATTGTCTAAGACTTTTAAAGATTTTAAAGCTAGCTAAATCAAAAAGTCATGCTATTGAA
GAAACAAAGCCGTTTTCAATACTATTAAATGGGGGTGGACACAGGTTTCAGAGCATCGAAAATCTAAGTGGTCAGGAAAT
AGCGATTCTATGATCTTAGTCACTATAAATCCTAAACTAATAAAACAACGATGACAAGCTTAGAACGTGACGTATTG
ATTAAATTGAGTGGTCCCAAAAATAATGGACAGACTGGAGTAGAAGCAAAGCTAAATGCAGCCTATGCTTCTGGTGGT
GCGGAAATGGCATTGATGACTGTTCAAGACTTATTAGATATTAATGTTGATTACTTTATGCAAATTAATATGCAAGGA
TTAGTTGATTTAGTCAATGCTGTTGGTGGTATAACAGTAACATAAATTTGACTTTCCAATATCAATTGCTGCCAAT
GAACCAGAGTACAAGGCTGTTGTTGAACCAGGGACACATAAAATAAATGGAGAACAAGCACTTGTTTATTCTCGTATG
CGCTATGATGATCCAGAGGGAGATTATGGGCGTCAAAAAGACAACGTGAAGTAATTCAAAAAGTCCTTAAAAAATA
TTGGCGTTAAATAGTATTAGTTTCATACAAAAAAATCTTTCCGCAGTAAGTAATAACATGCAAACTAATATTGAGATA
TCATCAAAAACGATTCCTAATTTGTTAGCTTATAAAGATTCAATTGGAACATATTAAATCTTATCAGTTGAAGGGTGAA
GACGCTACTTTATCAGATGGTGGCTCTTATCAAATTTTAACTAAGAAACATCTACTTGCAGTTCAAAATAGAATTAAG
AAAGAACTGGATAAAAAGCGTAGTAAACTCTGAAGACAAGCGCGATTCTATATGAAGATTACTATGGTACTACTGCT
AGTAATGATTCTTCTACTTATTATCATCAACACAAGAGAATAATTATAATACAACACCTTATTTCAGAAGCACCACCAAGT
TACAGTGGTAATACTACTTATAGTTCTGAGACTAATCAAACTCATCAAAATTAATAATAGTAGCACTCCTGCT
AGTAACATATAGCAGTAACACTAACACAGGTCAGGCTGATTCAAGTGAAGTGTCAATAATCATAACGGGGCTGCAACG
CCTAATCCA

SEQ ID NO. 2502: SAG0368 FROM THE 1169NT1 GBS TYPE V STRAIN

TATAATTTTTCGACTAATGAATTGTCTAAGACTTTTAAAGATTTTAAAGCTAGCTAAATCAAAAAGTCATGCTATTGAA
GAAACAAAGCCGTTTTCAATACTATTAAATGGGGGTGGACACAGGTTTCAGAGCATCGAAAATCTAAGTGGTCAGGAAA
TAGCGATTCTATGATCTTAGTCACTATAAATCCTAAACTAATAAAACAACGATGACAAGCTTAGAACGTGACGTATT
GATTAAATTGAGTGGTCCCAAAAATAATGGACAGACTGGCGTAGAAGCAAAGCTAAATGCAGCCTATGCTTCTGGTGG
TGCGGAAATGGCATTGATGACTGTTCAAGACTTATTAGATATTAATGTTGATTACTTTATGCAAATTAATATGCAAGG
ATTAGTTGATTTAGTCAATGCTGTTGGTGGTATAACAGTAACATAAATTTGACTTTCCAATATCAATTGCTGCCAA
TGAACCAGAGTACAAGGCTGTTGTTGAACCAGGGACACATAAAATAAATGGAGAACAAGCACTTGTTTATTCTCGTAT
GCGCTATGATGATCCAGAGGGAGATTATGGGCGTCAAAAAGACAACGTGAAGTAATTCAAAAAGTCCTTAAAAAATA
ATTGGCGTTAAATAGTATTAGTTTCATACAAAAAAATCTTTCCGCAGTAAGTAATAACATGCAAACTAATATTGAGAT
ATCATCAAAAACGATTCCTAATTTGTTAGCTTATAAAGATTCAATTGGAACATATTAAATCTTATCAGTTGAAGGGTGA
AGACGCTACTTTATCAGATGGTGGCTCTTATCAAATTTTAACTAAGAAACATCTACTTGCAGTTCAAAATAGAATTA
GAAAGAACTAGATAAAAAGCGTAGTAAACTCTGAAGACAAGCGCGATTCTATATGAAGATTACTATGGTACTACTGC
TAGTAATGATTCTTCTACTTATTATCATCAACACAAGAGAATAATTATAATACAACACCTTATTTCAGAAGCACCACCAAG
TTACAGTGGTAATACTACTTATAGTTCTGAGACTAATCAAACTCATCAAAAGTTACTATAATAGTAGCACTCCTGCT
TAATACTATAGCAGTAACACTAACACAGGTCAGGCTGATTCAAGTGAAGTGTCAATAATCATAATGGGGCTGCAAC
GCCTAATCCA

SEQ ID NO. 2503 SAG0368 FROM THE 18RS21 GBS TYPE II STRAIN

TATAATTTTTCGACTAATGAATTGTCTAAGACTTTTAAAGATTTTAAAGCTAGCTAAATCAAAAAGTCATGCTATTGAA
GAAACAAAGCCGTTTTCAATACTATTAAATGGGGGTGGACACAGGTTTCAGAGCATCGAAAATCTAAGTGGTCAGGAAAT
AGCGATTCTATGATCTTAGTCACTATAAATCCTAAACTAATAAAACAACGATGACAAGCTTAGAACGTGACGTATTG
ATTAAATTGAGTGGTCCCAAAAATAATGGACAGACTGGAGTAGAAGCAAAGCTAAATGCAGCCTATGCTTCTGGTGGT
GCGGAAATGGCATTGATGACTGTTCAAGACTTATTAGATATTAATGTTGATTACTTTATGCAAATTAATATGCAAGGA
TTAGTTGATTTAGTCAATGCTGTTGGTGGTATAACAGTAACATAAATTTGACTTTCCAATATCAATTGCTGCCAAT
GAACCAGAGTACAAGGCTGTTGTTGAACCAGGGACACATAAAATAAATGGAGAACAAGCACTTGTTTATTCTCGTATG
CGCTATGATGATCCAGAGGGAGATTATGGGCGTCAAAAAGACAACGTGAAGTAATTCAAAAAGTCCTTAAAAAATA
TTGGCGTTAAATAGTATTAGTTTCATACAAAAAAATCTTTCCGCAGTAAGTAATAACATGCAAACTAATATTGAGATA
TCATCAAAAACGATTCCTAATTTGTTAGCTTATAAAGATTCAATTGGAACATATTAAATCTTATCAGTTGAAGGGTGAA
GACGCTACTTTATCAGATGGTGGCTCTTATCAAATTTTAACTAAGAAACATCTACTTGCAGTTCAAAATAGAATTAAG
AAAGAACTGGATAAAAAGCGTAGTAAACTCTGAAGACAAGCGCGATTCTATATGAAGATTACTATGGTACTACTGCT
AGTAATGATTCTTCTACTTATTATCATCAACACAAGAGAATAATTATAATACAACACCTTATTTCAGAAGCACCACCAAGT
TACAGTGGTAATACTACTTATAGTTCTGAGACTAATCAAACTCATCAAAATTAATAATAGTAGCACTCCTGCT
AGTAACATATAGCAGTAACACTAACACAGGTCAGGCTGATTCAAGTGAAGTGTCAATAATCATAACGGGGCTGCAACG
CCTAATCCA

**Table 25: Comparative Sequences relating to SAG0368
(protein of unknown function)**

SEQ ID NO. 2504: SAG0368 FROM THE 2603 V/R GBS TYPE V STRAIN

TATAATTTTTCGACTAATGAATTGTCTAAGACTTTTAAAGATTTTAAGCTAGCTAAATCAAAAAGTCATGCTATTGAA
GAAACAAAGCCGTTTTCATACTATTAATGGGGGTGGACACAGGTTTCAGAGCATCGAAAATCTAAGTGGTCAGGAAAT
AGCGATTCTATGATCTTAGTCACTATAAATCCTAAAACTAATAAAAAACAGATGACAAGCTTAGAACGTGACGTATTG
ATTAAATTGAGTGGTCCCAAAAATAATGGACAGACTGGAGTAGAAGCAAAGCTAAATGCAGCCTATGCTTCTGGTGGT
GCGGAAATGGCATTTGATGACTGTTCAAGACTTATTAGATATTAATGTTGATTACTTTATGCAAATTAATATGCAAGGA
TTAGTTGATTTAGTCAATGCTGTTGGTGGTATAACAGTAACATAAATTTGACTTTCGAATATCAATTGCTGCCAAT
GAACCAGAGTACAAGGCTGTTGTTGAACCAGGGACACATAAAATAAATGGAGAACAGCACTTGTATTCTCGTATG
CGCTATGATGATCCAGAGGGAGATTATGGGCGTCAAAAAGACAACGTGAAGTAATTCAAAAAGTCCTTAAAAAATA
TTGGCGTTAAATAGTATTAGTTCATACAAAAAATCTTTCCGCAGTAAGTAATAACATGCAAATAATATTGAGATA
TCATCAAAAACGATTCTTAATTTGTTAGCTTATAAAGATTTCATTGGAACATATTAAATCTTATCAGTTGAAGGGTGAA
GACGCTACTTTTATCAGATGGTGGCTCTTATCAAAATTTTAAGTAAGAACATCTACTTGCAGTTCAAAATAGAAATTAAG
AAAGAACTGGATAAAAAGCGTAGTAAACTCTGAAGACAAGCGCGATTCTATATGAAGATTACTATGGTACTACTGCT
AGTAATGATTCTTCTACTTATTCATCAACACAAGAGAATAATTATAATACAACACCTTATTCAGAAGCACCACCAAGT
TACAGTGGTAATACTACTTATAGTTCTGAGACTAATCAAACTCATCAAAATTACTATAATAGTAGCACTCCTGCT
AGTAACATAGCAGTAACACTAACACAGGTGAGGCTGATTCAAGTGGAAGTGTCAATAATCATAACGGGGCTGCAACG
CCTAATCCA

SEQ ID NO. 2505: SAG0368 FROM THE A909 GBS TYPE Ia STRAIN

TATAATTTTTCGACTAATGAATTGTCTAAGACTTTTAAAGATTTTAAGCTAGCTAAATCAAAAAGTCATGCTATTGAA
GAAACAAAGCCGTTTTCATACTATTAATGGGGGTGGACACAGGTTTCAGAGCATCGAAAATCTAAGTGGTCAGGAAAT
AGCGATTCTATGATCTTAGTCACTATAAATCCTAAAACTAATAAAAAACAGATGACAAGCTTAGAACGTGACGTATTG
ATTAAATTGAGTGGTCCCAAAAATAATGGACAGACTGGAGTAGAAGCAAAGCTAAATGCAGCCTATGCTTCTGGTGGT
GCGGAAATGGCATTTGATGACTGTTCAAGACTTATTAGATATTAATGTTGATTACTTTATGCAAATTAATATGCAAGGA
TTAGTTGATTTAGTCAATGCTGTTGGTGGTATAACAGTAACATAAATTTGACTTTCGAATATCAATTGCTGCCAAT
GAACCAGAGTACAAGGCTGTTGTTGAACCAGGGACACATAAAATAAATGGAGAACAGCACTTGTATTCTCGTATG
CGCTATGATGATCCAGAGGGAGATTATGGGCGTCAAAAAGACAACGTGAAGTAATTCAAAAAGTCCTTAAAAAATA
TTGGCGTTAAATAGTATTAGTTCATACAAAAAATCTTTCCGCAGTAAGTAATAACATGCAAATAATATTGAGATA
TCATCAAAAACGATTCTTAATTTGTTAGCTTATAAAGATTTCATTGGAACATATTAAATCTTATCAGTTGAAGGGTGAA
GACGCTACTTTTATCAGATGGTGGCTCTTATCAAAATTTTAAGTAAGAACATCTACTTGCAGTTCAAAATAGAAATTAAG
AAAGAACTGGATAAAAAGCGTAGTAAACTCTGAAGACAAGCGCGATTCTATATGAAGATTACTATGGTACTACTGCT
AGTAATGATTCTTCTACTTATTCATCAACACAAGAGAATAATTATAATACAACACCTTATTCAGAAGCACCACCAAGT
TACAGTGGTAATACTACTTATAGTTCTGAGACTAATCAAACTCATCAAAATTACTATAATAGTAGCACTCCTGCT
AGTAACATAGCAGTAACACTAACACAGGTGAGGCTGATTCAAGTGGAAGTGTCAATAATCATAACGGGGCTGCAACG
CCTAATCCA

**SEQ ID NO. 2506: SAG0368 FROM THE CJB110 GBS NONTYPEABLE STRAIN (REVERSE
COMPLEMENT)**

TATAATTTTTCGACTAATGAATTGTCTAAGACTTTTAAAGATTTTAAGCTAGCTAAATCAAAAAGTCATGCTATTGAA
GAAACAAAGCCGTTTTCATACTATTAATGGGGGTGGACACAGGTTTCAGAGCATCGAAAATCTAAGTGGTCAGGAAAT
AGCGATTCTATGATCTTAGTCACTATAAATCCTAAAACTAATAAAAAACAGATGACAAGCTTAGAACGTGACGTATTG
ATTAAATTGAGTGGTCCCAAAAATAATGGACAGACTGGAGTAGAAGCAAAGCTAAATGCAGCCTATGCTTCTGGTGGT
GCGGAAATGGCATTTGATGACTGTTCAAGACTTATTAGATATTAATGTTGATTACTTTATGCAAATTAATATGCAAGGA
TTAGTTGATTTAGTCAATGCTGTTGGTGGTATAACAGTAACATAAATTTGACTTTCGAATATCAATTGCTGCCAAT
GAACCAGAGTACAAGGCTGTTGTTGAACCAGGGACACATAAAATAAATGGAGAACAGCACTTGTATTCTCGTATG
CGCTATGATGATCCAGAGGGAGATTATGGGCGTCAAAAAGACAACGTGAAGTAATTCAAAAAGTCCTTAAAAAATA
TTGGCGTTAAATAGTATTAGTTCATACAAAAAATCTTTCCGCAGTAAGTAATAACATGCAAATAATATTGAGATA
TCATCAAAAACGATTCTTAATTTGTTAGCTTATAAAGATTTCATTGGAACATATTAAATCTTATCAGTTGAAGGGTGAA
GACGCTACTTTTATCAGATGGTGGCTCTTATCAAAATTTTAAGTAAGAACATCTACTTGCAGTTCAAAATAGAAATTAAG
AAAGAACTGGATAAAAAGCGTAGTAAACTCTGAAGACAAGCGCGATTCTATATGAAGATTACTATGGTACTACTGCT
AGTAATGATTCTTCTACTTATTCATCAACACAAGAGAATAATTATAATACAACACCTTATTCAGAAGCACCACCAAGT
TACAGTGGTAATACTACTTATAGTTCTGAGACTAATCAAACTCATCAAAATTACTATAATAGTAGCACTCCTGCT
TAGTAACATAGCAGTAACACTAACACAGGTGAGGCTGATTCAAGTGGAAGTGTCAATAATCATAACGGGGCTGCAAC
GCCTAATCCA

**Table 25: Comparative Sequences relating to SAG0368
(protein of unknown function)**

SEQ ID NO. 2507: SAG0368 FROM THE COH1 GBS TYPE III STRAIN (REVERSE COMPLEMENT)

GATTTTAAGCTAGATAAAATCAAAAAGTCATGCTATTGAAGAAACAAAGCCGTTTCAATACTATTAAATGGGTGTGGAC
ACAGGTTTCAGAGCATCGAAAATCTAAGTGGTCAGGAAATAGCGATTCTATGATCTTAGTCACTATAAATCCTAAAAC
AATAAAACAACGATGACAAGCTTAGAACGTGACGTATTGATTAAATTGAGTGGTCCCAAAAATAATGGACAGACTGGC
GTAGAAGCAAAGCTAAATGCAGCCTATGCTTCTGGTGGTGCGGAAATGGCATTGATGACTGTTCAAGACTTATTAGAT
ATTAATGTTGATTACTTTATGCAAATTAATATGCAAGGATTAGTTGATTGGTCAATGCTGTTGGTGGTATAACAGTA
ACTAATAAATTTGACTTTCCAATATCAATTGCTGCCAATGAACCAGAGTACAAGGCTGTTGTTGAACCAGGGACACAT
AAAATAAATGGAGAACAAAGCACTTGTATTCTCGTATGCGCTATGATGATCCAGAGGGAGATTATGGGCGTCAAAAA
AGACAACGTGAAGTAATTCAAAAAGTCCTTAAAAAATATTGGCGTTAAATAGTATTAGTTCATACAAAAAATCTTT
TCCGCAGTAAGTAATAACATGCAACTAATATTGAGATATCATCAAAAACGATTCCTAATTTGTTAGCTTATAAAGAT
TCATTGGAACATATTAAATCTTATCAGTTGAAGGGTGAAGACGCTACTCTATCAGATGGTGGCTCTTATCAAATTTTA
ACTAAGAAACATCTACTTGCAGTTCAAAATAGAATTAAGAAAGAGCTGGATAAAAAGCGTAGTAAAACCTGTAAGACA
AGCGCGATTCTATATGAAGATTACTATGGTACTACTAGTAAATGATTCTTCTACTTATTCAACACAAGAGAAT
TATTATTATACAAACCCCTTATTCAGAAGCACCACCAAGTTACAGTGGTAATACTACTTATAGTTCTGAGACTAATCA
AACAACCTCATCAAAGTTACTATAATAGTAGCACTCCTGCTAGTAACTATAGCAGTAACACTAACACAGGTCAGGCTGA
TTCAAGTGAAGTGTTAATAATTATAACGGGGCTGCAACGCCAATCCAAACACAGGAACGCAACCAAGTACCAGGTCA
AACTAATCCA

SEQ ID NO. 2508: SAG0368 FROM THE H36b GBS TYPE Ib STRAIN

TATAATTTTTTCGACTAATGAATTGTCTAAGACTTTTAAAGATTTTAAGCTAGCTAAATCAAAAAGTCATGCTATTGAA
GAAACAAAGCCGTTTCAATACTATTAATGGGGGTGGACACAGGTTTCAGAGCATCGAAAATCTAAGTGGTCAGGAAAT
AGCGATTCTATGATCTTAGTCACTATAAATCCTAAAACCTAATAAACAACGATGACAAGCTTAGAACGTGACGTATTG
ATTAAATTGAGTGGTCCCAAAAATAATGGACAGACTGGAGTAGAAGCAAAGCTAAATGCAGCCTATGCTTCTGGTGGT
GCGGAAATGGCATTTGATGACTGTTCAAGACTTATAGATATTAAATGTTGATTACTTTATGCAAATTAATATGCAAGGA
TTAGTTGATTTAGTCAATGCTGTTGGTGGTATAACAGTAACATAAATTTGACTTTCCAATATCAATTGCTGCCAAT
GAACCAGAGTACAAGGCTGTTGTTGAACCAGGGACACATAAAATAAATGGAGAACAAAGCACTTGTTTATTCTCGTATG
CGCTATGATGATCCAGAGGGAGATTATGGGCGTCAAAAAGACAACGTGAAGTAATTCAAAAAGTCCTTAAAAAATA
TTGGCGTTAAATAGTA

SEQ ID NO. 2509: SAG0368 FROM THE _____

TTAGTTCATACAAAAAATCTTTCCGCAGTAAGTAATAACATGCAAACTAATATTGAGATATCATCAAAAACGATTC
CTAATTTGTTAGCTTATAAAGATTCAATTGGAACATATTAAATCTTATCAGTTGAAGGGTGAAGACGCTACTTTATCAG
ATGGTGGCTCTTATCAAATTTTAACTAAGAAACATCTACTTGCAGTTCAAAATAGAATTAAGAAAGAACTGGATAAAA
AGCGTAGTAAAACCTGTAAGACAAGCGCGATTCTATATGAAGATTACTATGGTACTACTGCTAGTAATGATTTCTTCTA
CTTATTCATCAACACAAGAGAATAATTATAATACACACCTTATTCAGAAGCACCACCAAGTTACAGTGGTAACTACTA
CTTATAGTTCTGAGACTAATCAAACAACCTCATCAAATTACTATAATAGTAGCACTCCTGCTAGTAACTATAGCAGTA
ACACTAACACAGGTCAGGCTGATTCAAGTGAAGTGTCAATAATCATAACGGGGCTGCAACGCCAATCCA

SEQ ID NO. 2510: SAG0368 FROM THE JM9130013 GBS TYPE VIII STRAIN (REVERSE COMPLEMENT)

TATAATTTTTTCGACTAATGAATTGTCTAAGACTTTTAAAGATTTTAAGCTAGCTAAATCAAAAAGTCATGCTATTGAA
GAAACAAAGCCGTTTCAATACTATTAATGGGGGTGGACACAGGTTTCAGAGCATCGAAAATCTAAGTGGTCAGGAAAT
AGCGATTCTATGATCTTAGTCACTATAAATCCTAAAACCTAATAAACAACGATGACAAGCTTAGAACGTGACGTATTG
ATTAAATTGAGTGGTCCCAAAAATAATGGACAGACTGGAGTAGAAGCAAAGCTAAATGCAGCCTATGCTTCTGGTGGT
GCGGAAATGGCATTTGATGACTGTTCAAGACTTATTAGATATTAAATGTTGATTACTTTATGCAAATTAATATGCAAGGA
TTAGTTGATTTAGTCAATGCTGTTGGTGGTATAACAGTAACATAAATTTGACTTTCCAATATCAATTGCTGCCAAT
GAACCAGAGTACAAGGCTGTTGTTGAACCAGGGACACATAAAATAAATGGAGAACAAAGCACTTGTTTATTCTCGTATG
CGCTATGATGATCCAGAGGGAGATTATGGGCGTCAAAAAGACAACGTGAAGTAATTCAAAAAGTCCTTAAAAAATA
TTGGCGTTAAATAGTATTAGTTTCATACAAAAAATCTTTCCGCAGTAAGTAATAACATGCAAACTAATATTGAGATA
TCATCAAAAACGATTCTCAATTTGTTAGCTTATAAAGATTCAATTGGAACATATTAAATCTTATCAGTTGAAGGGTGA
GACGCTACTTTATCAGATGGTGGCTCTTATCAAATTTTAACTAAGAAACATCTACTTGCAGTTCAAAATAGAATTAAG
AAGAAGCTGGATAAAAAGCGTAGTAAAACCTGTAAGACAAGCGCGATTCTATATGAAGATTACTATGGTACTACTGCT
AGTAATGATTTCTTACTTATTATCAACACAAGAGAATAATTATAATACACACCTTATTTCAGAAGCACCACCAAGT
TACAGTGGTAATCTATAGTTCTGAGACTAATCAAACAACCTCATCAAATTACTATAATAGTAGCACTCCTGCT
AGTAATATAGCAGTAACACTAACACAGGTCAGGCTGATTCAAGTGAAGTGTCAATAATCATAACGGGGCTGCAACG
CCTAATCCA

**Table 25: Comparative Sequences relating to SAG0368
(protein of unknown function)**

SEQ ID NO. 2511: SAG0368 FROM THE M781 GBS TYPE III STRAIN (REVERSE
COMPLEMENT)

TTCAATACTATTAATGGGTGTGGACACAGGTTTCAGAGCATCGAAAATCTAAGTGGTCAGGAAATAGCGATTCTATGAT
CTTAGTCACTATAAATCCTAACTAATAAAACAACGATGACAAGCTTAGAACGTGACGTATTGATTAAATTGAGTGG
TCCCAAAAATAATGGACAGACTGGCGTAGAAGCAAAGCTAAATGCAGCCTATGCTTCTGGTGGTGCAGAAATGGCATT
GATGACTGTTCAAGACTTATTAGATATTAATGTTGATTACTTTATGCAAATTAATATGCAAGGATTAGTTGATTTGGT
CAATGCTGTTGGTGGTATAACAGTAATAATAAATTTGACTTTCCAAATATCAATTGCTGCCAATGAACCAGAGTACAA
GGCTGTTGTTGAACAGGGACACATAAAATAAATGGAGAACAAAGCACTTGTATTCTCGTATGCGCTATGATGATCC
AGAGGGAGATTATGGGCGTCAAAAAGACAACGTGAAGTAATTCAAAAAGTCCTTAAAAAATATTGGCGTTAAATAG
TATTAGTTCATACAAAAAATTCCTTTCCGCAGTAAGTAATAACATGCAAACTAATATTGAGATATCATCAAAAACGAT
TCCTAATTTGTTAGCTTATAAAGATTCATTGGAACATATTAAATCTTATCAGTTGAAGGGTGAAGACGCTACTCTATC
AGATGGTGGCTCTTATCAAATTTTAACTAAGAAACATCTACTTGCAGTTCAAAATAGAATTAAGAAAGAGCTGGATAA
AAAGCGTAGTAAACTCTGAAGACAAGCGCGATTCTATATGAAGATTACTATGGTACTACTGCTAGTAATGATTCCTC
TACTTATTCATCAACACAAGAGAATAATTATAATACAACACCTTATTCAGAAGCACCACCAAGTTACAGTGGTAATAC
TACTTATAGTTCTGAGACTAATCAAACAACATCAAAAGTTACTATAATAGTAGCACTCCTGCTAGTAATATAGCAG
TAACACTAACACAGGTCAGGCTGATTCAAGTGGAAGTGTTAATAATTATAACGGGGCTGCAACGCCTAATCCAAACAC
AGGAACGCAACAGTACCAGGTCAAACCTAATCCA

SEQ2501 -----
SEQ2502 -----
SEQ2503 -----
SEQ2504 -----
SEQ2505 -----
SEQ2506 -----
SEQ2507 ATTTTAAGCTAGATAAATCAAAAAGTCATGCTATTGAAGAAACAAAGCCGTTTTCATA
SEQ2508 -----
SEQ2509 -----
SEQ2510 -----
SEQ2511 -----TTCAATA

SEQ2501 -----
SEQ2502 -----
SEQ2503 -----
SEQ2504 -----
SEQ2505 -----
SEQ2506 -----
SEQ2507 TATTAATGGGTGTGGACACAGGTTTCAGAGCATCGAAAATCTAAGTGGTCAGGAAATAGC
SEQ2508 -----
SEQ2509 -----
SEQ2510 -----
SEQ2511 TATTAATGGGTGTGGACACAGGTTTCAGAGCATCGAAAATCTAAGTGGTCAGGAAATAGC

SEQ2501 -----
SEQ2502 -----
SEQ2503 -----
SEQ2504 -----
SEQ2505 -----
SEQ2506 -----
SEQ2507 ATTCTATGATCTTAGTCACTATAAATCCTAACTAATAAAACAACGATGACAAGCTTA
SEQ2508 -----
SEQ2509 -----
SEQ2510 -----
SEQ2511 ATTCTATGATCTTAGTCACTATAAATCCTAACTAATAAAACAACGATGACAAGCTTA

**Table 25: Comparative Sequences relating to SAG0368
(protein of unknown function)**

SEQ2501	-----
SEQ2502	-----
SEQ2503	-----
SEQ2504	-----
SEQ2505	-----
SEQ2506	-----
SEQ2507	AACGTGACGTATTGATTAAATTGAGTGGTCCCAAAAATAATGGACAGACTGGCGTAGAA
SEQ2508	-----
SEQ2509	-----
SEQ2510	-----
SEQ2511	AACGTGACGTATTGATTAAATTGAGTGGTCCCAAAAATAATGGACAGACTGGCGTAGAA
SEQ2501	-----
SEQ2502	-----
SEQ2503	-----
SEQ2504	-----
SEQ2505	-----
SEQ2506	-----
SEQ2507	CAAAGCTAAATGCAGCCTATGCTTCTGGTGGTGCGGAAATGGCATTGATGACTGTTCAA
SEQ2508	-----
SEQ2509	-----
SEQ2510	-----
SEQ2511	CAAAGCTAAATGCAGCCTATGCTTCTGGTGGTGCGGAAATGGCATTGATGACTGTTCAA
SEQ2501	-----
SEQ2502	-----
SEQ2503	-----
SEQ2504	-----
SEQ2505	-----
SEQ2506	-----
SEQ2507	ACTTATTAGATATTAATGTTGATTACTTTATGCAAATTAATATGCAAGGATTAGTTGAT
SEQ2508	-----
SEQ2509	-----
SEQ2510	-----
SEQ2511	ACTTATTAGATATTAATGTTGATTACTTTATGCAAATTAATATGCAAGGATTAGTTGAT
SEQ2501	-----
SEQ2502	-----
SEQ2503	-----
SEQ2504	-----
SEQ2505	-----
SEQ2506	-----
SEQ2507	TGGTCAATGCTGTTGGTGGTATAACAGTAACTAATAAATTTGACTTTCCAATATCAATT
SEQ2508	-----
SEQ2509	-----
SEQ2510	-----
SEQ2511	TGGTCAATGCTGTTGGTGGTATAACAGTAACTAATAAATTTGACTTTCCAATATCAATT
SEQ2501	-----
SEQ2502	-----
SEQ2503	-----
SEQ2504	-----
SEQ2505	-----
SEQ2506	-----
SEQ2507	CTGCCAATGAACCAGAGTACAAGGCTGTTGTTGAACCAGGGACACATAAAATAAATGGA
SEQ2508	-----
SEQ2509	-----
SEQ2510	-----
SEQ2511	CTGCCAATGAACCAGAGTACAAGGCTGTTGTTGAACCAGGGACACATAAAATAAATGGA

**Table 25: Comparative Sequences relating to SAG0368
(protein of unknown function)**

SEQ2501	-----
SEQ2502	-----
SEQ2503	-----
SEQ2504	-----
SEQ2505	-----
SEQ2506	-----
SEQ2507	AACAAGCACTTGTTTATTCTCGTATGCGCTATGATGATCCAGAGGGAGATTATGGGCGT
SEQ2508	-----
SEQ2509	-----
SEQ2510	-----
SEQ2511	AACAAGCACTTGTTTATTCTCGTATGCGCTATGATGATCCAGAGGGAGATTATGGGCGT
SEQ2501	-----TATAATTTTTCG
SEQ2502	-----TATAATTTTTCG
SEQ2503	-----TATAATTTTTCG
SEQ2504	-----TATAATTTTTCG
SEQ2505	-----TATAATTTTTCG
SEQ2506	-----TATAATTTTTCG
SEQ2507	AAAAAAGACAACGTGAAGTAATTCAAAAAGTCCTTAAAAAATATTGGCGTTAAATAGT
SEQ2508	-----TATAATTTTTCG
SEQ2509	-----
SEQ2510	-----TATAATTTTTCG
SEQ2511	AAAAAAGACAACGTGAAGTAATTCAAAAAGTCCTTAAAAAATATTGGCGTTAAATAGT
SEQ2501	CTAATGAATTGTCTAAGACTTTTAAAGATTTTAAGCTAGCTAAATCAAAAAGTCATGCT
SEQ2502	CTAATGAATTGTCTAAGACTTTTAAAGATTTTAAGCTAGCTAAATCAAAAAGTCATGCT
SEQ2503	CTAATGAATTGTCTAAGACTTTTAAAGATTTTAAGCTAGCTAAATCAAAAAGTCATGCT
SEQ2504	CTAATGAATTGTCTAAGACTTTTAAAGATTTTAAGCTAGCTAAATCAAAAAGTCATGCT
SEQ2505	CTAATGAATTGTCTAAGACTTTTAAAGATTTTAAGCTAGCTAAATCAAAAAGTCATGCT
SEQ2506	CTAATGAATTGTCTAAGACTTTTAAAGATTTTAAGCTAGCTAAATCAAAAAGTCATGCT
SEQ2507	TTAGTTCAT-ACAAAAAAATCTTTCCGCAGTAAGTAA--TAACATGCAAACTAATATT
SEQ2508	CTAATGAATTGTCTAAGACTTTTAAAGATTTTAAGCTAGCTAAATCAAAAAGTCATGCT
SEQ2509	TTAGTTCAT-ACAAAAAAATCTTTCCGCAGTAAGTAA--TAACATGCAAACTAATATT
SEQ2510	CTAATGAATTGTCTAAGACTTTTAAAGATTTTAAGCTAGCTAAATCAAAAAGTCATGCT
SEQ2511	TTAGTTCAT-ACAAAAAAATCTTTCCGCAGTAAGTAA--TAACATGCAAACTAATATT
SEQ2501	TTGAAGAAACAAAGCCGTTTTC AATACTATTAATGGGGGTGGACACAGGTT CAGAGCAT
SEQ2502	TTGAAGAAACAAAGCCGTTTTC AATACTATTAATGGGGGTGGACACAGGTT CAGAGCAT
SEQ2503	TTGAAGAAACAAAGCCGTTTTC AATACTATTAATGGGGGTGGACACAGGTT CAGAGCAT
SEQ2504	TTGAAGAAACAAAGCCGTTTTC AATACTATTAATGGGGGTGGACACAGGTT CAGAGCAT
SEQ2505	TTGAAGAAACAAAGCCGTTTTC AATACTATTAATGGGGGTGGACACAGGTT CAGAGCAT
SEQ2506	TTGAAGAAACAAAGCCGTTTTC AATACTATTAATGGGGGTGGACACAGGTT CAGAGCAT
SEQ2507	AGATATCATCAAAAACGATTCCTAATTTGTTAGCTTATAAAGATTCA--TTGGAACAT
SEQ2508	TTGAAGAAACAAAGCCGTTTTC AATACTATTAATGGGGGTGGACACAGGTT CAGAGCAT
SEQ2509	AGATATCATCAAAAACGATTCCTAATTTGTTAGCTTATAAAGATTCA--TTGGAACAT
SEQ2510	TTGAAGAAACAAAGCCGTTTTC AATACTATTAATGGGGGTGGACACAGGTT CAGAGCAT
SEQ2511	AGATATCATCAAAAACGATTCCTAATTTGTTAGCTTATAAAGATTCA--TTGGAACAT
SEQ2501	GAAAATCTAAGT-GGTCAGGAAATAGCGATTCTATGATCTTAGTCACTATAAATCCTAA
SEQ2502	GAAAATCTAAGT-GGTCAGGAAATAGCGATTCTATGATCTTAGTCACTATAAATCCTAA
SEQ2503	GAAAATCTAAGT-GGTCAGGAAATAGCGATTCTATGATCTTAGTCACTATAAATCCTAA
SEQ2504	GAAAATCTAAGT-GGTCAGGAAATAGCGATTCTATGATCTTAGTCACTATAAATCCTAA
SEQ2505	GAAAATCTAAGT-GGTCAGGAAATAGCGATTCTATGATCTTAGTCACTATAAATCCTAA
SEQ2506	GAAAATCTAAGT-GGTCAGGAAATAGCGATTCTATGATCTTAGTCACTATAAATCCTAA
SEQ2507	TTAAATCTTATC-AGTTGAAGGGTGAAGACGCTACTCTATCAG--ATGGTGGCTCTTAT
SEQ2508	GAAAATCTAAGT-GGTCAGGAAATAGCGATTCTATGATCTTAGTCACTATAAATCCTAA
SEQ2509	TTAAATCTTATC-AGTTGAAGGGTGAAGACGCTACTCTATCAG--ATGGTGGCTCTTAT
SEQ2510	GAAAATCTAAGT-GGTCAGGAAATAGCGATTCTATGATCTTAGTCACTATAAATCCTAA
SEQ2511	TTAAATCTTATC-AGTTGAAGGGTGAAGACGCTACTCTATCAG--ATGGTGGCTCTTAT
SEQ2501	ACTAATAAAACAACGATGACAAGCTTAGAACGTGACGTATTGATTAAATTGAGTGGTCC

**Table 25: Comparative Sequences relating to SAG0368
(protein of unknown function)**

SEQ2502	ACTAATAAAACAACGATGACAAGCTTAGAACGTGACGTATTGATTAAATTGAGTGGTCC
SEQ2503	ACTAATAAAACAACGATGACAAGCTTAGAACGTGACGTATTGATTAAATTGAGTGGTCC
SEQ2504	ACTAATAAAACAACGATGACAAGCTTAGAACGTGACGTATTGATTAAATTGAGTGGTCC
SEQ2505	ACTAATAAAACAACGATGACAAGCTTAGAACGTGACGTATTGATTAAATTGAGTGGTCC
SEQ2506	ACTAATAAAACAACGATGACAAGCTTAGAACGTGACGTATTGATTAAATTGAGTGGTCC
SEQ2507	AAATTTTAACTAAGAAACATCTACTTGCAGTTCAAAATAGAATTAAGAAAGAGCTGGAT
SEQ2508	ACTAATAAAACAACGATGACAAGCTTAGAACGTGACGTATTGATTAAATTGAGTGGTCC
SEQ2509	AAATTTTAACTAAGAAACATCTACTTGCAGTTCAAAATAGAATTAAGAAAGAACTGGAT
SEQ2510	ACTAATAAAACAACGATGACAAGCTTAGAACGTGACGTATTGATTAAATTGAGTGGTCC
SEQ2511	AAATTTTAACTAAGAAACATCTACTTGCAGTTCAAAATAGAATTAAGAAAGAGCTGGAT
SEQ2501	AAAAATAATGGACAGACTGGAGTAGAAGCAAAG--CTAAATGCAGCCTATGCTTCTGGT
SEQ2502	AAAAATAATGGACAGACTGGCGTAGAAGCAAAG--CTAAATGCAGCCTATGCTTCTGGT
SEQ2503	AAAAATAATGGACAGACTGGAGTAGAAGCAAAG--CTAAATGCAGCCTATGCTTCTGGT
SEQ2504	AAAAATAATGGACAGACTGGAGTAGAAGCAAAG--CTAAATGCAGCCTATGCTTCTGGT
SEQ2505	AAAAATAATGGACAGACTGGAGTAGAAGCAAAG--CTAAATGCAGCCTATGCTTCTGGT
SEQ2506	AAAAATAATGGACAGACTGGAGTAGAAGCAAAG--CTAAATGCAGCCTATGCTTCTGGT
SEQ2507	AAAAGCGTAGTAAAACCTCTGAAGACAAGCGCGATTCTATATGAAGATTACTATGGTACT
SEQ2508	AAAAATAATGGACAGACTGGAGTAGAAGCAAAG--CTAAATGCAGCCTATGCTTCTGGT
SEQ2509	AAAAGCGTAGTAAAACCTCTGAAGACAAGCGCGATTCTATATGAAGATTACTATGGTACT
SEQ2510	AAAAATAATGGACAGACTGGAGTAGAAGCAAAG--CTAAATGCAGCCTATGCTTCTGGT
SEQ2511	AAAAGCGTAGTAAAACCTCTGAAGACAAGCGCGATTCTATATGAAGATTACTATGGTACT
SEQ2501	GTGC-GGAAATGGCATTGATGACTGTTCAAGACTTATTAGATATTAATGTTGATTACTT
SEQ2502	GTGC-GGAAATGGCATTGATGACTGTTCAAGACTTATTAGATATTAATGTTGATTACTT
SEQ2503	GTGC-GGAAATGGCATTGATGACTGTTCAAGACTTATTAGATATTAATGTTGATTACTT
SEQ2504	GTGC-GGAAATGGCATTGATGACTGTTCAAGACTTATTAGATATTAATGTTGATTACTT
SEQ2505	GTGC-GGAAATGGCATTGATGACTGTTCAAGACTTATTAGATATTAATGTTGATTACTT
SEQ2506	GTGC-GGAAATGGCATTGATGACTGTTCAAGACTTATTAGATATTAATGTTGATTACTT
SEQ2507	CTGCTAGTAATGATTCTTCTACTTATTTCATCAAC-ACAAGAGAATTATTATAT-ACAA
SEQ2508	GTGC-GGAAATGGCATTGATGACTGTTCAAGACTTATTAGATATTAATGTTGATTACTT
SEQ2509	CTGCTAGTAATGATTCTTCTACTTATTTCATCAAC-ACAAGAGAATAATTATAAT-ACAA
SEQ2510	GTGC-GGAAATGGCATTGATGACTGTTCAAGACTTATTAGATATTAATGTTGATTACTT
SEQ2511	CTGCTAGTAATGATTCTTCTACTTATTTCATCAAC-ACAAGAGAATAATTATAAT-ACAA
SEQ2501	ATGCAAATTAATATGCAAGGATTAGTTGATTAGTCAATGCTGTTGGTGGTATAACAGT
SEQ2502	ATGCAAATTAATATGCAAGGATTAGTTGATTAGTCAATGCTGTTGGTGGTATAACAGT
SEQ2503	ATGCAAATTAATATGCAAGGATTAGTTGATTAGTCAATGCTGTTGGTGGTATAACAGT
SEQ2504	ATGCAAATTAATATGCAAGGATTAGTTGATTAGTCAATGCTGTTGGTGGTATAACAGT
SEQ2505	ATGCAAATTAATATGCAAGGATTAGTTGATTAGTCAATGCTGTTGGTGGTATAACAGT
SEQ2506	ATGCAAATTAATATGCAAGGATTAGTTGATTAGTCAATGCTGTTGGTGGTATAACAGT
SEQ2507	ACCCTTATTTCAGAAGCACCACCAAGTTACAGTGGT-AATACTACTTATAGTT---CTGA
SEQ2508	ATGCAAATTAATATGCAAGGATTAGTTGATTAGTCAATGCTGTTGGTGGTATAACAGT
SEQ2509	ACC-TTATTTCAGAAGCACCACCAAGTTACAGTGGT-AATACTACTTATAGTT---CTGA
SEQ2510	ATGCAAATTAATATGCAAGGATTAGTTGATTAGTCAATGCTGTTGGTGGTATAACAGT
SEQ2511	ACC-TTATTTCAGAAGCACCACCAAGTTACAGTGGT-AATACTACTTATAGTT---CTGA
SEQ2501	ACTAATAAAATTTGACTTTCCAATATCAATTGCTGCCAATGAACCAGAGTACAAGGCTGT
SEQ2502	ACTAATAAAATTTGACTTTCCAATATCAATTGCTGCCAATGAACCAGAGTACAAGGCTGT
SEQ2503	ACTAATAAAATTTGACTTTCCAATATCAATTGCTGCCAATGAACCAGAGTACAAGGCTGT
SEQ2504	ACTAATAAAATTTGACTTTCCAATATCAATTGCTGCCAATGAACCAGAGTACAAGGCTGT
SEQ2505	ACTAATAAAATTTGACTTTCCAATATCAATTGCTGCCAATGAACCAGAGTACAAGGCTGT
SEQ2506	ACTAATAAAATTTGACTTTCCAATATCAATTGCTGCCAATGAACCAGAGTACAAGGCTGT
SEQ2507	ACTAATCAAAC-AACTCATCAA---AGTTACTAT-AATAG--TAGCACTCCTGCTAGT
SEQ2508	ACTAATAAAATTTGACTTTCCAATATCAATTGCTGCCAATGAACCAGAGTACAAGGCTGT
SEQ2509	ACTAATCAAAC-AACTCATCAA---AATTACTAT-AATAG--TAGCACTCCTGCTAGT
SEQ2510	ACTAATAAAATTTGACTTTCCAATATCAATTGCTGCCAATGAACCAGAGTACAAGGCTGT
SEQ2511	ACTAATCAAAC-AACTCATCAA---AGTTACTAT-AATAG--TAGCACTCCTGCTAGT

**Table 25: Comparative Sequences relating to SAG0368
(protein of unknown function)**

SEQ2501	GTTGAACCAGGGACACATAAAATAAATGGAGAACAAGCACTTGTTTATTCTCGTATGCG
SEQ2502	GTTGAACCAGGGACACATAAAATAAATGGAGAACAAGCACTTGTTTATTCTCGTATGCG
SEQ2503	GTTGAACCAGGGACACATAAAATAAATGGAGAACAAGCACTTGTTTATTCTCGTATGCG
SEQ2504	GTTGAACCAGGGACACATAAAATAAATGGAGAACAAGCACTTGTTTATTCTCGTATGCG
SEQ2505	GTTGAACCAGGGACACATAAAATAAATGGAGAACAAGCACTTGTTTATTCTCGTATGCG
SEQ2506	GTTGAACCAGGGACACATAAAATAAATGGAGAACAAGCACTTGTTTATTCTCGTATGCG
SEQ2507	ACTATAGCAGTAACAC - TAACACAGGTCAGGCTGATTCAAGTGAAGTGTTAATAATTA
SEQ2508	GTTGAACCAGGGACACATAAAATAAATGGAGAACAAGCACTTGTTTATTCTCGTATGCG
SEQ2509	ACTATAGCAGTAACAC - TAACACAGGTCAGGCTGATTCAAGTGAAGTGTCAATAATCA
SEQ2510	GTTGAACCAGGGACACATAAAATAAATGGAGAACAAGCACTTGTTTATTCTCGTATGCG
SEQ2511	ACTATAGCAGTAACAC - TAACACAGGTCAGGCTGATTCAAGTGAAGTGTTAATAATTA
SEQ2501	TATGATGATCCAGAGGGAGATTATGGGCGTCAAAAAAGACAACGTGAAGTAATTCAAAA
SEQ2502	TATGATGATCCAGAGGGAGATTATGGGCGTCAAAAAAGACAACGTGAAGTAATTCAAAA
SEQ2503	TATGATGATCCAGAGGGAGATTATGGGCGTCAAAAAAGACAACGTGAAGTAATTCAAAA
SEQ2504	TATGATGATCCAGAGGGAGATTATGGGCGTCAAAAAAGACAACGTGAAGTAATTCAAAA
SEQ2505	TATGATGATCCAGAGGGAGATTATGGGCGTCAAAAAAGACAACGTGAAGTAATTCAAAA
SEQ2506	TATGATGATCCAGAGGGAGATTATGGGCGTCAAAAAAGACAACGTGAAGTAATTCAAAA
SEQ2507	AACGGGGCTGCAACGCCTAATCCAAACACAGGAACGCAACCAGTACCAGTCAAATAA
SEQ2508	TATGATGATCCAGAGGGAGATTATGGGCGTCAAAAAAGACAACGTGAAGTAATTCAAAA
SEQ2509	AACGGGGCTGCAACGCCTAATCCA-----
SEQ2510	TATGATGATCCAGAGGGAGATTATGGGCGTCAAAAAAGACAACGTGAAGTAATTCAAAA
SEQ2511	AACGGGGCTGCAACGCCTAATCCAAACACAGGAACGCAACCAGTACCAGTCAAATAA
SEQ2501	GTCTTAAAAAAATATTGGCGTTAAATAGTATTAGTTCATACAAAAAAATCTTTCCGC
SEQ2502	GTCTTAAAAAAATATTGGCGTTAAATAGTATTAGTTCATACAAAAAAATCTTTCCGC
SEQ2503	GTCTTAAAAAAATATTGGCGTTAAATAGTATTAGTTCATACAAAAAAATCTTTCCGC
SEQ2504	GTCTTAAAAAAATATTGGCGTTAAATAGTATTAGTTCATACAAAAAAATCTTTCCGC
SEQ2505	GTCTTAAAAAAATATTGGCGTTAAATAGTATTAGTTCATACAAAAAAATCTTTCCGC
SEQ2506	GTCTTAAAAAAATATTGGCGTTAAATAGTATTAGTTCATACAAAAAAATCTTTCCGC
SEQ2507	CCA-----
SEQ2508	GTCTTAAAAAAATATTGGCGTTAAATAGTA-----
SEQ2509	-----
SEQ2510	GTCTTAAAAAAATATTGGCGTTAAATAGTATTAGTTCATACAAAAAAATCTTTCCGC
SEQ2511	CCA-----
SEQ2501	GTAAGTAATAACATGCAAACTAATATTGAGATATCATCAAAAACGATTCCCTAATTTGTT
SEQ2502	GTAAGTAATAACATGCAAACTAATATTGAGATATCATCAAAAACGATTCCCTAATTTGTT
SEQ2503	GTAAGTAATAACATGCAAACTAATATTGAGATATCATCAAAAACGATTCCCTAATTTGTT
SEQ2504	GTAAGTAATAACATGCAAACTAATATTGAGATATCATCAAAAACGATTCCCTAATTTGTT
SEQ2505	GTAAGTAATAACATGCAAACTAATATTGAGATATCATCAAAAACGATTCCCTAATTTGTT
SEQ2506	GTAAGTAATAACATGCAAACTAATATTGAGATATCATCAAAAACGATTCCCTAATTTGTT
SEQ2507	-----
SEQ2508	-----
SEQ2509	-----
SEQ2510	GTAAGTAATAACATGCAAACTAATATTGAGATATCATCAAAAACGATTCCCTAATTTGTT
SEQ2511	-----
SEQ2501	GCTTATAAAGATTCATTGGAACATATTAATCTTATCAGTTGAAGGGTGAAGACGCTAC
SEQ2502	GCTTATAAAGATTCATTGGAACATATTAATCTTATCAGTTGAAGGGTGAAGACGCTAC
SEQ2503	GCTTATAAAGATTCATTGGAACATATTAATCTTATCAGTTGAAGGGTGAAGACGCTAC
SEQ2504	GCTTATAAAGATTCATTGGAACATATTAATCTTATCAGTTGAAGGGTGAAGACGCTAC
SEQ2505	GCTTATAAAGATTCATTGGAACATATTAATCTTATCAGTTGAAGGGTGAAGACGCTAC
SEQ2506	GCTTATAAAGATTCATTGGAACATATTAATCTTATCAGTTGAAGGGTGAAGACGCTAC
SEQ2507	-----
SEQ2508	-----
SEQ2509	-----
SEQ2510	GCTTATAAAGATTCATTGGAACATATTAATCTTATCAGTTGAAGGGTGAAGACGCTAC
SEQ2511	-----

**Table 25: Comparative Sequences relating to SAG0368
(protein of unknown function)**

SEQ2501	TTATCAGATGGTGGCTCTTATCAAATTTTAACTAAGAAACATCTACTTGCAGTTCAAAA
SEQ2502	TTATCAGATGGTGGCTCTTATCAAATTTTAACTAAGAAACATCTACTTGCAGTTCAAAA
SEQ2503	TTATCAGATGGTGGCTCTTATCAAATTTTAACTAAGAAACATCTACTTGCAGTTCAAAA
SEQ2504	TTATCAGATGGTGGCTCTTATCAAATTTTAACTAAGAAACATCTACTTGCAGTTCAAAA
SEQ2505	TTATCAGATGGTGGCTCTTATCAAATTTTAACTAAGAAACATCTACTTGCAGTTCAAAA
SEQ2506	TTATCAGATGGTGGCTCTTATCAAATTTTAACTAAGAAACATCTACTTGCAGTTCAAAA
SEQ2507	-----
SEQ2508	-----
SEQ2509	-----
SEQ2510	TTATCAGATGGTGGCTCTTATCAAATTTTAACTAAGAAACATCTACTTGCAGTTCAAAA
SEQ2511	-----
SEQ2501	AGAATTAAGAAAGAACTGGATAAAAAAGCGTAGTAAACTCTGAAGACAAGCGCGATTCT
SEQ2502	AGAATTAAGAAAGAACTAGATAAAAAAGCGTAGTAAACTCTGAAGACAAGCGCGATTCT
SEQ2503	AGAATTAAGAAAGAACTGGATAAAAAAGCGTAGTAAACTCTGAAGACAAGCGCGATTCT
SEQ2504	AGAATTAAGAAAGAACTGGATAAAAAAGCGTAGTAAACTCTGAAGACAAGCGCGATTCT
SEQ2505	AGAATTAAGAAAGAACTGGATAAAAAAGCGTAGTAAACTCTGAAGACAAGCGCGATTCT
SEQ2506	AGAATTAAGAAAGAACTGGATAAAAAAGCGTAGTAAACTCTGAAGACAAGCGCGATTCT
SEQ2507	-----
SEQ2508	-----
SEQ2509	-----
SEQ2510	AGAATTAAGAAAGAACTGGATAAAAAAGCGTAGTAAACTCTGAAGACAAGCGCGATTCT
SEQ2511	-----
SEQ2501	TATGAAGATTACTATGGTACTACTGCTAGTAATGATTCTTCTACTTATTCATCAACACA
SEQ2502	TATGAAGATTACTATGGTACTACTGCTAGTAATGATTCTTCTACTTATTCATCAACACA
SEQ2503	TATGAAGATTACTATGGTACTACTGCTAGTAATGATTCTTCTACTTATTCATCAACACA
SEQ2504	TATGAAGATTACTATGGTACTACTGCTAGTAATGATTCTTCTACTTATTCATCAACACA
SEQ2505	TATGAAGATTACTATGGTACTACTGCTAGTAATGATTCTTCTACTTATTCATCAACACA
SEQ2506	TATGAAGATTACTATGGTACTACTGCTAGTAATGATTCTTCTACTTATTCATCAACACA
SEQ2507	-----
SEQ2508	-----
SEQ2509	-----
SEQ2510	TATGAAGATTACTATGGTACTACTGCTAGTAATGATTCTTCTACTTATTCATCAACACA
SEQ2511	-----
SEQ2501	GAGAATAATTATAATACAACACCTTATTCAGAAGCACCACCAAGTTACAGTGGTAATAC
SEQ2502	GAGAATAATTATAATACAACACCTTATTCAGAAGCACCACCAAGTTACAGTGGTAATAC
SEQ2503	GAGAATAATTATAATACAACACCTTATTCAGAAGCACCACCAAGTTACAGTGGTAATAC
SEQ2504	GAGAATAATTATAATACAACACCTTATTCAGAAGCACCACCAAGTTACAGTGGTAATAC
SEQ2505	GAGAATAATTATAATACAACACCTTATTCAGAAGCACCACCAAGTTACAGTGGTAATAC
SEQ2506	GAGAATAATTATAATACAACACCTTATTCAGAAGCACCACCAAGTTACAGTGGTAATAC
SEQ2507	-----
SEQ2508	-----
SEQ2509	-----
SEQ2510	GAGAATAATTATAATACAACACCTTATTCAGAAGCACCACCAAGTTACAGTGGTAATAC
SEQ2511	-----
SEQ2501	ACTTAT-AGTTCTGAGACTAATCAAACAACTCATCAAAATTACTATAATAGTAGCACTC
SEQ2502	ACTTAT-AGTTCTGAGACTAATCAAACAACTCATCAAAATTACTATAATAGTAGCACTC
SEQ2503	ACTTAT-AGTTCTGAGACTAATCAAACAACTCATCAAAATTACTATAATAGTAGCACTC
SEQ2504	ACTTAT-AGTTCTGAGACTAATCAAACAACTCATCAAAATTACTATAATAGTAGCACTC
SEQ2505	ACTTAT-AGTTCTGAGACTAATCAAACAACTCATCAAAATTACTATAATAGTAGCACTC
SEQ2506	ACTTATTAGTTCTGAGACTAATCAAACAACTCATCAAAATTACTATAATAGTAGCACTC
SEQ2507	-----
SEQ2508	-----
SEQ2509	-----
SEQ2510	ACTTAT-AGTTCTGAGACTAATCAAACAACTCATCAAAATTACTATAATAGTAGCACTC
SEQ2511	-----

**Table 25: Comparative Sequences relating to SAG0368
(protein of unknown function)**

SEQ2501	TGCTAGTAACTATAGCAGTAACACTAACACAGGTCAGGCTGATTCAAGTGGAAGTGTCA
SEQ2502	TGCTAATAACTATAGCAGTAACACTAACACAGGTCAGGCTGATTCAAGTGGAAGTGTCA
SEQ2503	TGCTAGTAACTATAGCAGTAACACTAACACAGGTCAGGCTGATTCAAGTGGAAGTGTCA
SEQ2504	TGCTAGTAACTATAGCAGTAACACTAACACAGGTCAGGCTGATTCAAGTGGAAGTGTCA
SEQ2505	TGCTAGTAACTATAGCAGTAACACTAACACAGGTCAGGCTGATTCAAGTGGAAGTGTCA
SEQ2506	TGCTAGTAACTATAGCAGTAACACTAACACAGGTCAGGCTGATTCAAGTGGAAGTGTCA
SEQ2507	-----
SEQ2508	-----
SEQ2509	-----
SEQ2510	TGCTAGTAACTATAGCAGTAACACTAACACAGGTCAGGCTGATTCAAGTGGAAGTGTCA
SEQ2511	-----
SEQ2501	TAATCATAACGGGGCTGCAACGCCTAATCCA
SEQ2502	TAATCATAATGGGGCTGCAACGCCTAATCCA
SEQ2503	TAATCATAACGGGGCTGCAACGCCTAATCCA
SEQ2504	TAATCATAACGGGGCTGCAACGCCTAATCCA
SEQ2505	TAATCATAACGGGGCTGCAACGCCTAATCCA
SEQ2506	TAATCATAACGGGGCTGCAACGCCTAATCCA
SEQ2507	-----
SEQ2508	-----
SEQ2509	-----
SEQ2510	TAATCATAACGGGGCTGCAACGCCTAATCCA
SEQ2511	-----

>SEQ ID NO 2550: 54_090 frame: 1
 YNFSTNELSKTFKDFKLAKSKSHAIEETKPFISILLMGVDTGSEHRKSKWSGNSDSMILVT
 INPKTNKTTMTSLERDVLIKLSGPKNNGQTGVEAKLNAAYASGGAEMALMTVQDILLDINV
 DYFMQINMQGLVDLVNAVGGITVTNKFDFFPISIAANEPEYKAVVEPGTHKINGEQALVYS
 RMRYYDDPEGDYGRQKRQREVIQKVLKKILALNSISSYKKILSAVSNMOTNIEISSKTIP
 NLLAYKDSLEHIKSYQLKGEDATLSDGGSYQILTKKHLAVQNRIKKELDKRSLTKTS
 AILYEDYYGTASNDSSSTYSSTQENNYNTTPYSEAPPSYSGNTTYSSETNQTHQNYNS
 STPASNYSSNTNTGQADSSGSVNNHNGAATPNP

>SEQ ID NO 2551: 54_1169NT frame: 1
 YNFSTNELSKTFKDFKLAKSKSHAIEETKPFISILLMGVDTGSEHRKSKLVRK. RFYDL
 SHYKS.N..NNDDKLRT.RID.IEWSQK.WTDWRRSKAKCSLCFWCGNGIDDCSRLIRY.C
 .LLYAN.YARIS.FSQCCWYNSN..I.LSNINCCQ.TRVQGCC.TRDT.NKWRTSTCLF
 SYAL..SRGLWASKKTT.SNSKSP.KNIGVK.Y.FIQKNSFRSK..HAN.Y.DIIKNDS
 .FVSL.RFIGTY.ILSVER.RRYFIRWLLSNFN.ETSTCSSK.N.ERTR.KA..NSEDK
 RDSI.RLLWYYC..FFYLFINTRE.L.YNTLFRSTTKLQW.YYL.F.D.SNNSSKLL..
 .HSC..L.Q.H.HRSG.FKWKQ.S.WGCNA.S

>SEQ ID NO 2552: 54_18RS21 frame: 1
 YNFSTNELSKTFKDFKLAKSKSHAIEETKPFISILLMGVDTGSEHRKSKWSGNSDSMILVT
 INPKTNKTTMTSLERDVLIKLSGPKNNGQTGVEAKLNAAYASGGAEMALMTVQDILLDINV
 DYFMQINMQGLVDLVNAVGGITVTNKFDFFPISIAANEPEYKAVVEPGTHKINGEQALVYS
 RMRYYDDPEGDYGRQKRQREVIQKVLKKILALNSISSYKKILSAVSNMOTNIEISSKTIP
 NLLAYKDSLEHIKSYQLKGEDATLSDGGSYQILTKKHLAVQNRIKKELDKRSLTKTS
 AILYEDYYGTASNDSSSTYSSTQENNYNTTPYSEAPPSYSGNTTYSSETNQTHQNYNS
 STPASNYSSNTNTGQADSSGSVNNHNGAATPNP

>SEQ ID NO 2553: 54_2603 frame: 1
 YNFSTNELSKTFKDFKLAKSKSHAIEETKPFISILLMGVDTGSEHRKSKWSGNSDSMILVT
 INPKTNKTTMTSLERDVLIKLSGPKNNGQTGVEAKLNAAYASGGAEMALMTVQDILLDINV
 DYFMQINMQGLVDLVNAVGGITVTNKFDFFPISIAANEPEYKAVVEPGTHKINGEQALVYS
 RMRYYDDPEGDYGRQKRQREVIQKVLKKILALNSISSYKKILSAVSNMOTNIEISSKTIP
 NLLAYKDSLEHIKSYQLKGEDATLSDGGSYQILTKKHLAVQNRIKKELDKRSLTKTS
 AILYEDYYGTASNDSSSTYSSTQENNYNTTPYSEAPPSYSGNTTYSSETNQTHQNYNS
 STPASNYSSNTNTGQADSSGSVNNHNGAATPNP

>SEQ ID NO 2554: 54_A909 frame: 1
 YNFSTNELSKTFKDFKLAKSKSHAIEETKPFISILLMGVDTGSEHRKSKWSGNSDSMILVT
 INPKTNKTTMTSLERDVLIKLSGPKNNGQTGVEAKLNAAYASGGAEMALMTVQDILLDINV
 DYFMQINMQGLVDLVNAVGGITVTNKFDFFPISIAANEPEYKAVVEPGTHKINGEQALVYS
 RMRYYDDPEGDYGRQKRQREVIQKVLKKILALNSISSYKKILSAVSNMOTNIEISSKTIP
 NLLAYKDSLEHIKSYQLKGEDATLSDGGSYQILTKKHLAVQNRIKKELDKRSLTKTS

**Table 25: Comparative Sequences relating to SAG0368
(protein of unknown function)**

AILYEDYYGTASNDSSSTYSSTQENNYNTTTPYSEAPPSYSGNTTYSSETNQTHQNYNS
STPASNYSSNTNTGQADSSGSVNNHNGAATPNP

>SEQ ID NO 2555:54_CJB110 frame: 1

YNFSTNELSKTFKDFKLAKSKSHAIETKPFISILLMGVDTGSEHRKSKWSGNSDSMILVT
INPKTNKTTMTSLERDVLIKLSGPKNNGQTGVEAKLNAAAYASGGAEMALMTVQDLLDINV
DYFMQINMQGLVDLVNAVGGITVTNKFDFFPISIAANEPEYKAVVEPGTHKINGEQALVYS
RMRYDDPEGDYGRQKRQREVIQKVLKKILALNSISSYKKILSAVSNNMQTNIEISSKTIP
NLLAYKDSLEHIKSYQLKGEDATLSDGGSYQILTKKHLAVQNRIKKELDKKRSKTLKTS
AILYEDYYGTASNDSSSTYSSTQENNYNTTTPYSEAPPSYSGNTTY.F.D.SNNSKLL..

>SEQ ID NO 2556:54_COH1 frame: 1

DFKLDKSKSHAIETKPFISILLMGVDTGSEHRKSKWSGNSDSMILVTINPKTNKTTMTSL
ERDVLIKLSGPKNNGQTGVEAKLNAAAYASGGAEMALMTVQDLLDINV DYFMQINMQGLVD
LVNAVGGITVTNKFDFFPISIAANEPEYKAVVEPGTHKINGEQALVYSRMRYDDPEGDYGR
QKRQREVIQKVLKKILALNSISSYKKILSAVSNNMQTNIEISSKTIPNLLAYKDSLEHIK
SYQLKGEDATLSDGGSYQILTKKHLAVQNRIKKELDKKRSKTLKTSAILYEDYYGTAS
NDSSSTYSSTQENNYTTPFRSTTKLQW.YYL.F.D.SNNSKLL...HSC..L.Q.H.H
RSG.FKWKC..L.RGCNA.SKHNRATSTRN.S

>SEQ ID NO 2557:54_H36B frame: 1

YNFSTNELSKTFKDFKLAKSKSHAIETKPFISILLMGVDTGSEHRKSKWSGNSDSMILVT
INPKTNKTTMTSLERDVLIKLSGPKNNGQTGVEAKLNAAAYASGGAEMALMTVQDLLDINV
DYFMQINMQGLVDLVNAVGGITVTNKFDFFPISIAANEPEYKAVVEPGTHKINGEQALVYS
RMRYDDPEGDYGRQKRQREVIQKVLKKILALNSISSYKKILSAVSNNMQTNIEISSKTIP
NLLAYKDSLEHIKSYQLKGEDATLSDGGSYQILTKKHLAVQNRIKKELDKKRSKTLKTS
AILYEDYYGTASNDSSSTYSSTQENNYNTTTPYSEAPPSYSGNTTYSSETNQTHQNYNS
STPASNYSSNTNTGQADSSGSVNNHNGAATPNP

>SEQ ID NO 2558:54_JM9130013 frame: 1

YNFSTNELSKTFKDFKLAKSKSHAIETKPFISILLMGVDTGSEHRKSKWSGNSDSMILVT
INPKTNKTTMTSLERDVLIKLSGPKNNGQTGVEAKLNAAAYASGGAEMALMTVQDLLDINV
DYFMQINMQGLVDLVNAVGGITVTNKFDFFPISIAANEPEYKAVVEPGTHKINGEQALVYS
RMRYDDPEGDYGRQKRQREVIQKVLKKILALNSISSYKKILSAVSNNMQTNIEISSKTIP
NLLAYKDSLEHIKSYQLKGEDATLSDGGSYQILTKKHLAVQNRIKKELDKKRSKTLKTS
AILYEDYYGTASNDSSSTYSSTQENNYNTTTPYSEAPPSYSGNTTYSSETNQTHQNYNS
STPASNYSSNTNTGQADSSGSVNNHNGAATPNP

>SEQ ID NO 2559:54_M781 frame: 2

SILLMGVDTGSEHRKSKWSGNSDSMILVTINPKTNKTTMTSLERDVLIKLSGPKNNGQTG
VEAKLNAAAYASGGAEMALMTVQDLLDINV DYFMQINMQGLVDLVNAVGGITVTNKFDFFP
ISIAANEPEYKAVVEPGTHKINGEQALVYSRMRYDDPEGDYGRQKRQREVIQKVLKKILAL
NSISSYKKILSAVSNNMQTNIEISSKTIPNLLAYKDSLEHIKSYQLKGEDATLSDGGSYQ
ILTKKHLAVQNRIKKELDKKRSKTLKTSAILYEDYYGTASNDSSSTYSSTQENNYNTTTP
YSEAPPSYSGNTTYSSETNQTHQSYNSSTPASNYSSNTNTGQADSSGSVNNYNGAATP
NPNTGTQPVPGQINP

SEQ2550	NFSTNELSKTFKDFKLAKSKSHAIETKPFISILLMGVDTGSEHRKSKWSGNSDSMILVT
SEQ2551	NFSTNELSKTFKDFKLAKSKSHAIETKPFISILLMGVDTGSEHRKSKLVRKRFDLSHY
SEQ2552	NFSTNELSKTFKDFKLAKSKSHAIETKPFISILLMGVDTGSEHRKSKWSGNSDSMILVT
SEQ2553	NFSTNELSKTFKDFKLAKSKSHAIETKPFISILLMGVDTGSEHRKSKWSGNSDSMILVT
SEQ2554	NFSTNELSKTFKDFKLAKSKSHAIETKPFISILLMGVDTGSEHRKSKWSGNSDSMILVT
SEQ2555	NFSTNELSKTFKDFKLAKSKSHAIETKPFISILLMGVDTGSEHRKSKWSGNSDSMILVT
SEQ2556	-----DFKLDKSKSHAIETKPFISILLMGVDTGSEHRKSKWSGNSDSMILVT
SEQ2557	NFSTNELSKTFKDFKLAKSKSHAIETKPFISILLMGVDTGSEHRKSKWSGNSDSMILVT
SEQ2558	NFSTNELSKTFKDFKLAKSKSHAIETKPFISILLMGVDTGSEHRKSKWSGNSDSMILVT
SEQ2559	-----SILLMGVDTGSEHRKSKWSGNSDSMILVT

SEQ2550	NPKTNKTTMTSLERDVLIKLSGPKNNGQTGVEAKLNAAAYASGGAEMALMTVQDLLDINV
SEQ2551	SNNDKLRTRIDIEWSQKWDWRRS-----KAKCSLCFWWCNGIDDCSRLIRYCLLY
SEQ2552	NPKTNKTTMTSLERDVLIKLSGPKNNGQTGVEAKLNAAAYASGGAEMALMTVQDLLDINV
SEQ2553	NPKTNKTTMTSLERDVLIKLSGPKNNGQTGVEAKLNAAAYASGGAEMALMTVQDLLDINV
SEQ2554	NPKTNKTTMTSLERDVLIKLSGPKNNGQTGVEAKLNAAAYASGGAEMALMTVQDLLDINV
SEQ2555	NPKTNKTTMTSLERDVLIKLSGPKNNGQTGVEAKLNAAAYASGGAEMALMTVQDLLDINV
SEQ2556	NPKTNKTTMTSLERDVLIKLSGPKNNGQTGVEAKLNAAAYASGGAEMALMTVQDLLDINV
SEQ2557	NPKTNKTTMTSLERDVLIKLSGPKNNGQTGVEAKLNAAAYASGGAEMALMTVQDLLDINV

**Table 25: Comparative Sequences relating to SAG0368
(protein of unknown function)**

SEQ2558	NPKTNKTTMTSLERDVLILKLSGPKNNGQTGVEAKLNAAYASGGAEMALMTVQDLLDINV
SEQ2559	NPKTNKTTMTSLERDVLILKLSGPKNNGQTGVEAKLNAAYASGGAEMALMTVQDLLDINV
SEQ2550	YFMQINMQGLVDLVNAVGGITVTNKFDFPISIAANEPEYKAVVEPGTHKINGEQALVYS
SEQ2551	NYARISFSQCCWWYNS-----NILSNINCCQTRVQGCCTRDITNKWRTSTCLFSY
SEQ2552	YFMQINMQGLVDLVNAVGGITVTNKFDFPISIAANEPEYKAVVEPGTHKINGEQALVYS
SEQ2553	YFMQINMQGLVDLVNAVGGITVTNKFDFPISIAANEPEYKAVVEPGTHKINGEQALVYS
SEQ2554	YFMQINMQGLVDLVNAVGGITVTNKFDFPISIAANEPEYKAVVEPGTHKINGEQALVYS
SEQ2555	YFMQINMQGLVDLVNAVGGITVTNKFDFPISIAANEPEYKAVVEPGTHKINGEQALVYS
SEQ2556	YFMQINMQGLVDLVNAVGGITVTNKFDFPISIAANEPEYKAVVEPGTHKINGEQALVYS
SEQ2557	YFMQINMQGLVDLVNAVGGITVTNKFDFPISIAANEPEYKAVVEPGTHKINGEQALVYS
SEQ2558	YFMQINMQGLVDLVNAVGGITVTNKFDFPISIAANEPEYKAVVEPGTHKINGEQALVYS
SEQ2559	YFMQINMQGLVDLVNAVGGITVTNKFDFPISIAANEPEYKAVVEPGTHKINGEQALVYS
SEQ2550	MRYDDPEGDYGROKQREVIQKVLKKILALNSISSYKKILSAVSNMQTNIEISSKTIP
SEQ2551	LSRGRLWASKKTTNSKSPKNIQVYFIQKNSFRSKHANYDIIKNDSEVSLRFITGYI-
SEQ2552	MRYDDPEGDYGROKQREVIQKVLKKILALNSISSYKKILSAVSNMQTNIEISSKTIP
SEQ2553	MRYDDPEGDYGROKQREVIQKVLKKILALNSISSYKKILSAVSNMQTNIEISSKTIP
SEQ2554	MRYDDPEGDYGROKQREVIQKVLKKILALNSISSYKKILSAVSNMQTNIEISSKTIP
SEQ2555	MRYDDPEGDYGROKQREVIQKVLKKILALNSISSYKKILSAVSNMQTNIEISSKTIP
SEQ2556	MRYDDPEGDYGROKQREVIQKVLKKILALNSISSYKKILSAVSNMQTNIEISSKTIP
SEQ2557	MRYDDPEGDYGROKQREVIQKVLKKILALNSISSYKKILSAVSNMQTNIEISSKTIP
SEQ2558	MRYDDPEGDYGROKQREVIQKVLKKILALNSISSYKKILSAVSNMQTNIEISSKTIP
SEQ2559	MRYDDPEGDYGROKQREVIQKVLKKILALNSISSYKKILSAVSNMQTNIEISSKTIP
SEQ2550	LLAYKDSLEHIKSYQLKGEDATLSDGGSYQILTKKHLAVQNRIKKELDKKRSKTLKTS
SEQ2551	L-SVERRRYFIRWLLSNFNETSTCSSKNERTRKANSEDKRDSIRLLWYFCFFYLFINT
SEQ2552	LLAYKDSLEHIKSYQLKGEDATLSDGGSYQILTKKHLAVQNRIKKELDKKRSKTLKTS
SEQ2553	LLAYKDSLEHIKSYQLKGEDATLSDGGSYQILTKKHLAVQNRIKKELDKKRSKTLKTS
SEQ2554	LLAYKDSLEHIKSYQLKGEDATLSDGGSYQILTKKHLAVQNRIKKELDKKRSKTLKTS
SEQ2555	LLAYKDSLEHIKSYQLKGEDATLSDGGSYQILTKKHLAVQNRIKKELDKKRSKTLKTS
SEQ2556	LLAYKDSLEHIKSYQLKGEDATLSDGGSYQILTKKHLAVQNRIKKELDKKRSKTLKTS
SEQ2557	LLAYKDSLEHIKSYQLKGEDATLSDGGSYQILTKKHLAVQNRIKKELDKKRSKTLKTS
SEQ2558	LLAYKDSLEHIKSYQLKGEDATLSDGGSYQILTKKHLAVQNRIKKELDKKRSKTLKTS
SEQ2559	LLAYKDSLEHIKSYQLKGEDATLSDGGSYQILTKKHLAVQNRIKKELDKKRSKTLKTS
SEQ2550	ILYEDYYGTTASNDSSSTYSSTQENNYNTTPYSEAPPSYSGNTTYSSETNQTHQNYNS
SEQ2551	ELY-----NTLFRST-----TKLQWYLFDSNNSKLLHSCLOH
SEQ2552	ILYEDYYGTTASNDSSSTYSSTQENNYNTTPYSEAPPSYSGNTTYSSETNQTHQNYNS
SEQ2553	ILYEDYYGTTASNDSSSTYSSTQENNYNTTPYSEAPPSYSGNTTYSSETNQTHQNYNS
SEQ2554	ILYEDYYGTTASNDSSSTYSSTQENNYNTTPYSEAPPSYSGNTTYSSETNQTHQNYNS
SEQ2555	ILYEDYYGTTASNDSSSTYSSTQENNYNTTPYSEAPPSYSGNTTYSFDSNNSKLL-----
SEQ2556	ILYEDYYGTTASNDSSSTYSSTQENNYNTTPYSEAPPSYSGNTTYSSETNQTHQNYNS
SEQ2557	ILYEDYYGTTASNDSSSTYSSTQENNYNTTPYSEAPPSYSGNTTYSSETNQTHQNYNS
SEQ2558	ILYEDYYGTTASNDSSSTYSSTQENNYNTTPYSEAPPSYSGNTTYSSETNQTHQNYNS
SEQ2559	ILYEDYYGTTASNDSSSTYSSTQENNYNTTPYSEAPPSYSGNTTYSSETNQTHQSYNS
SEQ2550	TPASNYSSNTNTGQADSSGSVNNHNGAATPNP-----
SEQ2551	RSGFKWKQCSWGCNAS-----
SEQ2552	TPASNYSSNTNTGQADSSGSVNNHNGAATPNP-----
SEQ2553	TPASNYSSNTNTGQADSSGSVNNHNGAATPNP-----
SEQ2554	TPASNYSSNTNTGQADSSGSVNNHNGAATPNP-----
SEQ2555	-----
SEQ2556	RSGFKWKCLRGCNASKHRNATSTRSNS-----
SEQ2557	TPASNYSSNTNTGQADSSGSVNNHNGAATPNP-----
SEQ2558	TPASNYSSNTNTGQADSSGSVNNHNGAATPNP-----
SEQ2559	TPASNYSSNTNTGQADSSGSVNNYNGAATPNPNTGTQPVPGQTNP

Table 26: Comparative Sequences relating to SAG0503 (lipase/acylhydrolase)

SEQ ID NO. 2601: SAG0503 FROM THE 090 GBS TYPE Ia STRAIN
(REVERSE COMPLEMENT)

GGGCACAAGTTTGTACAAAAAGCAGGCTCTATTTTTTCCTTGATCATTCCAAAATCAAATCCTAAATTAACAAAAA
AGACTTCCTAACAAAGAAAGTTATCCCACTTAAGTATGTTGCTCTTGAGATTCTCTGACCGAAGGTGTGGGCGATAC
AACCTCTCAAGGTGTTTGTCCCACTGCTATCAGAATCACTCCATAATCGATACTCTTACCAAGTGACTTCTGTTAA
TTATGGTGTGTCTGGGAATACTAGTCAACAAATTTTAAACGATGACGACAGATCCTCAAATCGAAAAAGATTTAGA
GAAAGCTGATTTATTGACGCTAACTGTTGGTGGTAATGATGTCTTGGCTGTTATTTCGTAAAGAGCTCAGTCATTTATC
ACTAAATTCCTTTGAGAAACCAGCAGAAGCATATAAGGAACGTTTGAAAGAAATACTTGCAAAAGCAAGACAAGATAA
TCCTAAATTGCCTATTTATGTTTTAGGCATTTATAATCCTTTTTACCTAAACTTTCCACAATTAAGTAAATGCAAAAC
CGTTATTGATAATTGGAATAAAGCTACAAAAGAAGTAGTTGATGCTTCAGAAAATGTTTATTTTGTCCCAATTAATGA
CCGCCTTTATAAGGAATAAATGGTAAAGAGGGTATTACAGAGTCATCAAATAGTCAGGCAAGTATCACTAATGATGC
TCTCTTTACTGGAGACCATTTTCATCCCAATAATATTGGCTATCAAATCATGTCTAACGCCGTTATGGAGAAAAATAA
TGAAACAAGAAAAACTGGCCGAACCCAGCTTTCTTGTACAAAG

SEQ ID NO. 2602: SAG0503 FROM THE H36b GBS TYPE Ib STRAIN
(REVERSE COMPLEMENT)

TTTGTACAAAAAGCAGGCTCTATTTTTTCCTTGATCATTCCAAAATCAAATCCTAAATTAACAAAAAAGACTTCCT
AACAAAGAAAGTTATCCCACTTAAGTATGTTGCTCTTGAGATTCTCTGACCGAAGGTGTGGGCGATACAACTCTCA
AGGTGGTTTTGTTCCTACTGCTATCAGAATCACTCCATAATCGATACTCTTACCAAGTGACTTCTGTTAATTATGGTGT
GTCTGGGAATACTAGTCAACAAATTTTAAACGATGACGACAGATCCTCAAATCGAAAAAGATTTAGAGAAAGCTGA
TTTATTGACGCTAACTGTTGGTGGTAATGATGTCTTGGCTGTTATTTCGTAAAGAGCTCAGTCATTTATCACTAAATTC
CTTTGAGAAACCAGCAGAAGCATATAAGGAACGTTTGAAAGAAATCCTTGCAAAAGCAAGACAAGATAATCCTAAAT
GCCTATTTATGTTTTAGGCATTTATAATCCTTTTTACCTAAACTTTCCACAATTAAGTAAATGCAAAACCGTTATTGA
TAATTGGAATAAAGCTACAAAAGAAGTAGTTGATGCTTCAGAAAATGTTTATTTTGTCCCAATTAATGACCGCTTTA
TAAGGAATAAATGGTAAAGAGGGTATTATAGAGTCATCAAATAGTCAGGCAAGTATCACTAATGATGCTCTCTTTAC
TGGAGACCATTTTCATCCCAATAATATTGGCTATCAAATCATGTCTAACGCCGTTATGGAGAAAAATAATGAAACAAG
AAAAAACTGGCCGAACCCAGCTTTCTTGTACAAAGTGGTCC

SEQ ID NO. 2603: SAG0503 FROM THE 18RS21 GBS TYPE II STRAIN (REVERSE
COMPLEMENT)

GTTTGTACAAAAAGCAGGCTCTATTTTTTCCTTGATCATTCCAAAATCAAATCCTAAATTAACAAAAAAGACTTCC
TAACAAAGAAAGTTATCCCACTTAAGTATGTTGCTCTTGAGATTCTCTGACCGAAGGTGTGGGCGATACAACTCTC
AAGGTGGTTTTGTTCCTACTGCTATCAGAATCACTCCATAATCGATACTCTTACCAAGTGACTTCTGTTAATTATGGTGT
TGCTCTGGGAATACTAGTCAACAAATTTTAAACGATGACGACAGATCCTCAAATCGAAAAAGATTTAGAGAAAGCTG
ATTTATTGACGCTAACTGTTGGTGGTAATGATGTCTTGGCTGTTATTTCGTAAAGAGCTCAGTCATTTATCACTAAAT
CCTTTGAGAAACCAGCAGAAGCATATAAGGAACGTTTGAAAGAAATCCTTGCAAAAGCAAGACAAGATAATCCTAAAT
TGCTATTTATGTTTTAGGCATTTATAATCCTTTTTACCTAAACTTTCCACAATTAAGTAAATGCAAAACCGTTATTG
ATAATTGGAATAAAGCTACAAAAGAAGTAGTTGATGCTTCAGAAAATGTTTATTTTGTCCCAATTAATGACCGCTTT
ATAAGGAATAAATGGTAAAGAGGGTATTACAGAGTCATCAAATAGTCAGGCAAGTATCACTAATGATGCTCTCTTTA
CTGGAGACCATTTTCATCCCAATAATATTGGCTATCAAATCATGTCTAACGCCGTTATGGAGAAAAATAATGAAACAA
GAAAAAACTGGCCGAACCCAGCTTTCTTGTACAA

SEQ ID NO. 2604: SAG0503 FROM THE COH1 GBS TYPE III STRAIN (REVERSE
COMPLEMENT)

GGACAAGTTTGTACAAAAAGCAGGCTCTATTTTTTCCTTGATCATTCCAAAATCAAATCCTAAATTAACAAAAAAG
ACTTCCTAACAAAGAAAGTTATCCCACTTAAGTATGTTGCTCTTGAGATTCTCTGACCGAAGGTGTGGGGGATACAA
CCTCTCAAGGTGTTTGTCCCACTGCTATCAGAATCACTCCATAATCGATACTCTTACCAAGTGACTTCTGTTAATT
ATGGTGTGTCTGGGAATACTAGTCAACAAATTTTAAACGATGACGACAGATCCTCAAATCGAAAAAGATTTAGAGA
AAGCTGATTTATTGACGCTAACTGTTGGTGGTAATGATGTCTTGGCTGTTATTTCGTAAAGAGCTCAGTCATTTATCAC
TAAATTCCTTTGAGAAACCAGCAGAAGCATATAAGGAACGTTTGAAAGAAATCCTTGCAAAAGCAAGACAAGATAATC
CTAAATTGCCTATTTATGTTTTAGGCATTTATAATCCTTTTTACCTAAACTTTCCACAATTAAGTAAATGCAAAACCG
TTATTGATAATTGGAATAAAGCTACAAAAGAAGTAGTTGATGCTTCAGAAAATGTTTATTTTGTCCCAATTAATGACC
GCCTTTATAAGGAATAAATGGTAAAGAGGGTATTACAGAGTCATCAAATAGTCAGGCAAGTATCACTAATGATGCTC
TCTTTACTGGAGACCATTTTCATCCCAATAATATTGGCTATCAAATCATGTCTAACGCCGTTATGGAGAAAAATAAT
AAACAAGAAAAAACTGGCCGAACCCAGCTTTCTTGTACAA

Table 26: Comparative Sequences relating to SAG0503 (lipase/acylhydrolase)

SEQ ID NO. 2605: SAG0503 FROM THE CJB110 GBS NONTYPEABLE STRAIN (REVERSE COMPLEMENT)

GTTTGTACAAAAAGCAGGCTCTATTTTTTCTTGATCATTTCCAAAATCAAATCCTAAATTAACAAAAAAGACTTCC
TAACAAAGAAAGTTATCCCACTTAACATATGTTGCTCTTGAGATTCTCTGACCGAAGGTGTGGGCGATACAACCTCTC
AAGGTGGTTTTGTCCACTGCTATCAGAATCACTCCATAATCGATACTCTTACCAAGTGACTTCTGTTAATTATGGTG
TGTCTGGGAATACTAGTCAACAAATTTTAAACGATGACGACAGATCCTCAAATCGAAAAAGATTTAGAGAAAGCTG
ATTTATTGACGCTAACTGTTGGTGGTAATGATGTCTTGGCTGTTATTCGTAAAGAGCTCAGTCATTTATCACTAAATT
CCTTTGAGAAACCAGCAGAACATATAAGGAACGTTTGAAAGAAATCTTGCAAAAGCAAGACAAGATAATCCTAAAT
TGCCTATTTATGTTTTAGGCATTTATAATCCTTTTTTACCTAAACTTTCCACAATTAATAAAATGCAAACCGTTATTG
ATAATTGGAATAAAGCTACAAAAGAAGTAGTTGATGCTTCAGAAAATGTTATTTTGTCCCAATTAATGACCGCCTTT
ATAAGGGAATAAATGGTAAAGAGGGTATTACAGAGTCATCAAATAGTCAGGCAAGTATCACTAATGATGCTCTCTTTA
CTGGAGACCATTTCATCCCAATAATATTGGCTATCAAATCATGTCTAACGCCGTTATGGAGAAAATAAATGAAACAA
GAAAAAAGCTGGCCGAACCCAGCTTTCTTGTACAA

SEQ ID NO. 2606: SAG0503 FROM THE 1169NT1 GBS TYPE V STRAIN (REVERSE COMPLEMENT)

GTTTGTACAAAAAGCAGGCTCTATTTTTTCTTGATCATTTCCAAAATCAAATCCTAAATTAACAAAAAAGACTTCC
TAACAAAGAAAGTTATCCCACTTAACATATGTTGCTCTTGAGATTCTCTGACCGAAGGTGTGGGGGATACAACCTCTC
AAGGTGGTTTTGTCCACTGCTATCAGAATCACTCCATAATCGATACTCTTACCAAGTGACTTCTGTTAATTATGGTG
TGTCTGGGAATACTAGTCAACAAATTTTAAACGATGACGACAGATCCTCAAATCGAAAAAGATTTAGAGAAAGCTG
ATTTATTGACGCTAACTGTTGGTGGTAATGATGTCTTGGCTGTTATTCGTAAAGAGCTCAGTCATTTATCACTAAATT
CCTTTGAGAAACCAGCAGAACATATAAGGAACGTTTGAAAGAAATCTTGCAAAAGCAAGACAAGATAATCCTAAAT
TGCCTATTTATGTTTTAGGCATTTATAATCCTTTTTTACCTAAACTTTCCACAATTAATAAAATGCAAACCGTTATTG
ATAATTGGAATAAAGCTACAAAAGAAGTAGTTGATGCTTCAGAAAATGTTATTTTGTCCCAATTAATGACCGCCTTT
ATAAGGGAATAAATGGTAAAGAGGGTATTACAGAGTCATCAAATAGTCAGGCAAGTATCACTAATGATGCTCTCTTTA
CTGGAGACCATTTCATCCCAATAATATTGGCTATCAAATCATGTCTAACGCCGTTATGGAGAAAATAAATGAAACAA
GAAAAAAGCTGGCCGAACCCAGCTTTCTTGTACAA

SEQ ID NO. 2607: SAG0503 FROM THE JM9130013 GBS TYPE VIII STRAIN (REVERSE COMPLEMENT)

GTTTGTACAAAAAGCAGGCTCTATTTTTTCTTGATCATTTCCAAAATCAAATCCTAAATTAACAAAAAAGACTTCC
TAACAAAGAAAGTTATCCCACTTAACATATGTTGCTCTTGAGATTCTCTGACCGAAGGTGTGGGCGATACAACCTCTC
AAGGTGGTTTTGTTCCTGCTATCAGAATCACTCCATAATCGATACTCTTACCAAGTGACTTCTGTTAATTATGGTG
TGTCTGGGAATACTAGTCAACAAATTTTAAACGATGACGACAGATCCTCAAATCGAAAAAGATTTAGAGAAAGCTG
ATTTATTGACGCTAACTGTTGGTGGTAATGATGTCTTGGCTGTTATTCGTAAAGAGCTCAGTCATTTATCACTAAATT
CCTTTGAGAAACCAGCAGAACATATAAGGAACGTTTGAAAGAAATCCTTGCAAAAGCAAGACAAGATAATCCTAAAT
TGCCTATTTATGTTTTAGGCATTTATAATCCTTTTTTACCTAAACTTTCCACAATTAATAAAATGCAAACCGTTATTG
ATAATTGGAATAAAGCTACAAAAGAAGTAGTTGATGCTTCAGAAAATGTTATTTTGTCCCAATTAATGACCGCCTTT
ATAAGGGAATAAATGGTAAAGAGGGTATTACAGAGTCATCAAATAGTCAGGCAAGTATCACTAATGATGCTCTCTTTA
CTGGAGACCATTTCATCCCAATAATATTGGCTATCAAATCATGTCTAACGCCGTTATGGAGAAAATAAATGAAACAA
GAAAAAAGCTGGCCGAACCCAGCTTTCTTGTACAA

SEQ ID NO. 2608: SAG0503 FROM THE 2603 V/R GBS TYPE V STRAIN (REVERSE COMPLEMENT)

AGTTTGTACAAAAAGCAGGCTCTATTTTTTCTTGATCATTTCCAAAATCAAATCCTAAATTAACAAAAAAGACTTCC
CTAACAAAGAAAGTTATCCCACTTAACATATGTTGCTCTTGAGATTCTCTGACCGAAGGTGTGGGCGATACAACCTCT
CAAGGTGGTTTTGTTCCTGCTATCAGAATCACTCCATAATCGATACTCTTACCAAGTGACTTCTGTTAATTATGGT
GTGCTGGGAATACTAGTCAACAAATTTTAAACGATGACGACAGATCCTCAAATCGAAAAAGATTTAGAGAAAGCT
GATTTATTGACGCTAACTGTTGGTGGTAATGATGTCTTGGCTGTTATTCGTAAAGAGCTCAGTCATTTATCACTAAAT
TCCTTTGAGAAACCAGCAGAACATATAAGGAACGTTTGAAAGAAATCCTTGCAAAAGCAAGACAAGATAATCCTAAA
TTGCCTATTTATGTTTTAGGCATTTATAATCCTTTTTTACCTAAACTTTCCACAATTAATAAAATGCAAACCGTTATT
GATAATTGGAATAAAGCTACAAAAGAAGTAGTTGATGCTTCAGAAAATGTTTATTTTGTCCCAATTAATGACCGCCTT
TATAAGGGAATAAATGGTAAAGAGGGTATTACAGAGTCATCAAATAGTCAGGCAAGTATCACTAATGATGCTCTCTTT
ACTGGAGACCATTTCATCCCAATAATATTGGCTATCAAATCATGTCTAACGCCGTTATGGAGAAAATAAATGAAACAA
AGAAAAAAGCTGGCCGAACCCAGCTTTCTTGTACAAAGTG

Table 26: Comparative Sequences relating to SAG0503 (lipase/acylhydrolase)

SEQ ID NO. 2609: SAG0503 FROM THE M781 GBS TYPE III STRAIN
(REVERSE COMPLEMENT)

GGACAAGTTTGTACAAAAAGCAGGCTCTATTTTTTCCTTGATCATTCCTAAATTAACAAAAAAG
ACTTCCTAACAAAGAAAGTTATCCCACTTAACATATGTTGCTCTTGAGATTCTCTGACCGAAGGTGTGGGGATACAA
CCTCTCAAGGTGGTTTTGTCCCACTGCTATCAGAATCACTCCATAATCGATACTCTTACCAAGTGACTTCTGTTAATT
ATGGTGTGCTGGGAATACTAGTCAACAAATTTTAAACGTATGACGACAGATCCTCAAATCGAAAAAGATTTAGAGA
AAGCTGATTTATTGACGCTAACTGTTGGTGGTAATGATGCTTGGCTGTTATTTCGTAAAGAGCTCAGTCATTTATC
TAAATTCCTTTGAGAAACAGCAGAAGCATATAAGGAACGTTTGAAGAAATTCCTGCAAAAGCAAGACAAGATAATC
CTAAATTCCTATTTATGTTTTAGGCATTTATAATCCTTTTACCTAACTTTCCACAATTAATAAATGCAAAACCG
TTATTGATAATTGGAATAAAGCTACAAAGAAGTAGTTGATGCTTCAGAAAATGTTTATTTGTCCCAATTAATGACC
GCCTTTATAAGGGAATAAATGGTAAAGAGGGTATTACAGAGTCATCAATAGTCAGGCAAGTATCACTAATGATGCTC
TCTTTACTGGAGACCATTTTCATCCCAATAATATTGGCTATCAAAATCATGTCTAACGCCGTTATGGAGAAAAATAATG
AAACAAGAAAAAAGCTGGCCGAACCCAGCTTTCTTGTACAAA

SEQ2601 GGACAAGTTTGTACAAAAAGCAGGCTCTATTTTTTCCTTGATCATTCCTAAATTAAC
SEQ2602 -----TTTGTACAAAAAGCAGGCTCTATTTTTTCCTTGATCATTCCTAAATTAAC
SEQ2603 -----GTTTGTACAAAAAGCAGGCTCTATTTTTTCCTTGATCATTCCTAAATTAAC
SEQ2604 GGACAAGTTTGTACAAAAAGCAGGCTCTATTTTTTCCTTGATCATTCCTAAATTAAC
SEQ2605 -----GTTTGTACAAAAAGCAGGCTCTATTTTTTCCTTGATCATTCCTAAATTAAC
SEQ2606 -----GTTTGTACAAAAAGCAGGCTCTATTTTTTCCTTGATCATTCCTAAATTAAC
SEQ2607 -----GTTTGTACAAAAAGCAGGCTCTATTTTTTCCTTGATCATTCCTAAATTAAC
SEQ2608 -----AGTTTGTACAAAAAGCAGGCTCTATTTTTTCCTTGATCATTCCTAAATTAAC
SEQ2609 GGACAAGTTTGTACAAAAAGCAGGCTCTATTTTTTCCTTGATCATTCCTAAATTAAC

SEQ2601 TCCTAAATTAACAAAAAAGACTTCCTAACAAAGAAAGTTATCCCACTTAACATATGTTGC
SEQ2602 TCCTAAATTAACAAAAAAGACTTCCTAACAAAGAAAGTTATCCCACTTAACATATGTTGC
SEQ2603 TCCTAAATTAACAAAAAAGACTTCCTAACAAAGAAAGTTATCCCACTTAACATATGTTGC
SEQ2604 TCCTAAATTAACAAAAAAGACTTCCTAACAAAGAAAGTTATCCCACTTAACATATGTTGC
SEQ2605 TCCTAAATTAACAAAAAAGACTTCCTAACAAAGAAAGTTATCCCACTTAACATATGTTGC
SEQ2606 TCCTAAATTAACAAAAAAGACTTCCTAACAAAGAAAGTTATCCCACTTAACATATGTTGC
SEQ2607 TCCTAAATTAACAAAAAAGACTTCCTAACAAAGAAAGTTATCCCACTTAACATATGTTGC
SEQ2608 TCCTAAATTAACAAAAAAGACTTCCTAACAAAGAAAGTTATCCCACTTAACATATGTTGC
SEQ2609 TCCTAAATTAACAAAAAAGACTTCCTAACAAAGAAAGTTATCCCACTTAACATATGTTGC

SEQ2601 TCTTGGAGATTCTCTGACCGAAGGTGTGGGCGATACAACCTCTCAAGGTGGTTTTGTCCC
SEQ2602 TCTTGGAGATTCTCTGACCGAAGGTGTGGGCGATACAACCTCTCAAGGTGGTTTTGTCCC
SEQ2603 TCTTGGAGATTCTCTGACCGAAGGTGTGGGCGATACAACCTCTCAAGGTGGTTTTGTCCC
SEQ2604 TCTTGGAGATTCTCTGACCGAAGGTGTGGGCGATACAACCTCTCAAGGTGGTTTTGTCCC
SEQ2605 TCTTGGAGATTCTCTGACCGAAGGTGTGGGCGATACAACCTCTCAAGGTGGTTTTGTCCC
SEQ2606 TCTTGGAGATTCTCTGACCGAAGGTGTGGGCGATACAACCTCTCAAGGTGGTTTTGTCCC
SEQ2607 TCTTGGAGATTCTCTGACCGAAGGTGTGGGCGATACAACCTCTCAAGGTGGTTTTGTCCC
SEQ2608 TCTTGGAGATTCTCTGACCGAAGGTGTGGGCGATACAACCTCTCAAGGTGGTTTTGTCCC
SEQ2609 TCTTGGAGATTCTCTGACCGAAGGTGTGGGCGATACAACCTCTCAAGGTGGTTTTGTCCC

SEQ2601 ACTGCTATCAGAATCACTCCATAATCGATACTCTTACCAAGTGACTTCTGTTAATTATGG
SEQ2602 ACTGCTATCAGAATCACTCCATAATCGATACTCTTACCAAGTGACTTCTGTTAATTATGG
SEQ2603 ACTGCTATCAGAATCACTCCATAATCGATACTCTTACCAAGTGACTTCTGTTAATTATGG
SEQ2604 ACTGCTATCAGAATCACTCCATAATCGATACTCTTACCAAGTGACTTCTGTTAATTATGG
SEQ2605 ACTGCTATCAGAATCACTCCATAATCGATACTCTTACCAAGTGACTTCTGTTAATTATGG
SEQ2606 ACTGCTATCAGAATCACTCCATAATCGATACTCTTACCAAGTGACTTCTGTTAATTATGG
SEQ2607 ACTGCTATCAGAATCACTCCATAATCGATACTCTTACCAAGTGACTTCTGTTAATTATGG
SEQ2608 ACTGCTATCAGAATCACTCCATAATCGATACTCTTACCAAGTGACTTCTGTTAATTATGG
SEQ2609 ACTGCTATCAGAATCACTCCATAATCGATACTCTTACCAAGTGACTTCTGTTAATTATGG

SEQ2601 TGTGTCTGGGAATACTAGTCAACAAATTTTAAACGTATGACGACAGATCCTCAAATCGA
SEQ2602 TGTGTCTGGGAATACTAGTCAACAAATTTTAAACGTATGACGACAGATCCTCAAATCGA
SEQ2603 TGTGTCTGGGAATACTAGTCAACAAATTTTAAACGTATGACGACAGATCCTCAAATCGA
SEQ2604 TGTGTCTGGGAATACTAGTCAACAAATTTTAAACGTATGACGACAGATCCTCAAATCGA
SEQ2605 TGTGTCTGGGAATACTAGTCAACAAATTTTAAACGTATGACGACAGATCCTCAAATCGA
SEQ2606 TGTGTCTGGGAATACTAGTCAACAAATTTTAAACGTATGACGACAGATCCTCAAATCGA
SEQ2607 TGTGTCTGGGAATACTAGTCAACAAATTTTAAACGTATGACGACAGATCCTCAAATCGA
SEQ2608 TGTGTCTGGGAATACTAGTCAACAAATTTTAAACGTATGACGACAGATCCTCAAATCGA
SEQ2609 TGTGTCTGGGAATACTAGTCAACAAATTTTAAACGTATGACGACAGATCCTCAAATCGA

SEQ2601 AAAAGATTTAGAGAAAGCTGATTTATTGACGCTAACTGTTGGTGGTAATGATGCTTGGC
SEQ2602 AAAAGATTTAGAGAAAGCTGATTTATTGACGCTAACTGTTGGTGGTAATGATGCTTGGC

Table 26: Comparative Sequences relating to SAG0503 (lipase/acylhydrolase)

SEQ2603	AAAAGATTTAGAGAAAGCTGATTATTGACGCTAACTGTTGGTGGTAATGATGCTCTGGC
SEQ2604	AAAAGATTTAGAGAAAGCTGATTATTGACGCTAACTGTTGGTGGTAATGATGCTCTGGC
SEQ2605	AAAAGATTTAGAGAAAGCTGATTATTGACGCTAACTGTTGGTGGTAATGATGCTCTGGC
SEQ2606	AAAAGATTTAGAGAAAGCTGATTATTGACGCTAACTGTTGGTGGTAATGATGCTCTGGC
SEQ2607	AAAAGATTTAGAGAAAGCTGATTATTGACGCTAACTGTTGGTGGTAATGATGCTCTGGC
SEQ2608	AAAAGATTTAGAGAAAGCTGATTATTGACGCTAACTGTTGGTGGTAATGATGCTCTGGC
SEQ2609	AAAAGATTTAGAGAAAGCTGATTATTGACGCTAACTGTTGGTGGTAATGATGCTCTGGC
SEQ2601	TGTTATTCGTAAAGAGCTCAGTCATTTATCACTAAATTCCTTTGAGAAACCAGCAGAAGC
SEQ2602	TGTTATTCGTAAAGAGCTCAGTCATTTATCACTAAATTCCTTTGAGAAACCAGCAGAAGC
SEQ2603	TGTTATTCGTAAAGAGCTCAGTCATTTATCACTAAATTCCTTTGAGAAACCAGCAGAAGC
SEQ2604	TGTTATTCGTAAAGAGCTCAGTCATTTATCACTAAATTCCTTTGAGAAACCAGCAGAAGC
SEQ2605	TGTTATTCGTAAAGAGCTCAGTCATTTATCACTAAATTCCTTTGAGAAACCAGCAGAAGC
SEQ2606	TGTTATTCGTAAAGAGCTCAGTCATTTATCACTAAATTCCTTTGAGAAACCAGCAGAAGC
SEQ2607	TGTTATTCGTAAAGAGCTCAGTCATTTATCACTAAATTCCTTTGAGAAACCAGCAGAAGC
SEQ2608	TGTTATTCGTAAAGAGCTCAGTCATTTATCACTAAATTCCTTTGAGAAACCAGCAGAAGC
SEQ2609	TGTTATTCGTAAAGAGCTCAGTCATTTATCACTAAATTCCTTTGAGAAACCAGCAGAAGC
SEQ2601	ATATAAGGAACGTTTGAAAGAAATCTTGCAAAAGCAAGACAAGATAATCCTAAATTGCC
SEQ2602	ATATAAGGAACGTTTGAAAGAAATCCTTGCAAAAGCAAGACAAGATAATCCTAAATTGCC
SEQ2603	ATATAAGGAACGTTTGAAAGAAATCCTTGCAAAAGCAAGACAAGATAATCCTAAATTGCC
SEQ2604	ATATAAGGAACGTTTGAAAGAAATCCTTGCAAAAGCAAGACAAGATAATCCTAAATTGCC
SEQ2605	ATATAAGGAACGTTTGAAAGAAATCTTGCAAAAGCAAGACAAGATAATCCTAAATTGCC
SEQ2606	ATATAAGGAACGTTTGAAAGAAATCCTTGCAAAAGCAAGACAAGATAATCCTAAATTGCC
SEQ2607	ATATAAGGAACGTTTGAAAGAAATCCTTGCAAAAGCAAGACAAGATAATCCTAAATTGCC
SEQ2608	ATATAAGGAACGTTTGAAAGAAATCCTTGCAAAAGCAAGACAAGATAATCCTAAATTGCC
SEQ2609	ATATAAGGAACGTTTGAAAGAAATCTTGCAAAAGCAAGACAAGATAATCCTAAATTGCC
SEQ2601	TATTTATGTTTTAGGCATTATAATCCTTTTACCTAAACTTTCCACAATTAACATAAAAT
SEQ2602	TATTTATGTTTTAGGCATTATAATCCTTTTACCTAAACTTTCCACAATTAACATAAAAT
SEQ2603	TATTTATGTTTTAGGCATTATAATCCTTTTACCTAAACTTTCCACAATTAACATAAAAT
SEQ2604	TATTTATGTTTTAGGCATTATAATCCTTTTACCTAAACTTTCCACAATTAACATAAAAT
SEQ2605	TATTTATGTTTTAGGCATTATAATCCTTTTACCTAAACTTTCCACAATTAACATAAAAT
SEQ2606	TATTTATGTTTTAGGCATTATAATCCTTTTACCTAAACTTTCCACAATTAACATAAAAT
SEQ2607	TATTTATGTTTTAGGCATTATAATCCTTTTACCTAAACTTTCCACAATTAACATAAAAT
SEQ2608	TATTTATGTTTTAGGCATTATAATCCTTTTACCTAAACTTTCCACAATTAACATAAAAT
SEQ2609	TATTTATGTTTTAGGCATTATAATCCTTTTACCTAAACTTTCCACAATTAACATAAAAT
SEQ2601	GCAAACCGTTATTGATAATTGGAATAAAGCTACAAAAGAAGTAGTTGATGCTTCAGAAAA
SEQ2602	GCAAACCGTTATTGATAATTGGAATAAAGCTACAAAAGAAGTAGTTGATGCTTCAGAAAA
SEQ2603	GCAAACCGTTATTGATAATTGGAATAAAGCTACAAAAGAAGTAGTTGATGCTTCAGAAAA
SEQ2604	GCAAACCGTTATTGATAATTGGAATAAAGCTACAAAAGAAGTAGTTGATGCTTCAGAAAA
SEQ2605	GCAAACCGTTATTGATAATTGGAATAAAGCTACAAAAGAAGTAGTTGATGCTTCAGAAAA
SEQ2606	GCAAACCGTTATTGATAATTGGAATAAAGCTACAAAAGAAGTAGTTGATGCTTCAGAAAA
SEQ2607	GCAAACCGTTATTGATAATTGGAATAAAGCTACAAAAGAAGTAGTTGATGCTTCAGAAAA
SEQ2608	GCAAACCGTTATTGATAATTGGAATAAAGCTACAAAAGAAGTAGTTGATGCTTCAGAAAA
SEQ2609	GCAAACCGTTATTGATAATTGGAATAAAGCTACAAAAGAAGTAGTTGATGCTTCAGAAAA
SEQ2601	TGTTTATTTTGTCCCAATTAATGACCGCCTTTATAAGGGAATAAATGGTAAAGAGGGTAT
SEQ2602	TGTTTATTTTGTCCCAATTAATGACCGCCTTTATAAGGGAATAAATGGTAAAGAGGGTAT
SEQ2603	TGTTTATTTTGTCCCAATTAATGACCGCCTTTATAAGGGAATAAATGGTAAAGAGGGTAT
SEQ2604	TGTTTATTTTGTCCCAATTAATGACCGCCTTTATAAGGGAATAAATGGTAAAGAGGGTAT
SEQ2605	TGTTTATTTTGTCCCAATTAATGACCGCCTTTATAAGGGAATAAATGGTAAAGAGGGTAT
SEQ2606	TGTTTATTTTGTCCCAATTAATGACCGCCTTTATAAGGGAATAAATGGTAAAGAGGGTAT
SEQ2607	TGTTTATTTTGTCCCAATTAATGACCGCCTTTATAAGGGAATAAATGGTAAAGAGGGTAT
SEQ2608	TGTTTATTTTGTCCCAATTAATGACCGCCTTTATAAGGGAATAAATGGTAAAGAGGGTAT
SEQ2609	TGTTTATTTTGTCCCAATTAATGACCGCCTTTATAAGGGAATAAATGGTAAAGAGGGTAT
SEQ2601	TACAGAGTCATCAAAATAGTCAGGCAAGTATCACTAATGATGCTCTCTTTACTGGAGACCA
SEQ2602	TACAGAGTCATCAAAATAGTCAGGCAAGTATCACTAATGATGCTCTCTTTACTGGAGACCA
SEQ2603	TACAGAGTCATCAAAATAGTCAGGCAAGTATCACTAATGATGCTCTCTTTACTGGAGACCA
SEQ2604	TACAGAGTCATCAAAATAGTCAGGCAAGTATCACTAATGATGCTCTCTTTACTGGAGACCA
SEQ2605	TACAGAGTCATCAAAATAGTCAGGCAAGTATCACTAATGATGCTCTCTTTACTGGAGACCA
SEQ2606	TACAGAGTCATCAAAATAGTCAGGCAAGTATCACTAATGATGCTCTCTTTACTGGAGACCA
SEQ2607	TACAGAGTCATCAAAATAGTCAGGCAAGTATCACTAATGATGCTCTCTTTACTGGAGACCA
SEQ2608	TACAGAGTCATCAAAATAGTCAGGCAAGTATCACTAATGATGCTCTCTTTACTGGAGACCA
SEQ2609	TACAGAGTCATCAAAATAGTCAGGCAAGTATCACTAATGATGCTCTCTTTACTGGAGACCA
SEQ2601	TTTTCATCCCAATAATATTGGCTATCAAAATCATGTCTAACGCCGTTATGGAGAAAATAAA
SEQ2602	TTTTCATCCCAATAATATTGGCTATCAAAATCATGTCTAACGCCGTTATGGAGAAAATAAA

Table 26: Comparative Sequences relating to SAG0503 (lipase/acylhydrolase)

SEQ2603	TTTTCATCCCAATAATATTGGCTATCAAATCATGTCTAACGCCGTTATGGAGAAAATAAA
SEQ2604	TTTTCATCCCAATAATATTGGCTATCAAATCATGTCTAACGCCGTTATGGAGAAAATAAA
SEQ2605	TTTTCATCCCAATAATATTGGCTATCAAATCATGTCTAACGCCGTTATGGAGAAAATAAA
SEQ2606	TTTTCATCCCAATAATATTGGCTATCAAATCATGTCTAACGCCGTTATGGAGAAAATAAA
SEQ2607	TTTTCATCCCAATAATATTGGCTATCAAATCATGTCTAACGCCGTTATGGAGAAAATAAA
SEQ2608	TTTTCATCCCAATAATATTGGCTATCAAATCATGTCTAACGCCGTTATGGAGAAAATAAA
SEQ2609	TTTTCATCCCAATAATATTGGCTATCAAATCATGTCTAACGCCGTTATGGAGAAAATAAA
SEQ2601	TGAAACAAGAAAAAACTGGCCGAACCCAGCTTTCTTGTACAAAG-----
SEQ2602	TGAAACAAGAAAAAACTGGCCGAACCCAGCTTTCTTGTACAAAGTGGTCC-----
SEQ2603	TGAAACAAGAAAAAACTGGCCGAACCCAGCTTTCTTGTACAA-----
SEQ2604	TGAAACAAGAAAAAACTGGCCGAACCCAGCTTTCTTGTACAA-----
SEQ2605	TGAAACAAGAAAAAACTGGCCGAACCCAGCTTTCTTGTACAA-----
SEQ2606	TGAAACAAGAAAAAACTGGCCGAACCCAGCTTTCTTGTACAA-----
SEQ2607	TGAAACAAGAAAAAACTGGCCGAACCCAGCTTTCTTGTACAA-----
SEQ2608	TGAAACAAGAAAAAACTGGCCGAACCCAGCTTTCTTGTACAAAGTGG-----
SEQ2609	TGAAACAAGAAAAAACTGGCCGAACCCAGCTTTCTTGTACAAATABCMARATVSTNCSRA
SEQ2601	-----
SEQ2602	-----
SEQ2603	-----
SEQ2604	-----
SEQ2605	-----
SEQ2606	-----
SEQ2607	-----
SEQ2608	-----
SEQ2609	NGTSAGASACYHYDAS

>SEQ ID NO 2650:103_090 frame: 2

IFSLIIPKSNPKLTKKDFLTKKVIPLNYVALGDSLTEGVGDTSQGGFVPL
 LLESLNHRYSYQVTSVNYGVSGNTSQILKRMTTDPQIEKDLEKADLLTLTVGGNDVLAVIR
 VIRKELSHLSLNSFEKPAEAYKERLKEILAKARQDNPKLPYVVLGIYNPFYLNFPQLTKM
 QTVIDNWNKATKEVVDASENVYFVPINDRLYKGINGKEGITESSNSQASITNDALFTGDH
 FHPNNIGYQIMSNVMEKINETRKNWP

>SEQ ID NO 2651:103_H36B frame: 2

IFSLIIPKSNPKLTKKDFLTKKVIPLNYVALGDSLTEGVGDTSQGGFVPLLS
 ESLHNHRYSYQVTSVNYGVSGNTSQILKRMTTDPQIEKDLEKADLLTLTVGGNDVLAVIR
 KELSHLSLNSFEKPAEAYKERLKEILAKARQDNPKLPYVVLGIYNPFYLNFPQLTKMQTV
 IDNWNKATKEVVDASENVYFVPINDRLYKGINGKEGITESSNSQASITNDALFTGDHFP
 NNIGYQIMSNVMEKINETRKNWP

>SEQ ID NO 2652:103_18RS21 frame: 3

IFSLIIPKSNPKLTKKDFLTKKVIPLNYVALGDSLTEGVGDTSQGGFVPLLS
 ESLHNHRYSYQVTSVNYGVSGNTSQILKRMTTDPQIEKDLEKADLLTLTVGGNDVLAVIR
 KELSHLSLNSFEKPAEAYKERLKEILAKARQDNPKLPYVVLGIYNPFYLNFPQLTKMQTV
 IDNWNKATKEVVDASENVYFVPINDRLYKGINGKEGITESSNSQASITNDALFTGDHFP
 NNIGYQIMSNVMEKINETRKNWP

>SEQ ID NO 2653:103_COH1 frame: 3

IFSLIIPKSNPKLTKKDFLTKKVIPLNYVALGDSLTEGVGDTSQGGFVPL
 LLESLNHRYSYQVTSVNYGVSGNTSQILKRMTTDPQIEKDLEKADLLTLTVGGNDVLAVIR
 IRKELSHLSLNSFEKPAEAYKERLKEILAKARQDNPKLPYVVLGIYNPFYLNFPQLTKMQ
 TVIDNWNKATKEVVDASENVYFVPINDRLYKGINGKEGITESSNSQASITNDALFTGDHFP
 HPNNIGYQIMSNVMEKINETRKNWP

>SEQ ID NO 2654:103_CJB110 frame: 3

IFSLIIPKSNPKLTKKDFLTKKVIPLNYVALGDSLTEGVGDTSQGGFVPLLS
 ESLHNHRYSYQVTSVNYGVSGNTSQILKRMTTDPQIEKDLEKADLLTLTVGGNDVLAVIR
 KELSHLSLNSFEKPAEAYKERLKEILAKARQDNPKLPYVVLGIYNPFYLNFPQLTKMQTV
 IDNWNKATKEVVDASENVYFVPINDRLYKGINGKEGITESSNSQASITNDALFTGDHFP
 NNIGYQIMSNVMEKINETRKNWP

>SEQ ID NO 2655:103_1169NT frame: 3

IFSLIIPKSNPKLTKKDFLTKKVIPLNYVALGDSLTEGVGDTSQGGFVPLLS
 ESLHNHRYSYQVTSVNYGVSGNTSQILKRMTTDPQIEKDLEKADLLTLTVGGNDVLAVIR
 KELSHLSLNSFEKPAEAYKERLKEILAKARQDNPKLPYVVLGIYNPFYLNFPQLTKMQTV
 IDNWNKATKEVVDASENVYFVPINDRLYKGINGKEGITESSNSQASITNDALFTGDHFP
 NNIGYQIMSNVMEKINETRKNWP

Table 26: Comparative Sequences relating to SAG0503 (lipase/acylhydrolase)

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>SEQ ID NO 2656:103_JM9130013 frame: 3
IFSLIIPKSNPKLTKKDFLTKKVIPLNYVALGDSLTEGVGDTTSQGGFVPLLS
ESLHNRYSYQVTSVNYGVSGNTSQQILKRMTTDPQIEKDLEKADLLTLTVGGNDVLAVIR
KELSHLSLNSFEKPAEAYKERLKEILAKARQDNPKLPIYVLGIYNPFYLNFPQLTKMQTV
IDNWNKATKEVVDASENVYFVPINDRLYKINGKEGITESSNSQASITNDALFTGDHFP
NNIGYQIMSNVMEKINETRKNWP
>SEQ ID NO 2657:103_2603 frame: 1
IFSLIIPKSNPKLTKKDFLTKKVIPLNYVALGDSLTEGVGDTTSQGGFVPLL
SESLHNRYSYQVTSVNYGVSGNTSQQILKRMTTDPQIEKDLEKADLLTLTVGGNDVLAVI
RKELSHLSLNSFEKPAEAYKERLKEILAKARQDNPKLPIYVLGIYNPFYLNFPQLTKMQT
VIDNWNKATKEVVDASENVYFVPINDRLYKINGKEGITESSNSQASITNDALFTGDHFP
PNNIGYQIMSNVMEKINETRKNWP

>SEQ ID NO 2658:103_M781 frame: 3
IFSLIIPKSNPKLTKKDFLTKKVIPLNYVALGDSLTEGVGDTTSQGGFVPL
LSLSESLHNRYSYQVTSVNYGVSGNTSQQILKRMTTDPQIEKDLEKADLLTLTVGGNDVLAV
IRKELSHLSLNSFEKPAEAYKERLKEILAKARQDNPKLPIYVLGIYNPFYLNFPQLTKMQ
TVIDNWNKATKEVVDASENVYFVPINDRLYKINGKEGITESSNSQASITNDALFTGDHF
HPNNIGYQIMSNVMEKINETRKNWP

SEQ2650      IFSLIIPKSNPKLTKKDFLTKKVIPLNYVALGDSLTEGVGDTTSQGGFVPLLSLSESLHNRY
SEQ2651      IFSLIIPKSNPKLTKKDFLTKKVIPLNYVALGDSLTEGVGDTTSQGGFVPLLSLSESLHNRY
SEQ2652      IFSLIIPKSNPKLTKKDFLTKKVIPLNYVALGDSLTEGVGDTTSQGGFVPLLSLSESLHNRY
SEQ2653      IFSLIIPKSNPKLTKKDFLTKKVIPLNYVALGDSLTEGVGDTTSQGGFVPLLSLSESLHNRY
SEQ2654      IFSLIIPKSNPKLTKKDFLTKKVIPLNYVALGDSLTEGVGDTTSQGGFVPLLSLSESLHNRY
SEQ2655      IFSLIIPKSNPKLTKKDFLTKKVIPLNYVALGDSLTEGVGDTTSQGGFVPLLSLSESLHNRY
SEQ2656      IFSLIIPKSNPKLTKKDFLTKKVIPLNYVALGDSLTEGVGDTTSQGGFVPLLSLSESLHNRY
SEQ2657      IFSLIIPKSNPKLTKKDFLTKKVIPLNYVALGDSLTEGVGDTTSQGGFVPLLSLSESLHNRY
SEQ2658      IFSLIIPKSNPKLTKKDFLTKKVIPLNYVALGDSLTEGVGDTTSQGGFVPLLSLSESLHNRY

SEQ2650      SYQVTSVNYGVSGNTSQQILKRMTTDPQIEKDLEKADLLTLTVGGNDVLAVIRKELSHLS
SEQ2651      SYQVTSVNYGVSGNTSQQILKRMTTDPQIEKDLEKADLLTLTVGGNDVLAVIRKELSHLS
SEQ2652      SYQVTSVNYGVSGNTSQQILKRMTTDPQIEKDLEKADLLTLTVGGNDVLAVIRKELSHLS
SEQ2653      SYQVTSVNYGVSGNTSQQILKRMTTDPQIEKDLEKADLLTLTVGGNDVLAVIRKELSHLS
SEQ2654      SYQVTSVNYGVSGNTSQQILKRMTTDPQIEKDLEKADLLTLTVGGNDVLAVIRKELSHLS
SEQ2655      SYQVTSVNYGVSGNTSQQILKRMTTDPQIEKDLEKADLLTLTVGGNDVLAVIRKELSHLS
SEQ2656      SYQVTSVNYGVSGNTSQQILKRMTTDPQIEKDLEKADLLTLTVGGNDVLAVIRKELSHLS
SEQ2657      SYQVTSVNYGVSGNTSQQILKRMTTDPQIEKDLEKADLLTLTVGGNDVLAVIRKELSHLS
SEQ2658      SYQVTSVNYGVSGNTSQQILKRMTTDPQIEKDLEKADLLTLTVGGNDVLAVIRKELSHLS

SEQ2650      LNSFEKPAEAYKERLKEILAKARQDNPKLPIYVLGIYNPFYLNFPQLTKMQTVIDNWNKA
SEQ2651      LNSFEKPAEAYKERLKEILAKARQDNPKLPIYVLGIYNPFYLNFPQLTKMQTVIDNWNKA
SEQ2652      LNSFEKPAEAYKERLKEILAKARQDNPKLPIYVLGIYNPFYLNFPQLTKMQTVIDNWNKA
SEQ2653      LNSFEKPAEAYKERLKEILAKARQDNPKLPIYVLGIYNPFYLNFPQLTKMQTVIDNWNKA
SEQ2654      LNSFEKPAEAYKERLKEILAKARQDNPKLPIYVLGIYNPFYLNFPQLTKMQTVIDNWNKA
SEQ2655      LNSFEKPAEAYKERLKEILAKARQDNPKLPIYVLGIYNPFYLNFPQLTKMQTVIDNWNKA
SEQ2656      LNSFEKPAEAYKERLKEILAKARQDNPKLPIYVLGIYNPFYLNFPQLTKMQTVIDNWNKA
SEQ2657      LNSFEKPAEAYKERLKEILAKARQDNPKLPIYVLGIYNPFYLNFPQLTKMQTVIDNWNKA
SEQ2658      LNSFEKPAEAYKERLKEILAKARQDNPKLPIYVLGIYNPFYLNFPQLTKMQTVIDNWNKA

SEQ2650      TKEVVDASENVYFVPINDRLYKINGKEGITESSNSQASITNDALFTGDHFPNNIGYQI
SEQ2651      TKEVVDASENVYFVPINDRLYKINGKEGITESSNSQASITNDALFTGDHFPNNIGYQI
SEQ2652      TKEVVDASENVYFVPINDRLYKINGKEGITESSNSQASITNDALFTGDHFPNNIGYQI
SEQ2653      TKEVVDASENVYFVPINDRLYKINGKEGITESSNSQASITNDALFTGDHFPNNIGYQI
SEQ2654      TKEVVDASENVYFVPINDRLYKINGKEGITESSNSQASITNDALFTGDHFPNNIGYQI
SEQ2655      TKEVVDASENVYFVPINDRLYKINGKEGITESSNSQASITNDALFTGDHFPNNIGYQI
SEQ2656      TKEVVDASENVYFVPINDRLYKINGKEGITESSNSQASITNDALFTGDHFPNNIGYQI
SEQ2657      TKEVVDASENVYFVPINDRLYKINGKEGITESSNSQASITNDALFTGDHFPNNIGYQI
SEQ2658      TKEVVDASENVYFVPINDRLYKINGKEGITESSNSQASITNDALFTGDHFPNNIGYQI

SEQ2650      MSNAVMEKINETRKNWP
SEQ2651      MSNAVMEKINETRKNWP
SEQ2652      MSNAVMEKINETRKNWP
SEQ2653      MSNAVMEKINETRKNWP
SEQ2654      MSNAVMEKINETRKNWP
SEQ2655      MSNAVMEKINETRKNWP
SEQ2656      MSNAVMEKINETRKNWP
SEQ2657      MSNAVMEKINETRKNWP
SEQ2658      MSNAVMEKINETRKNWP

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**Table 27: Comparative Sequences relating to SAG1473
(cell wall surface anchor family protein)**

**SEQ ID NO. 2701: SAG1473 FROM THE 1169NT1 GBS TYPE V STRAIN
(REVERSE COMPLEMENT)**

GATACAAGTGATAAGAATACTGACACGAGTGTCTGACTACGACCTTATCTGAGGAGAAAAGATCAGATGA
ACTAGACCAGTCTAGTACTGGTTCCTTCTTGAAAATGAATCGAGTTCATCAAGTGAACCAGAAACAAATC
CGTCAACTAATCCACCTACAACAGAACCATCGCAACCCCTCACCTAGTGAAGAGAACAAAGCCTGATGGTAGA
ACGAAGACAGAAATTGGCAATAATAAGGATATTTCTAGTGGAACAAAAGTATTAATTTTCAGAAGATAGTAT
TAAGAATTTTAGTAAAGCAAGTAGTGATCAAGAAGAAGTGGATCGCGATGAATCATCATCTTCAAAAAGCAA
GTGATGGGAAAAAAGGCCACAGTAAGCCTAAAAAGGAA

SEQ ID NO. 2702: SAG1473 FROM THE 18RS21 GBS TYPE II STRAIN

GATACAAGTGATAAGAATACTGACACGAGTGTCTGACTACGACCTTATCTGAGGAGAAAAGATCAGATGA
ACTAGACCAGTCTAGTACTGGTTCCTTCTTGAAAATGAATCGAGTTCATCAAGTGAACCAGAAACAAATC
CGTCAACTAATCCACCTACAACAGAACCATCGCAACCCCTCACCTAGTGAAGAGAACAAAGCCTGATGGTAGA
ACGAAGACAGAAATTGGCAATAATAAGGATATTTCTAGTGGAACAAAAGTATTAATTTTCAGAAGATAGTAT
TAAGAATTTTAGTAAAGCAAGTAGTGATCAAGAAGAAGTGGATCGCGATGAATCATCATCTTCAAAAAGCAA
ATGATGGGAAAAAAGGCCACAGTAAGCCTAAAAAGGAA

SEQ ID NO. 2703: SAG1473 FROM THE 2603 V/R GBS TYPE V STRAIN

GATACAAGTGATAAGAATACTGACACGAGTGTCTGACTACGACCTTATCTGAGGAGAAAAGATCAGATGA
ACTAGACCAGTCTAGTACTGGTTCCTTCTTGAAAATGAATCGAGTTCATCAAGTGAACCAGAAACAAATC
CGTCAACTAATCCACCTACAACAGAACCATCGCAACCCCTCACCTAGTGAAGAGAACAAAGCCTGATGGTAGA
ACGAAGACAGAAATTGGCAATAATAAGGATATTTCTAGTGGAACAAAAGTATTAATTTTCAGAAGATAGTAT
TAAGAATTTTAGTAAAGCAAGTAGTGATCAAGAAGAAGTGGATCGCGATGAATCATCATCTTCAAAAAGCAA
ATGATGGGAAAAAAGGCCACAGTAAGCCTAAAAAGGAA

SEQ ID NO. 2704: SAG1473 FROM THE 090 GBS TYPE Ia STRAIN

GACCAGTCTAGTACTGGTTCCTTCTTGAAAATGAATCGAGTTCATCAAGTGAACCAGAAACAAATCCGTC
AACTAATCCACCTACAACAGAACCATCGCAACCCCTCACCTAGTGAAGAGAACAAAGCCTGATGGTAGAACGA
AGACAGAAATTGGCAATAATAAGGATATTTCTAGTGGAACAAAAGTATTAATTTTCAGAAGATAGTATTAAG
AATTTTAGTAAAGCAAGTAGTGATCAAGAAGAAGTGGATCGCGATGAATCATCATCTTCAAAAAGCAAATGA
TGGGAAAAAAGGCCACAGTAAGCCTAAAAAGGAA

SEQ ID NO. 2705: SAG1473 FROM THE A909 GBS TYPE Ia STRAIN

GATACAAGTGATAAGAATACTGACACGAGTGTCTGACTACGACCTTATCTGAGGAGAAAAGATTAGATGA
ACTAGACCAGTCTAGTACTGGTTCCTTCTTGAAAATGAATCGAGTTCATCAAGTGAACCAGAAACAAATC
CCTCAACTAATCCACCTACAACAGAACCATCGCAACCCCTCACCTAGTGAAGAGAACAAAGCCTGATGGTAGC
ACGAAGACAGAAATTGGCAATAATAAGGATATTTCTAGTGGAACAAAAGTATTAATTTTCAGAAGATAGTAT
TAAGAATTTTAGTAAAGCAAGTAGTGATCAAGAAGAAGTGGATCGCGATGAATCATCATCTTCAAAAAGCAA
ATGATGAGAAAAAAGGCCACAGTAAGCCTAAAAAGGAA

SEQ ID NO. 2706: SAG1473 FROM THE CJB110 GBS NONTYPEABLE STRAIN

GATACAAGTGATAAGAATACTGACACGAGTGTCTGACTACGACCTTATCTGAGGAGAAAAGATCAGATGA
ACTAGACCAGTCTAGTACTGGTTCCTTCTTGAAAATGAATCGAGTTCATCAAGTGAACCAGAAACAAATC
CGTCAACTAATCCACCTACAACAGAACCATCGCAACCCCTCACCTAGTGAAGAGAACAAAGCCTGATGGTAGA
ACGAAGACAGAAATTGGCAATAATAAGGATATTTCTAGTGGAACAAAAGTATTAATTTTCAGAAGATAGTAT
TAAGAATTTTAGTAAAGCAAGTAGTGATCAAGAAGAAGTGGATCGCGATGAATCATCATCTTCAAAAAGCAA
ATGATGGGAAAAAAGGCCACAGTAAGCCTAAAAAGGAA

**Table 27: Comparative Sequences relating to SAG1473
(cell wall surface anchor family protein)**

SEQ ID NO. 2707: SAG1473 FROM THE COH1 GBS TYPE III STRAIN
(REVERSE COMPLEMENT)

GATACAAGTGATAAGAATACTGACACGAGTGTCGTGACTACGACCTTATCTGAGGAGAAAAGATCAGATGA
ACTAGACCAGTCTAGTACTGGTTCTTCTTCTGAAAATGAATCAAGTTCATCAAGTGAACCAGAAACAAATC
CCTCAACTAATCCACCTACAACAGAACCATCGCAACCCCTCACCTAGTGAAGAGAACAAGCCTGATGGGAGC
ACGAAGACAGAAATTGGCAATAATAAGGATATTTCTAGTGGAACAAAAGTATTAATTTTCAGAAGATAGTAT
TAAGAATTTTAGTAAAGCAAGTAGTGATCAAGAAGAAGTGGAACGCGATGAATCATCATCTTCAAAAGCAA
ATGATGAGAAAAAAGGCCACAGTAAGCCTAAAAAGGAA

SEQ ID NO. 2708: SAG1473 FROM THE H36b GBS TYPE Ib STRAIN

GATACAAGTGATAAGAATACTGACACGAGTGTCGTGACTACGACCTTATCTGAGGAGAAAAGATTAGATGA
ACTAGACCAGTCTAGTACTGGTTCTTCTTCTGAAAATGAATCGAGTTCATCAAGTGAACCAGAAACAAATC
CCTCAACTAATCCACCTACAACAGAACCATCGCAACCCCTCACCTAGTGAAGAGAACAAGCCTGATGGTAGC
ACGAAGACAGAAATTGGCAATAATAAGGATATTTCTAGTGGAACAAAAGTATTAATTTTCAGAAGATAGTAT
TAAGAATTTTAGTAAAGCAAGTAGTGATCAAGAArAAGTGATCGCGATGAATCATCATCTTCAAAAGCAA
ATGATGAGAAAAAAGGCCACAGTAAGCCTAAAAAGGAA

SEQ ID NO. 2709: SAG1473 FROM THE JM910013 GBS TYPE VIII STRAIN

GATACAAGTGATAAGAATACTGACACGAGTGTCGTGACTACGACCTTATCTGAGGAGAAAAGATTAGATGA
ACTAGACCAGTCTAGTACTGGTTCTTCTTCTGAAAATGAATCGAGTTCATCAAGTGAACCAGAAACAAATC
CCTCAACTAATCCACCTACAACAGAACCATCGCAACCCCTCACCTAGTGAAGAGAACAAGCCTGATGGTAGC
ACGAAGACAGAAATTGGCAATAATAAGGATATTTCTAGTGGAACAAAAGTATTAATTTTCAGAAGATAGTAT
TAAGAATTTTAGTAAAGCAAGTAGTGATCAAGAAGAAGTGGAACGCGATGAATCATCATCTTCAAAAGCAA
ATGATGAGAAAAAAGGCCACAGTAAGCCTAAAAAGGAA

SEQ ID NO. 2710: SAG1473 FROM THE M732 GBS TYPE III STRAIN

GATACAAGTGATAAGAATACTGACACGAGTGTCGTGACTACGACCTTATCTGAGGAGAAAAGATCAGATGA
ACTAGACCAGTCTAGTACTGGTTCTTCTTCTGAAAATGAATCAAGTTCATCAAGTGAACCAGAAACAAATC
CCTCAACTAATCCACCTACAACAGAACCATCGCAACCCCTCACCTAGTGAAGAGAACAAGCCTGATGGGAGC
ACGAAGACAGAAATTGGCAATAATAAGGATATTTCTAGTGGAACAAAAGTATTAATTTTCAGAAGATAGTAT
TAAGAATTTTAGTAAAGCAAGTAGTGATCAAGAAGAAGTGGAACGCGATGAATCATCATCTTCAAAAGCAA
ATGATGAGAAAAAAGGCCACAGTAAGCCTAAAAAGGAA

SEQ ID NO. 2711: SAG1473 FROM THE M781 GBS TYPE III STRAIN

GATACAAGTGATAAGAATACTGACACGAGTGTCGTGACTACGACCTTATCTGAGGAGAAAAGATCAGATGA
ACTAGACCAGTCTAGTACTGGTTCTTCTTCTGAAAATGAATCAAGTTCATCAAGTGAACCAGAAACAAATC
CCTCAACTAATCCACCTACAACAGAACCATCGCAACCCCTCACCTAGTGAAGAGAACAAGCCTGATGGGAGC
ACGAAGACAGAAATTGGCAATAATAAGGATATTTCTAGTGGAACAAAAGTATTAATTTTCAGAAGATAGTAT
TAAGAATTTTAGTAAAGCAAGTAGTGATCAAGAAGAAGTGGAATCGCGATGAATCATCATCTTCAAAAGCAA
ATGATGAGAAAAAAGGCCACAGTAAGCCTAAAAAGGAA

SEQ2701	ATACAAGTGATAAGAATACTGACACGAGTGTCGTGACTACGACCTTATCTGAGGAGAAA
SEQ2702	ATACAAGTGATAAGAATACTGACACGAGTGTCGTGACTACGACCTTATCTGAGGAGAAA
SEQ2703	ATACAAGTGATAAGAATACTGACACGAGTGTCGTGACTACGACCTTATCTGAGGAGAAA
SEQ2704	-----
SEQ2705	ATACAAGTGATAAGAATACTGACACGAGTGTCGTGACTACGACCTTATCTGAGGAGAAA
SEQ2706	ATACAAGTGATAAGAATACTGACACGAGTGTCGTGACTACGACCTTATCTGAGGAGAAA
SEQ2707	ATACAAGTGATAAGAATACTGACACGAGTGTCGTGACTACGACCTTATCTGAGGAGAAA
SEQ2709	ATACAAGTGATAAGAATACTGACACGAGTGTCGTGACTACGACCTTATCTGAGGAGAAA
SEQ2710	ATACAAGTGATAAGAATACTGACACGAGTGTCGTGACTACGACCTTATCTGAGGAGAAA
SEQ2711	ATACAAGTGATAAGAATACTGACACGAGTGTCGTGACTACGACCTTATCTGAGGAGAAA

**Table 27: Comparative Sequences relating to SAG1473
(cell wall surface anchor family protein)**

SEQ2701	GATCAGATGAAC TAGACCAGTCTAGTACTGGTTCTTCTTCTGAAAATGAATCGAGTTCA
SEQ2702	GATCAGATGAAC TAGACCAGTCTAGTACTGGTTCTTCTTCTGAAAATGAATCGAGTTCA
SEQ2703	GATCAGATGAAC TAGACCAGTCTAGTACTGGTTCTTCTTCTGAAAATGAATCGAGTTCA
SEQ2704	-----GACCAGTCTAGTACTGGTTCTTCTTCTGAAAATGAATCGAGTTCA
SEQ2705	GATTAGATGAAC TAGACCAGTCTAGTACTGGTTCTTCTTCTGAAAATGAATCGAGTTCA
SEQ2706	GATCAGATGAAC TAGACCAGTCTAGTACTGGTTCTTCTTCTGAAAATGAATCGAGTTCA
SEQ2707	GATCAGATGAAC TAGACCAGTCTAGTACTGGTTCTTCTTCTGAAAATGAATCAAGTTCA
SEQ2709	GATTAGATGAAC TAGACCAGTCTAGTACTGGTTCTTCTTCTGAAAATGAATCGAGTTCA
SEQ2710	GATCAGATGAAC TAGACCAGTCTAGTACTGGTTCTTCTTCTGAAAATGAATCAAGTTCA
SEQ2711	GATCAGATGAAC TAGACCAGTCTAGTACTGGTTCTTCTTCTGAAAATGAATCAAGTTCA
SEQ2701	TCAAGTGAACCAGAAA CAAATCCGTCAACTAATCCACCTACAACAGAACCATCGCAACCC
SEQ2702	TCAAGTGAACCAGAAA CAAATCCGTCAACTAATCCACCTACAACAGAACCATCGCAACCC
SEQ2703	TCAAGTGAACCAGAAA CAAATCCGTCAACTAATCCACCTACAACAGAACCATCGCAACCC
SEQ2704	TCAAGTGAACCAGAAA CAAATCCGTCAACTAATCCACCTACAACAGAACCATCGCAACCC
SEQ2705	TCAAGTGAACCAGAAA CAAATCCCTCAACTAATCCACCTACAACAGAACCATCGCAACCC
SEQ2706	TCAAGTGAACCAGAAA CAAATCCGTCAACTAATCCACCTACAACAGAACCATCGCAACCC
SEQ2707	TCAAGTGAACCAGAAA CAAATCCCTCAACTAATCCACCTACAACAGAACCATCGCAACCC
SEQ2709	TCAAGTGAACCAGAAA CAAATCCCTCAACTAATCCACCTACAACAGAACCATCGCAACCC
SEQ2710	TCAAGTGAACCAGAAA CAAATCCCTCAACTAATCCACCTACAACAGAACCATCGCAACCC
SEQ2711	TCAAGTGAACCAGAAA CAAATCCCTCAACTAATCCACCTACAACAGAACCATCGCAACCC
SEQ2701	TCACCTAGTGAAGAGAACAAGCCTGATGGTAGAACGAAGACAGAAATTGGCAATAATAAG
SEQ2702	TCACCTAGTGAAGAGAACAAGCCTGATGGTAGAACGAAGACAGAAATTGGCAATAATAAG
SEQ2703	TCACCTAGTGAAGAGAACAAGCCTGATGGTAGAACGAAGACAGAAATTGGCAATAATAAG
SEQ2704	TCACCTAGTGAAGAGAACAAGCCTGATGGTAGAACGAAGACAGAAATTGGCAATAATAAG
SEQ2705	TCACCTAGTGAAGAGAACAAGCCTGATGGTAGCACGAAGACAGAAATTGGCAATAATAAG
SEQ2706	TCACCTAGTGAAGAGAACAAGCCTGATGGTAGAACGAAGACAGAAATTGGCAATAATAAG
SEQ2707	TCACCTAGTGAAGAGAACAAGCCTGATGGGAGCACGAAGACAGAAATTGGCAATAATAAG
SEQ2709	TCACCTAGTGAAGAGAACAAGCCTGATGGTAGCACGAAGACAGAAATTGGCAATAATAAG
SEQ2710	TCACCTAGTGAAGAGAACAAGCCTGATGGGAGCACGAAGACAGAAATTGGCAATAATAAG
SEQ2711	TCACCTAGTGAAGAGAACAAGCCTGATGGGAGCACGAAGACAGAAATTGGCAATAATAAG
SEQ2701	GATATTTCTAGTGGAACAAAAGTATTAATTTTCAGAAGATAGTATTAAGAATTTTAGTAAA
SEQ2702	GATATTTCTAGTGGAACAAAAGTATTAATTTTCAGAAGATAGTATTAAGAATTTTAGTAAA
SEQ2703	GATATTTCTAGTGGAACAAAAGTATTAATTTTCAGAAGATAGTATTAAGAATTTTAGTAAA
SEQ2704	GATATTTCTAGTGGAACAAAAGTATTAATTTTCAGAAGATAGTATTAAGAATTTTAGTAAA
SEQ2705	GATATTTCTAGTGGAACAAAAGTATTAATTTTCAGAAGATAGTATTAAGAATTTTAGTAAA
SEQ2706	GATATTTCTAGTGGAACAAAAGTATTAATTTTCAGAAGATAGTATTAAGAATTTTAGTAAA
SEQ2707	GATATTTCTAGTGGAACAAAAGTATTAATTTTCAGAAGATAGTATTAAGAATTTTAGTAAA
SEQ2709	GATATTTCTAGTGGAACAAAAGTATTAATTTTCAGAAGATAGTATTAAGAATTTTAGTAAA
SEQ2710	GATATTTCTAGTGGAACAAAAGTATTAATTTTCAGAAGATAGTATTAAGAATTTTAGTAAA
SEQ2711	GATATTTCTAGTGGAACAAAAGTATTAATTTTCAGAAGATAGTATTAAGAATTTTAGTAAA
SEQ2701	GCAAGTAGTGATCAAGAAGAAGTGGATCGCGATGAATCATCATCTTCAAAAGCAAATGAT
SEQ2702	GCAAGTAGTGATCAAGAAGAAGTGGATCGCGATGAATCATCATCTTCAAAAGCAAATGAT
SEQ2703	GCAAGTAGTGATCAAGAAGAAGTGGATCGCGATGAATCATCATCTTCAAAAGCAAATGAT
SEQ2704	GCAAGTAGTGATCAAGAAGAAGTGGATCGCGATGAATCATCATCTTCAAAAGCAAATGAT
SEQ2705	GCAAGTAGTGATCAAGAAGAAGTGGATCGCGATGAATCATCATCTTCAAAAGCAAATGAT
SEQ2706	GCAAGTAGTGATCAAGAAGAAGTGGATCGCGATGAATCATCATCTTCAAAAGCAAATGAT
SEQ2707	GCAAGTAGTGATCAAGAAGAAGTGGATCGCGATGAATCATCATCTTCAAAAGCAAATGAT
SEQ2709	GCAAGTAGTGATCAAGAAGAAGTGGATCGCGATGAATCATCATCTTCAAAAGCAAATGAT
SEQ2710	GCAAGTAGTGATCAAGAAGAAGTGGATCGCGATGAATCATCATCTTCAAAAGCAAATGAT
SEQ2711	GCAAGTAGTGATCAAGAAGAAGTGGATCGCGATGAATCATCATCTTCAAAAGCAAATGAT

**Table 27: Comparative Sequences relating to SAG1473
(cell wall surface anchor family protein)**

SEQ2701	GGGAAAAAAGGCCACAGTAAGCCTAAAAAGGAA-----
SEQ2702	GGGAAAAAAGGCCACAGTAAGCCTAAAAAGGAA-----
SEQ2703	GGGAAAAAAGGCCACAGTAAGCCTAAAAAGGAA-----
SEQ2704	GGGAAAAAAGGCCACAGTAAGCCTAAAAAGGAA-----
SEQ2705	GAGAAAAAAGGCCACAGTAAGCCTAAAAAGGAA-----
SEQ2706	GGGAAAAAAGGCCACAGTAAGCCTAAAAAGGAA-----
SEQ2707	GAGAAAAAAGGCCACAGTAAGCCTAAAAAGGAASGATACAAGTGATAAGAATACTGACAC
SEQ2709	GAGAAAAAAGGCCACAGTAAGCCTAAAAAGGAA-----
SEQ2710	GAGAAAAAAGGCCACAGTAAGCCTAAAAAGGAA-----
SEQ2711	GAGAAAAAAGGCCACAGTAAGCCTAAAAAGGAATABCMARATVSTNCSRATNGTSAGCWA
SEQ2701	-----
SEQ2702	-----
SEQ2703	-----
SEQ2704	-----
SEQ2705	-----
SEQ2706	-----
SEQ2707	AGTGTCGTGACTACGACCTTATCTGAGGAGAAAAGATTAGATGAACTAGACCAGTCTAG
SEQ2709	-----
SEQ2710	-----
SEQ2711	TRACANCHRAMYRTN-----
SEQ2701	-----
SEQ2702	-----
SEQ2703	-----
SEQ2704	-----
SEQ2705	-----
SEQ2706	-----
SEQ2707	ACTGGTTCTTCTTCTGAAAATGAATCGAGTTCATCAAGTGAAACCAGAAACAAATCCCTC
SEQ2709	-----
SEQ2710	-----
SEQ2711	-----
SEQ2701	-----
SEQ2702	-----
SEQ2703	-----
SEQ2704	-----
SEQ2705	-----
SEQ2706	-----
SEQ2707	ACTAATCCACCTACAACAGAACCATCGCAACCCTCACCTAGTGAAGAGAACAAGCCTGA
SEQ2709	-----
SEQ2710	-----
SEQ2711	-----
SEQ2701	-----
SEQ2702	-----
SEQ2703	-----
SEQ2704	-----
SEQ2705	-----
SEQ2706	-----
SEQ2707	GGTAGCACGAAGACAGAAATTGGCAATAATAAGGATATTTCTAGTGGAACAAAAGTATT
SEQ2709	-----
SEQ2710	-----
SEQ2711	-----

**Table 27: Comparative Sequences relating to SAG1473
(cell wall surface anchor family protein)**

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SEQ2701  -----
SEQ2702  -----
SEQ2703  -----
SEQ2704  -----
SEQ2705  -----
SEQ2706  -----
SEQ2707  ATTTTCAGAAAGATAGTATTAAGAATTTTAGTAAAGCAAGTAGTGATCAAGAARAAGTGG
SEQ2709  -----
SEQ2710  -----
SEQ2711  -----

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SEQ2701  -----
SEQ2702  -----
SEQ2703  -----
SEQ2704  -----
SEQ2705  -----
SEQ2706  -----
SEQ2707  CGCGATGAATCATCATCTTCAAAAGCAAATGATGAGAAAAAAGGCCACAGTAAGCCTAA
SEQ2709  -----
SEQ2710  -----
SEQ2711  -----

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SEQ2701  -----
SEQ2702  -----
SEQ2703  -----
SEQ2704  -----
SEQ2705  -----
SEQ2706  -----
SEQ2707  AAGGAA
SEQ2709  -----
SEQ2710  -----
SEQ2711  -----

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>SEQ ID NO 2750:4_1169NT frame: 1
DTSDKNTDTSVVTTLSEEKRSDELDQSSTGSSSENESSSSSEPETNPSTNPPTTEPSQP
SPSEENKPDGRKTKEIGNNKDISSGTVLISEDSIKNFSKASSDQEEVDRDESSSSKASD
GKKGHSKPKKE

>SEQ ID NO 2751:4_18RS21 frame: 1
DTSDKNTDTSVVTTLSEEKRSDELDQSSTGSSSENESSSSSEPETNPSTNPPTTEPSQP
SPSEENKPDGRKTKEIGNNKDISSGTVLISEDSIKNFSKASSDQEEVDRDESSSSKAND
GKKGHSKPKKE

>SEQ ID NO 2752:4_2603 frame: 1
DTSDKNTDTSVVTTLSEEKRSDELDQSSTGSSSENESSSSSEPETNPSTNPPTTEPSQP
SPSEENKPDGRKTKEIGNNKDISSGTVLISEDSIKNFSKASSDQEEVDRDESSSSKAND
GKKGHSKPKKE

>SEQ ID NO 2753:4_090 frame: 1
DQSSTGSSSENESSSSSEPETNPSTNPPTTEPSQSPSEENKPDGRKTKEIGNNKDISSG
TKVLISEDSIKNFSKASSDQEEVDRDESSSSKANDGKKGHSKPKKE

>SEQ ID NO 2754:4_A909 frame: 1
DTSDKNTDTSVVTTLSEEKRSDELDQSSTGSSSENESSSSSEPETNPSTNPPTTEPSQP
SPSEENKPDGSTKTEIGNNKDISSGTVLISEDSIKNFSKASSDQEEVDRDESSSSKAND
EKKGHSKPKKE

>SEQ ID NO 2755:4_CJB110 frame: 1
DTSDKNTDTSVVTTLSEEKRSDELDQSSTGSSSENESSSSSEPETNPSTNPPTTEPSQP
SPSEENKPDGRKTKEIGNNKDISSGTVLISEDSIKNFSKASSDQEEVDRDESSSSKAND
GKKGHSKPKKE

**Table 27: Comparative Sequences relating to SAG1473
(cell wall surface anchor family protein)**

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>SEQ ID NO 2756:4_COH1 frame: 1
DTSDKNTDTSVVTTLSEEKRSDELDQSSSTGSSSENESSSSSEPETNPSTNPPTTEPSQP
SPSEENKPDGSTKTEIGNNKDISSGTVLISEDSEIKNFSKASSDQEEVERDESSSSKAND
EKKGHSKPKKE

>SEQ ID NO 2757:4_H36B frame: 1
DTSDKNTDTSVVTTLSEEKRLDELDQSSSTGSSSENESSSSSEPETNPSTNPPTTEPSQP
SPSEENKPDGSTKTEIGNNKDISSGTVLISEDSEIKNFSKASSDQEXVDRDESSSSKAND
EKKGHSKPKKE

>SEQ ID NO 2758:4_JM9130013 frame: 1
DTSDKNTDTSVVTTLSEEKRLDELDQSSSTGSSSENESSSSSEPETNPSTNPPTTEPSQP
SPSEENKPDGSTKTEIGNNKDISSGTVLISEDSEIKNFSKASSDQEEVDRDESSSSKAND
EKKGHSKPKKE

>SEQ ID NO 2759:4_M732 frame: 1
DTSDKNTDTSVVTTLSEEKRSDELDQSSSTGSSSENESSSSSEPETNPSTNPPTTEPSQP
SPSEENKPDGSTKTEIGNNKDISSGTVLISEDSEIKNFSKASSDQEEVERDESSSSKAND
EKKGHSKPKKE

>SEQ ID NO 2760:4_M781 frame: 1
DTSDKNTDTSVVTTLSEEKRSDELDQSSSTGSSSENESSSSSEPETNPSTNPPTTEPSQP
SPSEENKPDGSTKTEIGNNKDISSGTVLISEDSEIKNFSKASSDQEEVDRDESSSSKAND
EKKGHSKPKKE

SEQ2750      TSDKNTDTSVVTTLSEEKRSDELDQSSSTGSSSENESSSSSEPETNPSTNPPTTEPSQP
SEQ2751      TSDKNTDTSVVTTLSEEKRSDELDQSSSTGSSSENESSSSSEPETNPSTNPPTTEPSQP
SEQ2752      TSDKNTDTSVVTTLSEEKRSDELDQSSSTGSSSENESSSSSEPETNPSTNPPTTEPSQP
SEQ2753      -----DQSSSTGSSSENESSSSSEPETNPSTNPPTTEPSQP
SEQ2754      TSDKNTDTSVVTTLSEEKRLDELDQSSSTGSSSENESSSSSEPETNPSTNPPTTEPSQP
SEQ2755      TSDKNTDTSVVTTLSEEKRSDELDQSSSTGSSSENESSSSSEPETNPSTNPPTTEPSQP
SEQ2756      TSDKNTDTSVVTTLSEEKRSDELDQSSSTGSSSENESSSSSEPETNPSTNPPTTEPSQP
SEQ2757      TSDKNTDTSVVTTLSEEKRLDELDQSSSTGSSSENESSSSSEPETNPSTNPPTTEPSQP
SEQ2758      TSDKNTDTSVVTTLSEEKRLDELDQSSSTGSSSENESSSSSEPETNPSTNPPTTEPSQP
SEQ2759      TSDKNTDTSVVTTLSEEKRSDELDQSSSTGSSSENESSSSSEPETNPSTNPPTTEPSQP
SEQ2760      TSDKNTDTSVVTTLSEEKRSDELDQSSSTGSSSENESSSSSEPETNPSTNPPTTEPSQP

SEQ2750      SPSEENKPDGRKTEIGNNKDISSGTVLISEDSEIKNFSKASSDQEEVDRDESSSSKASD
SEQ2751      SPSEENKPDGRKTEIGNNKDISSGTVLISEDSEIKNFSKASSDQEEVDRDESSSSKAND
SEQ2752      SPSEENKPDGRKTEIGNNKDISSGTVLISEDSEIKNFSKASSDQEEVDRDESSSSKAND
SEQ2753      SPSEENKPDGRKTEIGNNKDISSGTVLISEDSEIKNFSKASSDQEEVDRDESSSSKAND
SEQ2754      SPSEENKPDGSTKTEIGNNKDISSGTVLISEDSEIKNFSKASSDQEEVDRDESSSSKAND
SEQ2755      SPSEENKPDGRKTEIGNNKDISSGTVLISEDSEIKNFSKASSDQEEVDRDESSSSKAND
SEQ2756      SPSEENKPDGSTKTEIGNNKDISSGTVLISEDSEIKNFSKASSDQEEVERDESSSSKAND
SEQ2757      SPSEENKPDGSTKTEIGNNKDISSGTVLISEDSEIKNFSKASSDQEXVDRDESSSSKAND
SEQ2758      SPSEENKPDGSTKTEIGNNKDISSGTVLISEDSEIKNFSKASSDQEEVDRDESSSSKAND
SEQ2759      SPSEENKPDGSTKTEIGNNKDISSGTVLISEDSEIKNFSKASSDQEEVERDESSSSKAND
SEQ2760      SPSEENKPDGSTKTEIGNNKDISSGTVLISEDSEIKNFSKASSDQEEVDRDESSSSKAND

SEQ2750      KKGHSKPKKE
SEQ2751      KKGHSKPKKE
SEQ2752      KKGHSKPKKE
SEQ2753      KKGHSKPKKE
SEQ2754      KKGHSKPKKE
SEQ2755      KKGHSKPKKE
SEQ2756      KKGHSKPKKE
SEQ2757      KKGHSKPKKE
SEQ2758      KKGHSKPKKE
SEQ2759      KKGHSKPKKE
SEQ2760      KKGHSKPKKE

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**Table 28: Comparative Sequences relating to SAG1552
(conserved hypothetical protein)**

SEQ ID NO. 2801: SAG1552 FROM THE 1169NT1 GBS TYPE V STRAIN
(REVERSE COMPLEMENT)

TTTGTGTAAAGGTGATACTGTACTTCACAAGCCCACCAATAAACCTTTTGTGTAAAGGAGTAGACGTTGAGTCT
TCCTTAGCAGGTTATCATCACAACGATTTTCCTATTACTCAAAAAACGTATCGTGAGTGGTCCATTTAATTTCCAAC
ATGGGGGCAAATACTGTAAGAGTCAAAGTACCGATGAATGTTGCATTTTACGATGCTTTATATCACCACAACAAAGCA
TCAAAGAGGCCACTGTATTTGTTGCAAGGAATACGTATAGATTCTTATCGCAATAATGCTTCTATAACAGCTTTTAAT
GATAATTATAGGGGGTATTTAAACGAGAAGCAAAGGCGTGTGGATATTCTCCATGGGCGTAAGCAAGTATGGAAT
ACTGATTTTGGTAGCCGTCATTATCATATGATCTTAGTCCTTGGGTACTTGGTTATGTCTAGGGGATGATTGGAAT
AGTGGTACTGTGCGTTATACTAATCATCAAGAGAAAAAACGCAATATAAAGGACGTTATTTTAAACTTCTGCGGCA
GCTAATCCATTTGAGTCAATGCTAGCTCAAGTTATGGATGAATTGACACATTATGAGACAGCTAAATATGGTTGGCAA
CATTTGATTAGTTTTTCAAACCTACCAACAACAGACCCCTTTTCGTTATCGAAAACCATTTGAGGCACAGGCTCCTAAA
TACGTACAATAAATGTAGAAAATATTCAAGCTAATTCGAATGTTAAAGCAGGTATTTTTCGAGCATATAAAGCTATT
GATTTCCATCCTCGATACAAGGATTATCTATTATTGATAAAGAGAATATCAGTAAAGAAGATAGACAAAAGATTAAA
GAACCTTCTTTGTACAGGGATACGTTAACTGCTAAATGCTTATCACAATAATCCCTGTTCTAGTCACGGGTTATGGC
TATTCGACAGCGAGAGGTATTGCCAAAAAGAAATGATAAACGTCCTCTGCCGATTAATGAAAAAGAACAGGTCAG
CGTTTACTAGAAGATTATGAATCTTTTATATCATCCGCTAGTTTTGGAGCGACTATCAATGCATGGCAAGACGATTGG
AATGCAAGGGCGTGGAAATACATCCTTCGCCACAAATAAACATAGTCAATTCTATGGGGGGATGCACAAGTATTTAAT
CAAGGTTATGGTTTATTAGGCTTTAAACGCAAAACATCATTATCAAGTTGATGGTAAAGAGGCAAGGAGAGTGG
AAACATCCTCTG

SEQ ID NO. 2802: SAG1552 FROM THE _____

ATGACTAGTGCAACAGGAGATGACTTATATGCTAGCAGTGATGAAAGCTATCTCTACCTTGCGATTAAACAAAACCT
GAAAACTAAAAGAAAAACGATTATTACCAATAGATATTACACCAAAATCTGGTAGTAGAAAAATGAATGGTAGTAAG
GTCACATTTTCTAAATCTAGTGACTTTGTATTGTCTATTGATCCAAATGGCAAGTCTGAATTATTTGTCCAAGAGCGC
TATAATGCCCTTAAAGCGAACTATCTCGACAGCTTAAAGGTAAGATTATTTATGCTTTCCACCAAGAAGAAGACAGT
AGTAATTTTGAGCAGATCAATATGGTATTGAGAAATACAAAGATTGTTGAAGACATGGAAAAAGTAAAGCAACAGAG
AGGTTCTTACCAACTCATCTACTGGTCTTCTCAAAACAGGAACAATTGATAGGCACCAAAAAACATTGATTACAA
ACAGATATTTGCTTTGGAAAGGACTTTATAGAGGTCAGAAATCCGTCGAGTTGTTGAATTTTTCTGATCCATCATCT
CAAAAAATTCAGGATGATTACTTTAAACATTATGGTGTGAAGGAGTTAGAAATTGAGAGCATTGCTTTAGGATTAGGT
GCTAATAGCAAAGAAAACACACTGATAAAGATGGCAGATTATCGTTTGAATAATTGGGAGAGACCCGATACCAAAACC
TTTTTAAAGACTCCTATTATAGTATTTAAGAAAGAA

SEQ ID NO. 2803: SAG1552 FROM THE 18RS21 GBS TYPE II STRAIN

AAGGGCTTATTAAGAAAAATACAAGAACTAATTTGTGTAAAGGTGATACTGTACTTCACAAGCCCACCAATAAA
CCTTTTGTGTAAAGGAGTAGACGTTGAGTCTTCCTTAGCGGGTTATCATCACAACGATTTTCCTATTACTCAAAAA
ACGTATCGTGAATGGTCCATTTAATTTCCAACATGGGGGCAAATACTGTAAGAGTCAAGGTACCGATGAATGTTGCA
TTTTACGATGCCTTATATCACCACAACAAAGCATCAAAGAGCCACTGTATTGTTGCAAGGAATACGTATAGATTCT
TATCGCAATAAGCTTCTTATAACAGCTTTTAATGATAATTATAGGGGGTATTTAAACGAGAAGCAAAGGCGTGTG
GATATTTCTCCATGGGCGTAAGCAAGTATGGAATACTGATTGGGTAGCCGTCATTATCATTATGATCTTAGTCCTTGG
GTACTTGGTTATGTCTGAGGGGATGATTGGAATAGTGGTACTGTGCGTTATACTAATCATCAAGAGAAAAAACGCAA
TATAAAGGACGTTATTTTAAACTTCTGTGGCAGCTAATCCATTTGAGGTCATGCTAGCTCAAGTAATGGATGAATTG
ACACATTATGAGACAGCTAAATATGGTTGGCAACATTTGATTAGTTTTTCAAACCTACCAACAACAGACCCCTTTTCAT
TATCGAAAACCATTTGAGGCACAGGCTCCTAAATACGTACAATAAATGTAGAAAATATTCAAGCTAATCAAATGTT
AAAGCAGGTATGTTTGCAGCATATAAAGCTATTGATTTCCATCCTCGATACAAGGATTATCTATTATTGATAAAGAG
AATATCAGTAAAGAAGATAGACAAAAGATTAAAGAACCTTCTTTGTACAGGGATACGTTAAACTGCTAAATGCTTAT
CACAAAATCCCTGTTCTAGTCACGGGTTATGGCTATTGACAGCGAGAGGTATTGGCCAAAAAGAAATGATAAACGT
CCTCTGCCGATTAATGAAAAAGAAACAGGTGAGGCTTTACTAGAAGATTATGAATCTTTTATATCATCCGCTAGTTTT
GGAGCGACTATCAATGCATGGCAAGACGATTGGAATGCAAGGGCGTGGAAATACATCTTTCGCCACAAATAAACATAGT
CAATTCCTATGGGGGGATGCACAAGTATTTAATCAAGGTTATGGTTTATTAGGCTTTAAACGCAAAACATCATTAT
CAAGTTGATGGTAAAGAGGCAAGGAGAGTGGAAACATCCTCTGATGACTAGTGAACAGGAGATGACTTATATGCT
AGCAGTGATGAAAGCTATCTTACCTTGCGATTAAACAAAAACCTGAAAACTAAAAGAAAAACGATTATTACCAATA
GATATTACCAAAAACTGGTAGTAGAAAAATGAATGGTAGTAAGGTCACATTTTCTAAATCTAGTGACTTTGTATTG
TCTATTGATCCAAATGGCAAGTCTGAATTATTGTCCAAAGAGCGCTATAATGCCTTAAAGCGAACTATCTTCGACAG
CTTAACGGTAAAGATTTTATGCTTTCCACCAAGAAGAACAGTAGTAATTTTGGAGCAGATAAATATGGTATTGAGA
AATACAAAGATTGTTGAAGACATGAAAAAGTAAAGCAACAGAGAGGTTCTTACCACTCATCTACTGGTCTTCTC
AAAAAGGAACCACTGATAGGCACCAAAAAACATTTGATTACAAACAGATATTTCTGTTTGGAAAGGACTTTATAGAG
GTCAGAATTCGTCGAGGTTGTTGAATTTTTCTGATCCATCATCTCAAAAAATTCACGATGATTACTTTAAACATTAT
GGTGTGAAGGAGTTAGAAATTGAGAGCATTGCTTTAGGATTAGGTGCTAATAGCAAAGAAAAACACACTGATAAAGATG
GCAGATTATCGTTTGAATAATTGGGAGAGACCCGATACCAAAACCTTTTAAAGACTCCTATTATGTATTAAGAAAG
AA

**Table 28: Comparative Sequences relating to SAG1552
(conserved hypothetical protein)**

**SEQ ID NO. 2804: SAG1552 FROM THE 2603 V/R GBS TYPE V STRAIN
(REVERSE COMPLEMENT)**

TATTAAAAGAAAATACAAGAACTAACTTTGTTGTTAAAGGTGATACTGTACTTCACAAGCCCACCAATAAACCTTTTG
TTGTTAAAGGAGTAGACGTTGAGTCTTCCTTAGCGGGTTATCATCACAACGATTTTCCTATTACTCAAAAAACGTATC
GTGAATGGTTCCATTTAATTTCCAACATGGGGGCAAATACTGTAAGAGTCAAGGTACCGATGAATGTTGCATTTTACG
ATGCCTTATATCACCACAACAAAGCATCAAAGAGGCCACTGTATTTGTTGCAAGGAATACGTATAGATTCTTATCGCA
ATAATGCTTCTATAACAGCTTTTAAATGATAATTATAGGGGGTATTTAAAACGAGAAGCAAAAGGCGTTGTGGATATTC
TCCATGGGCGTAAGCAAGTATGGAATACTGATTGGGTAGCCGTCATTATCATATGATCTTAGTCCTTGGGTACTTG
GTTATGTCGTAGGGGATGATTGGAATAGTGGTACTGTCGCTTATACTAATCATCAAGAGAAAAAACGCAATATAAAG
GACGTTATTTTAAACTTCTGTGGCAGCTAATCCATTTGAGGTCATGCTAGCTCAAGTAATGGATGAATTGACACATT
ATGAGACAGCTAAATATGGTTGGCAACATTTGATTAGTTTTTCAAACCTCACCACAACAGACCCCTTTTCATTATCGAA
AACCATTTGAGGCACAGGCTCCTAAATACGTACAATAAATGTAGAAAATATTCAAGCTAATTCAAATGTTAAAGCAG
GTATGTTTGCAGCATATAAAGCTATTGATTTCCTCGATACAAGGATTATCTATTATTTGATAAAGAGAATATCA
GTAAGAAGATAGACAAAAGATTAAAGAACTTTCTTTGTCACAGGGATACGTTAACTGCTAAATGCTTATCACA
TCCCTGTTCTAGTCAACGGTTATGGCTATTGCGACAGGAGGTATTGCCAAAAAGAAATTGATAAAGCGTCTCTGC
CGATTAATGAAAAAGAACAAAGGTCAGCGTTTACTAGAAGATTATGAATCTTTTATATCATCCGTTAGTTTTGGAGCGA
CTATCAATGCATGGCAAGACGATTGGAATGCAAGGGCGTGGAAATACATCTTTCCGCCACAATAAACATAGTCAATTCC
TATGGGGGGATGCACAAGTATTTAATCAAGGTTATGGTTTATTAGGCTTTAAAAACGCAAAACATCATTATCAAGTTG
ATGGTAAAAGAGGCAAGAGGAGAGTGGAAACATCCTCTGATGACTAGTGCAACAGGAGATGACTTATATGCTAGCAGTG
ATGAAAGCTATCTCTACCTTGGGATTAAAAACAAAACCTGAAAACTAAAAGAAAAACGATTATTACCAATAGATATTA
CACCAAAATCTGGTAGTAGAAAAATGAATGGTAGTAAGGTCACATTTTCTAAATCTAGTGACTTTGTATTGTCTATTG
ATCCAAATGGCAAGTCTGAATTATTTGTCCAAGAGCGCTATAATGCCTTAAAAGCGAACTATCTTCGACAGCTTAAACG
GTAAGATTTTTATGCTTTCCACCAAAGAAGAACAGTAGTAATTTTGAGCAGATAAATATGGTATTGAGAAATACAA
AGATTGTTGAAGACATGGAAAAAGTAAAAAGCAACAGAGAGGTTCTTACCAACTCATCCTACTGCTCTTCTCAAAACAG
GAACAACCTGATAGGCACCAAAAAACATTTGATTCAAAACAGATATTTCTGTTTGGAAAGGACTTTATAGAGGTCAGAA
TTCCGTGGCAGTTGTTGAATTTTCTGATCCATCATCTCAAAAAATTACAGATGATTACTTTAAACATTATGGTGTGA
AGGAGTTAGAAATTGAGAGCATTTGCTTTAGGATTAGGTGCTAATAGCAAAGAAAAACACTGATAAAGATGGCAGATT
ATCCTTTGAAAAATTGGGAGAGACCCGATACCAAAACCTTTTAAAAGACTCCTATTATAGTATTAAGAAAGAAATGGT
CTAAAGAAAGAGAGAGAACATATGGTCCA

**SEQ ID NO. 2805: SAG1552 FROM THE A909 GBS TYPE Ia STRAIN
(REVERSE COMPLEMENT)**

AAGGCTTATTAAAGAAAAATACAAGAACTAACTTTGTTGTTAAAGGTGATACTGTACTTCACAAGCCCACCAATAAA
CCTTTTGTGTTAAAGGAGTAGACGTTGAGTCTTCCTTAGCGGGTTATCATCACAACGATTTTCCTATTACTCAAAAA
ACGTATCGTGAATGTTCCATTTAATTTCCAACATGGGGGCAAATACTGTAAGAGTCAAGGTACCGATGAATGTTGCA
TTTTACGATGCCTTATATCACCACAACAAAGCATCAAAGAGGCCACTGTATTTGTTGCAAGGAATACGTATAGATTCT
TATCGCAATAATGCTTCTATAACAGCTTTTAAATGATAATTATAGGGGGTATTTAAAACGAGAAGCAAAAGGCGTTGTG
GATATTCTCCATGGGCGTAAGCAAGTATGGAATACTGATTGGGTAGCCGTCATTATCATATGATCTTAGTCCTTGG
GTACTTGGTTATGTCGTAGGGGATGATTGGAATAGTGGTACTGTCGCTTATACTAATCATCAAGAGAAAAAACGCAA
TATAAAGGACGTTATTTTAAACTTCTGTGGCAGCTAATCCATTTGAGGTCATGCTAGCTCAAGTAATGGATGAATTG
ACACATTATGAGACAGCTAAATATGGTTGGCAACATTTGATTAGTTTTTCAAACCTCACCACAACAGACCCCTTTTCAT
TATCGAAAAACATTTGAGGCACAGGCTCCTAAATACGTACAATAAATGTAGAAAAATATTCAAGCTAATTCAAATGTT
AAAGCAGGTATGTTTGCAGCATATAAAGCTATTGATTTCATCCTCGATACAAGGATTATCTATTATTTGATAAAGAG
AATATCAGTAAAGAGATAGACAAAAGATTAAAGAACTTTCTTTGTCAAGGGATACGTTAACTGCTAAATGCTTAT
CACAAAAACCTGTTCTAGTCACGGGTTATGGCTATTCGACAGCGAGAGGTATTGCCAAAAAGAAATTGATAAAGCT
CCTCTGCCGATTAAATGAAAAAGAACAAAGGTCAGCGTTTACTAGAAGATTATGAATCTTTTATATCATCCGGTAGTTT
GGAGCGACTATCAATGCATGGCAAGACGATTGGAATGCAAGGGCGTGAATACATCTTTCCGCCACAATAAACATAGT
CAATTCCTATGGGGGATGCACAAGTATTTAATCAAGGTTATGGTTTATTAGGCTTTAAAACGCAAAACATCATTAT
CAAGTTGATGGTAAAGAGGCAAGGAGAGTGGAAACATCCTCTGATGACTAGTGCAACAGGAGATGACTTATATGCT
AGCAGTGATGAAAGCTATCTCTACCTTGGGATTAAAAACAAAACCTGAAAACTAAAAGAAAAACGATTATTACCAATA
GATATTACCAAAAAATCTGGTAGTAGAAAAATGAAATGGTAGTAAGGTCACATTTTCTAAATCTAGTGACTTTGTATTG
TCTATTGATCCAAATGGCAAGTCTGAATTATTTGTCCAAGAGCGCTATAATGCCTTAAAAGCGAACTATCTTCGACAG
CTTAAAGGTAAGATTATTTATGCTTTCCACCAAAGAAGAACAGTAGTAATTTTGAGCAGATAAATATGGTATTGAGA
AATACAAAGATTGTTGAAGACATGGAAAAAGTAAAAAGCAACAGAGAGGTTCTTACCAACTCATCCTACTGGTCTTCTC
AAAACAGGAACACTGATAGGCACCAAAAAACATTTGATTCAAAACAGATATTTCTGTTTGGAAAGGACTTTATAGAG
GTCAGAATTCCGTGGCAGTTGTTGAATTTTCTGATCCATCATCTCAAAAGAAATTCACGATGATTACTTTAAACATTAT
GGTGTGAAGGAGTTAGAAAATTGAGAGCCATTGCTTTAGGATTAGGTGCTAATAGCAAAGAAAAACACTGATAAAGA
TGGCAGATTATCGTTTGA AAAAATTGGGAGAGACCCGATACCAAAACCTTTTAAAAGA

**Table 28: Comparative Sequences relating to SAG1552
(conserved hypothetical protein)**

SEQ ID NO. 2806: SAG1552 FROM THE CJB110 GBS NONTYPEABLE STRAIN

TATTACTTTGATGGTAGTTTGTATTACCAAAGGGCTTATTTAAAGAAAATACAAGAACTAACTTTGTTGTTAAAGGT
GATACTGTACTTCACAAGCCCACCAATAAACCTTTTGTGTTTAAAGGAGTAGACGTTGAGTCTTCCTTAGCGGGTTAT
CATCACAACGATTTTCCTATTACTCAAAAAACGTATCGTGAATGGTTCATTTAATTTCCAACATGGGGGCAAATACT
GTAAGAGTCAAGGTACCGATGAATGTTGCATTTTACGATGCCTTATATCACCACAACAAAGCATCAAAGAGGCCACTG
TATTTGTTGCAAGGAATACGTATAGATTCTTATCGCAATAATGCTTCTATAACAGCTTTTAAATGATAATTATAGGGGG
TATTTAAACGAGAAAGCAAAGGCGTTGTGGATATCTCCATGGGCGTAAGCAAGTATGGAATACAGATTTTGGTAGC
CGTCATTATCATTATGATCTTAGTCCTTGGGTACTTGGTTATGTCTAGGGGATGATTGGAATAGTGGTACTGTCCGT
TATACTAATCATCAAGAGAAAAAACGCAATATAAAGGACGTTATTTAAACTTCTGTGGCAGCTAATCCATTGAG
GTCATGCTAGCTCAAGTAATGGATGAATTGACACATTATGAGACAGCTAAATATGGTTGGCAACATTTGATTAGTTTT
TCAAACCTACCAACAACAGACCCTTTTCATTATCGAAAACCATTTGAGGCACAGGCTCCTAAATACGTACAATAAAT
GTAGAAAATATTCAGCTAATTCAAATGTTAAAGCAGGTATGTTTGCAGCATATAAGCTATTGATTTCCATCCTCGA
TACAAGGATTATCTATTATTGATAAAGAGAATATCAGTAAAGAAGATAGACAAAAGATTAAAGAACTTTCTTTGTCA
CAGGGATACGTTAACTGCTAAATGCTTATCACAAAATCCCTGTTCTAGTCACGGGTTATGGCTATTTCGACAGCGAGA
GGTATTGCCCAAAAAGAAATTGATAAACGTCCTCTGCGGATTATGAAAAAGAACAGGTCAGCGTTTACTAGAAGAT
TATGAATCTTTTATATCATCCGGTAGTTTGGAGCGACTATCAATGCATGGCAAGACGATTGGAATGCAAGGGCGTGG
AATACATCTTTCCGCCACAAATAACATAATCAATTCCTATGGGGGATGCACAAGTATTTAATCAAGGTTATGGTTTA
TTAGGCTTTAAAAACGCAAAACATCATTATCAAGTTGATGGTAAAGAGGCAAGGAGAGTGGAAACATCCTCTGATG
ACTAGTGCAACAGGAGATGACTTATATGCTAGCAGTGATGAAAGCTATCTCTACCTTGGCATTTAAACAAAACCTGAA
AACTAAAAGAAAAACGATTATTACCAATAGATATTACACAAAATCTGGTAGTAGAAAAATGAATGGTAGTAAGGTC
ACATTTTCTAAATCTAGTGACTTTGTATTGTCTATTGATCCAAATGGCAAGTCTGAATTATTTGTCCAAGAGCGCTAT
AATGCCTTAAAGCGAATATCTTCGACAGCTTAAACGGTAAAGATTTTATGCTTTCCACCAAGAAGAACAGTAGT
AATTTTGAGCAGATAAAATATGGTATTTGAGAAAATACAAAGATTGTTGAAGACATGGAAAAAGTAAAGCAACAGAGAGG
TTCTTACCAACTCATCTACTGGTCTTCTCAAAACAGGAACAACCTGATAGGCACCAAAAAACATTTGATTACAAAACA
GATATTTCTGTTTGGAAAGGACTTTATAGAGGTCAGAATTCCTGTCAGTGTGTTGAATTTTCTGATCCATCATCTCAA
AAAATTCACGATGATTACTTTAAACATTATGGTGTGAAGGAGTTAGAAATTGAGAGCATTGCTTTAGGATTAGGTGCT
AATAGCAAAGAAAAACACTGATAAAGATGGCAGATTATCGTTTGAAAAATTGGGAGAGACCCGATACCAAAACCTTT
TTAAAGACTCCTATTATGTATTAAAGAAAGA

SEQ ID NO. 2807: SAG1552 FROM THE COH1 GBS TYPE III STRAIN

TTTACCACAGGGCTTATTTAAAGAAAATACAAGAACTAACTTTGTTGTTAAAGGTGATACTGTACTTCACAAGCCCAC
CAATAAACCTTTTGTGTTAAAGGAGTAGACGTTGAGTCTTCCTTAGCGGGTTATCATCACAACGATTTTCTATTAC
TCAAAAACGATATCGTGAATGGTTCATTTAATTTCCAACATGGGGGCAAATACTGTAAGAGTCAAGGTACCGATGAA
TGTTGCATTTTACGATGCCTTATATCACCACAACAAAGAATCAAAGAGGCCACTGTATTTGTGCAAGGAATACGTAT
AGATTCTTATCGCAATAATGCTTCTATAACAGCTTTTAATGATAATTATAGGGGGTATTTAAACGAGAAGCAAAGG
CGTTGTGGATATTTCCATGGGCGTAAGCAAGTATGGAATACTGATTTTGGTAGCCGTCATTATCATTATGATCTTAG
TCCTTGGGTACTTGGTTATGTCTAGGGGATGATTGGAATAGTGGTACTGTCTGCTTATACTAATCATCAAGAGAAAAA
AACGCAATATAAAGGACGTTATTTTAAACTTCTGTGGCAGCTAATCCATTTGAGGTCATGCTAGCTCAAGTAATGGA
TGAATTGACACATTATGAGACAGCTAAATATGGTTGGCAACATTGATTAGTTTTCAAACTCACCAACAACAGACCC
TTTTATTATCGAAAACCATTTGAGGCACAGGCTCCTAAATACGTACAATAAATGTAGAAAAATATTCAAGCTAATTC
AAATGTTAAAGCAGGTATGTTTGCAGCATATAAAGCTATTGATTTCCATCCTCGATACAAGGATTATCTATTATTTGA
TAAAGAGAATATCAGTAAAGAAGATAGACAAAAGATTAAAGAATCTTTTGTGTCACAGGGATACGTTAACTGCTAAA
TGCTTATCACAAAATCCCTGTTCTAGTCACGGGTATGGCTATTGACAGCGAGAGGTATTGCCAAAAAGAAATTGA
TAAACGTCTCTGCCGATTATGAAAAAGAACAGGTGAGCGTTTACTAGAAGATTATGAATCTTTTATATCATCCGG
TAGTTTTGGAGCGACTATCAATGCATGGCAAGACGATTGGAATGCAAGGGCGTGAATACATCTTTCGCCACAAATAA
ACATAGTCAATTCCTATGGGGGGATGCACAAGTATTTAATCAAGGTTATGGTTTATTAGGCTTTAAAAACGCAAAACA
TCATTATCAAGTTGATGGTAAAGAGGCAAGGAGAGTGGAAACATCCTCTGATGACTAGTGCAACAGGAGATGACTT
ATATGCTAGCAGTGATGAAAGCTATCTCTACCTTGCGATTAAAAACAAACCTGAAAACTAAAAGAAAAACGATTATT
ACCAATAGATATTACACAAAATCTGGTAGTAGAAAAATGAATGGTAGTAAGGTCACATTTTCTAAATCTAGTGACTT
TGTATTGTCTATTGATCCAAATGGCAAGTCTGAATTTATTTGTCCAAGAGCGCTATAATGCCTTTAAAGCGAATCTCT
TCGACAGCTTAAACGTTAAAGATTTTATGCTTTCCACCAAGAAAGACAGTAGTAATTTTGAGCAGATAAATATGGT
ATTGAGAAATACAAAGATTGTTGAAGACATGGAAAAAGTAAAGCAACAGAGAGGTTCTTACCAACTCATCTACTGG
TCCTTCTCAAAACAGGAACAACCTGATAGGCACCAAAAAACATTTGATTACAAACAGATATTTGTTTGGAAAGGACTT
TATAGAGGTGAGAATTCCTGTCAGTTGTTGAATTTTCTGATCCATCATCTCAAAAAATTCACGATGATTACTTTAA
ACATTATGGTGTGAAGGAGTTAGAAATTGAGAGCATTGCTTTAGGATTAGGTGCTAATAGCAAAAGAAACACACTGAT
AAAGATGGCAGATTATCGTTTGAAAAATTGGGAGAGACCCGATACCAAAACCTTTTAAAGACT

**Table 28: Comparative Sequences relating to SAG1552
(conserved hypothetical protein)**

SEQ ID NO. 2808: SAG1552 FROM THE H36b GBS TYPE Ib STRAIN

AAGGGGCTTATTAAAGAAATACAAGAATACTTTGTTGTTAAAGGTGATACTGTACTTCACAAGCCCACCAATAA
ACCTTTTGTGTTTAAAGGAGTAGACGTTGAGTCTTCCTTAGCGGGTTATCATCACAACGATTTTCCTATTACTCAAAA
AACGTATCGTGAATGGTTCCATTTAATTTCCAACATGGGGGCAAATACTGTAAGAGTCAAGGTACCGATGAATGTTGC
ATTTTACGATGCCTTATATCACCACAACAAAGCATCAAAGAGGCCACTGTATTTGTTGCAAGGAATACGTATAGATTTC
TTATCGCAATAATGCTTCTATAACAGCTTTTAATGATAATTATAGGGGGTATTTAAACGAGAAGCAAAAGGCGTTGT
GGATATTCTCCATGGGCGTAAGCAAGTATGGAATACTGATTTTGGTAGCAGTCATTATCATTTATGATCTTAGTCTCTTG
GGTACTTGGTTATGTGCTAGGGGATGATGGACATAGTGGTACTGTGCTTTATACTAATCATCAAGAGGAGAAAAACG
CAATATAAAGGACGTTATTTTAAACTTCTGTGGCAGCTAATCCATTTGAGGTCATGCTAGCTCAAGTAATGGATGAA
TTGACACATTATGAGACAGCTAAATATGGTTGGCAACATTTGATTAGTTTTCAAACTCACCACAACAGACCCCTTTT
CATTATCGAAAACCATTTGAGGCACAGGCTCCTAAATACGTACAACATAATGTAGAAAATATTCAAGCTAATTCGAAT
GTTAAAGCAGGTATGTTTGCAGCATATAAAGCTATTGATTTCCATCCTCGATACAAGGATTATCTATTATTGATAAA
GAGAATATCAGTAAAGAAGATAGACAAAAGATTAAAGAATCTTCTTTGTCAAGGGATACGTTAAACTGCTAAATGCT
TATCACAATAATCCCTGTTCTAGTCACGGGTTATGGCTACTCGACAGCGAGAGGTATTGCCCAAAAGAAATGATAAA
CGTCTCTGCCGATTAAATGAAAAGAACAAAGGTACAGCGTTTACTAGAAGATTATGAATCTTTATATCATCCGGTAGT
TTTGGAGCGACTATCAATGCATGGCAAGACGATTGGAATGCAAGGGTGTGGAATACATCCTTCGCCACAAATAACAT
AGTCAATTCCTATGGGGGGATGCACAAGTATTTAATCAAGGTATGTTTTATAGGCTTTAAAAACGCAAAACATCAT
TATCAGGTTGATGGTAAAGAGGCAAGAAGAGTGGAAACATCCTCTGATGACTAGTGCAACAGGAGATGACTTATAT
GCTAGCAGTGATGAAAGCTATCTCTACCTTGCATTAAAAACAAACCTGAAAACTAAAAAGAAAAACGATTATTACCA
ATAGATATTACACCAAAATCTGGTAGTAGAAAAATGAATGGTAGTAAGGTCACATTTTCTAAATCTAGTGACTTTGTA
TTGTCTATTGATCCAATGGCAAGTCTGAATTTATTTGTCCAGAGCGCTATAACGCCTTAAAGCGAACTATCTTCGA
CAGCTTAATGGTAAAGATTTTATGCTTTCCACCAAGAAGAAGACAGTAGTAATTTTGGAGCAGATAAATATGGTATTG
AGAAATACAAAGATTGTTGAAGACATGAAAAAGTAAAGCAACAGAGAGGTTCTTACCACTCATCTTGGTCTTT
CTCAAAACAGGAACAACTGATAGGCACCAAAAAACATTTGATTACAAACAGATATTTCTGTTTGGAAAGGACTTTATA
GAGGTCAGAATTCCTGTCAGTTGTTGAATTTTCTGATCCATCATCTCAAAAAATTACAGATGATTACTTTAAACAT
TATGGTGTGAAGAGTTAGAAATTGAGAGCATTGCTTTAGGATTAGGTGCTAATAGCAAAGAAAAACACACTGTATAAG
ATGGCAGATTATCGTTTGAATAATTGGGAGAGACCCGATACCAAAACCTTTTAAAGACTCCTATTATAGT

SEQ ID NO. 2809: SAG1552 FROM THE JM9130013 GBS TYPE VIII STRAIN

ACTTTGTTGTTAAAGGTGATACTGTACTTCACAAGCCCACCAATAAACCTTTGTTGTTAAAGGAGTAGACGTTGAGT
CTTCCTTAGCGGGTTATCATCACAACGATTTTCCTATTACTCAAAAAACGATATCGTGAATGGTTCCATTTAATTTCCA
ACATGGGGGCAATACTGTAAGAGTCAAGGTACCGATGAATGTTGCATTTTACGATGCCTTATATCACCACAACAAAG
CATCAAAAGAGGCCACTGTATTTGTTGCAAGGAATACGTATAGATTCTTATCGCAATAATGCTTCTATAACAGCTTTTA
ATGATAATTATAGGGGGTATTTAAACGAGAAGCAAAAGGCGTTGTGGATATTCTCCATGGGCGTAAGCAAGTATGGA
ATACTGATTTTGTGAGCAGTCATTATCATTTATGATCTTAGTCTTGGGTACTTGGTTATGTGCTAGGGGATGATTGGA
ATAGTGGTACTGTGCTTATACTAATCATCAAGAGAAAAAACGCAATATAAAGGACGTTATTTTAAACTTCTGTGG
CAGTAATCCATTTGAGGTCATGCTAGCTCAAGTAATGGATGAATTGACACATTATGAGACAGCTAAATATGGTTGGC
AACATTTGATTAGTTTTCAAACTCACCACAACAGACCCCTTTTATTATCGAAAACCATTTGAGGCACAGGCTCCTA
AATACGTACAATAAATGTAGAAAATATTCAAGCTAATTCGAATGTTAAAGCAGGTATGTTGTCAGCATATAAAGCTA
TTGATTTCCATCCTCGATACAAGGATTATCTATTATTTGATAAAGAGAATATCAGTAAAGAAGATAGACAAAAGATTA
AAGAATTTCTTTGTACAGGGATACGTTAAACTGCTAAATGCTTATCACAATAATCCCTGTTCTAGTCACGGGTTATG
GCTACTCGACAGCGAGAGGTTATGCCCCAAAAGAAATTGATAAAGCTCCTCTGCCGATTAAAGAAAAGAACAGGTC
AGCGTTTACTAGAAGATTATGAATCTTTTATATCATCCGGTAGTTTGGAGCGACTATCAATGCATGGCAAGACGATT
GGAATGCAAGGGTGTGGAATACATCCTTCGCCACAAATAAACATAGTCAATTCCTATGGGGGGATGCACAAGTATTTA
ATCAAGGTTATGGTTTATTAGGCTTTAAAAACGCAAAACATCATTATCAGGTTGATGGTAAAAGAGGCAAGAAAGAGT
GGAACATCCTCTGATGACTAGTGCAACAGGAGATGACTTATGCTAGCAGTGATGAAAGCTATCTCTACCTTGCGA
TTAAAAACAAAACCTGAAAAACTAAAAAGAAAACGATTATTACCAATAGATATTACACCAAAATCTGGTAGTAGAAAA
TGAATGGTAGTAAGGTCACATTTTCTAAATCTAGTGACTTTGTATTGTCTATTGATCCAAATGGCAAGTCTGAATTAT
TTGTCCAAGAGCGCTATAACGCCTTAAAGCGAACTATCTTCGACAGCTTAATGGTAAAGATTTTATGCTTTCCAC
CAAAGAAGAACAGTAGTAATTTGAGCAGATAAATATGGTATTGAGAAATACAAAGATTGTTGAAGACATGAAAAAG
TAAAGCAACAGAGAGGTTCTTACCACTCCTTACTGCTTCTCTCAAAACAGGAACAACTGATAGGCACCAAAAA
CATTTGATTACAAAACAGATATTTCTGTTTGGAAAGGACTTTATAGAGGTCAGAATTCCTGTCAGTTGTTGAATTTT
CTGATCCATCATCTCAAAAAATTACAGATGATTACTTTAAACATTATGGTGTGAAGAGTTAGAAATTGAGAGCATTG
CTTTAGGATTAGGTGCTAATAGCAAAGAAAAACACTGATAAAGATGGCAGATTATCGTTTGAATAATTGGGAGAGAC
CCGATACCAAAACCTTTTAAAGACTCCTATTATAGTATTAAAGAA

**Table 28: Comparative Sequences relating to SAG1552
(conserved hypothetical protein)**

SEQ ID NO. 2810: SAG1552 FROM THE M732 GBS TYPE III STRAIN

TACAAGAACTAATCTTTGTTGTTAAAGGTGATACTGTACTTCACAAGCCACCAATAAACCTTTTGTGTTAAAGGAGT
AGACGTTGAGTCTTCCTTAGCGGGTATCATCACACGATTTTCCTATTACTCAAAAACGTATCGTGAATGGTTCCA
TTTAATTTCCAACATGGGGGCAAATACTGTAAGAGTCAAGGTACCGATGAATGTTGCATTTTACGATGCCTTATATCA
CCACAACAAAGAATCAAGAGGGCCACTGTATTTGTGCAAGGAATACGTATAGATTCTTATCGCAATAATGCTTCTAT
AACAGCTTTTAATGATAATTATAGGGGGTATTTAAACGAGAAAGCAAGGCGTTGTGGATATTCTCCATGGGCGTAA
GCAAGTATGGAATACGATTTTGGTAGCCGTCATTATCATTATGATCTTAGTCCTTGGGTACTTGGTTATGTCGTAGG
GGATGATTGCAATAGTGGTACTGTGCTTATACTAATCATCAAGAGAAAAAACGCAATATAAAGGACGTTATTTTAA
AACTTCTGTGGCAGCTAATCCATTTGAGGTCATGCTAGCTCAAGTAATGGATGAATTGACACATTATGAGACAGCTAA
ATATGGTTGGCAACATTTGATTAGTTTTCAAAACACCAACACAGACCCTTTTCATTATCGAAAACCATTTGAGGC
ACAGGCTCCTAAATACGTACAATAAATGTAGAAAATATTCAAGCTAATTCAAATGTTAAAGCAGGTATGTTTCAGC
ATATAAAGCTATTGATTTCCATCCTCGATACAAGGATTATCTATTATTTGATAAAGAGAATATCAGTAAAGAAGATAG
ACAAAAGATTAAAGAACTTTCTTTGTACAGGGATACGTTAAACTGCTAAATGCTTATCACAAAATCCCTGTTCTAGT
CACGGGTATGGCTATTCGACAGCGAGAGGTATTGCCAAAAAGAAATTGATAAACGTCCTCTGCCGATTAATGAAAA
AGAACAAGGTCAGCGTTTACTAGAACGATTATGAATCTTTTATATCATCCGGTAGTTTGGAGCGACTATCAATGCATG
GCAAGACGATTGGAATGCAAGGGCGTGAATACATCTTTCGCCACAAATAACATAGTCAATTCCTATGGGGGGATGC
ACAAGTATTTAATCAAGGTTATGTTTATTAGGCTTTAAAAACGCAAAACATCATTATCAAGTTGATGGTAAAGAGG
CAAAGGAGAGTGGAAACATCCTCTGATGACTAGTGCAACAGGAGATGACTTATATGCTAGCAGTGATGAAAGCTATCT
CTACCTTGCATTTAAACAAAACCTGAAAAACTAAAAAGAAAACGATTATTACCAATAGATATTACACCAAAATCTGG
TAGTAGAAAAATGAATGGTAGTAAGGTCACATTTTCTAAATCTAGTGACTTTGTATTGTCTATTGATCCAAATGGCAA
GTCTGAATTATTTGTCCAAGAGCGCTATAATGCCTTAAAAGCGAACTATCTTCGACAGCTTAACGGTAAAGATTTTAA
TGCTTTCCCAACAAAGAAGACAGTAGTAATTTTGTAGCAGATAAATATGGTATTGAGAAATACAAAGATTGTTGAAGA
CATGGAAAAAGTAAAGCAACAGAGAGGTTCTTACCAACTCATCCTACTGGTCTTCTCAAAACAGGAACAACCTGATAG
GCACCAAAAAACATTTGATTACAAACAGATATTTCTGTTTGGAAAGGACTTTATAGAGGTGAGAATTCCTGGCAGTT
GTTGAATTTTCTGATCCATCATCTCAAAAATTCACGATGATTACTTTAAACATTATGGTGTGAAGGAGTTAGAAAT
TGAGAGCATTGCTTTAGGATTAGGTGCTAATAGCAAGAAAACACACTGATAAAGATGGCAGATTATCGTTTGAAAAA
TTGGGAGAGACCCGATACCAAAACCTTTTAAAGACTCCTATTATAGTATTAAG

SEQ ID NO. 2811: SAG1552 FROM THE M781 GBS TYPE III STRAIN

TTTGATGGTAGTTTGTATTTACCACAGGGCTTATTAAGAAAAATACAAGAACTAATCTTTGTTGTTAAAGGTGATACT
GTACTTCACAAGCCACCAATAAACCTTTTGTGTTTAAAGGAGTAGACGTTGAGTCTTCCTTAGCGGGTATCATCAC
AACGATTTTCCTATTACTCAAAAAACGTATCGTGAATGGTTCCATTTAATTTCCAACATGGGGGCAAATACTGTAAGA
GTCAAGGTACCGATGAATGTTGCAATTTTACGATGCCTTATATCACCAACAACAAAGAATCAAAGAGGCCACTGTATTG
TTGCAAGGAATACGTATAGATTCTTATCGCAATAATGCTTCTATAACAGCTTTTAAATGATAATTATAGGGGGTATTTA
AAACGAGAAGCAAAAGCGTGTGTGATATTCTCCATGGGCGTAAAGCAAGTATGGAATACGTATTTGGTAGCCGTCAT
TATCATTATGATCTTAGTCCTTGGGTACTTGGTTATGTGCTAGGGGATGATTGGAATAGTGGTACTGTGCTTATACT
AATCATCAAGAGAAAAACGCAATATAAAGGACGTTATTTTAAACTTCTGTGGCAGCTAATCCATTTGAGGTCATG
CTAGCTCAAGTAATGGATGAATTGACACATTATGAGACAGCTAAATATGGTTGGCAACATTGATTAGTTTTCAAAAC
TCACCAACAACAGACCCTTTTCAATTATCGAAAACCATTTGAGGCACAGGCTCCTAAATACGTACAATAAATGTAGAA
AATATTCAAGCTAATTCAAATGTTAAAGCAGGTATGTTTGCAGCATATAAAGCTATTGATTTCCTCGATACAAG
GATTATCTATTATTTGATAAAGAGAATATCAGTAAAGAAGATAGACAAAAGATTAAAGAACTTTCTTTGTACAGGGA
TACGTTAAACTGCTAAATGCTTATCACAAAATCCCTGTTCTAGTCACGGGTTATGGCTATTTCGACAGCGAGAGGTATT
GCCCCAAAAAGAAATTGATAAACGTCCTCTGCCGATTAATGAAAAAGAACAGGTCAGCGTTTACTAGAAGATTATGAA
TCTTTTATATCATCCGGTAGTTTTGGAGCGACTATCAATGCATGGCAAGACGATTGGAATGCAAGGGCGTGAATACA
TCTTTCCGCCACAAATAAATAGTCAATTCCTATGGGGGGATGCACAAGTATTTAATCAAGGTTATGGTTTATTAGGC
TTTAAAAACGCAAAACATCATTATCAAGTTGATGGTAAAGAGGCAAGGAGAGTGGAAACATCCTCTGATGACTAGT
GCAACAGGAGATGACTTATATGCTAGCAGTGATGAAAGCTATCTCTACCTTGCATTTAAACAAAACCTGAAAACTA
AAAGAAAAACGATTATTACCAATAGATATTACACCAAAATCTGGTAGTAGAAAAATGAATGGTAGTAAGGTCACATTT
TCTAAATCTAGTGACTTTGTATTGTCTATTGATCCAAATGGCAAGTCTGAATTATTTGTCCAAGAGCGCTATAATGCC
TTAAAGCGAACTATCTTCGACAGCTTAACGGTAAAGATTTTATGCTTTCCCAACAAAGAAGACAGTAGTAATTTT
GAGCAGATAAATATGGTATTGAGAAATACAAAGATTGTTGAAAGCATGAAAAAGTAAAGCAACAGAGAGGTTCTTA
CCAACCTCATCCTACTGGTCTTCTCAAAACAGGAACAACCTGATAGGCACCAAAAAACATTTGATTACAAACAGATATT
TCGTTTGGAAAGGACTTTATAGAGGTGAGAATTCGTTGGCAGTTGTTGAATTTTCTGATCCATCATCTCAAAAAT
CACGATGATTACTTTAAACATTATGGTGTGAAGGAGTTAGAAATGAGAGCATTGCTTTAGGATTAGGTGCTAATAGC
AAAGAAAAACACTGATAAAGATGGCAGATTATCGTTTGA AAAATTTGGGAGAGACCCGATACCAAAACCTTTTAAAA
GACTCCTATTATAGTATTAAGAAAGATGG

**Table 28: Comparative Sequences relating to SAG1552
(conserved hypothetical protein)**

SEQ2801	-----
SEQ2802	-----
SEQ2803	-----AAGGGCTTATTTAAAGAAAAATACAAGAACT
SEQ2804	-----TATTTAAAGAAAAATACAAGAACT
SEQ2805	-----AAGGGCTTATTTAAAGAAAAATACAAGAACT
SEQ2806	ATTACTTTGATGGTAGTTTGTATTTACCAAAGGGCTTATTTAAAGAAAAATACAAGAACT
SEQ2807	-----TTTACCACAGGGCTTATTTAAAGAAAAATACAAGAACT
SEQ2808	-----AAGGGCTTATTTAAAGAAAAATACAAGAACT
SEQ2809	-----
SEQ2810	-----TACAAGAACT
SEQ2811	-----TTTGATGGTAGTTTGTATTTACCACAGGGCTTATTTAAAGAAAAATACAAGAACT
SEQ2801	--TTTGTGTGTTAAAGGTGATACTGTACTTCACAAGCCCACCAATAAACCTTTTGTGTGTT
SEQ2802	-----
SEQ2803	ACTTTGTGTGTTAAAGGTGATACTGTACTTCACAAGCCCACCAATAAACCTTTTGTGTGTT
SEQ2804	ACTTTGTGTGTTAAAGGTGATACTGTACTTCACAAGCCCACCAATAAACCTTTTGTGTGTT
SEQ2805	ACTTTGTGTGTTAAAGGTGATACTGTACTTCACAAGCCCACCAATAAACCTTTTGTGTGTT
SEQ2806	ACTTTGTGTGTTAAAGGTGATACTGTACTTCACAAGCCCACCAATAAACCTTTTGTGTGTT
SEQ2807	ACTTTGTGTGTTAAAGGTGATACTGTACTTCACAAGCCCACCAATAAACCTTTTGTGTGTT
SEQ2808	ACTTTGTGTGTTAAAGGTGATACTGTACTTCACAAGCCCACCAATAAACCTTTTGTGTGTT
SEQ2809	ACTTTGTGTGTTAAAGGTGATACTGTACTTCACAAGCCCACCAATAAACCTTTTGTGTGTT
SEQ2810	ACTTTGTGTGTTAAAGGTGATACTGTACTTCACAAGCCCACCAATAAACCTTTTGTGTGTT
SEQ2811	ACTTTGTGTGTTAAAGGTGATACTGTACTTCACAAGCCCACCAATAAACCTTTTGTGTGTT
SEQ2801	AAGGAGTAGACGTTGAGTCTTCCTTAGCAGGTTATCATCAACGATTTTCCTATTACT
SEQ2802	-----
SEQ2803	AAGGAGTAGACGTTGAGTCTTCCTTAGCGGGTTATCATCAACGATTTTCCTATTACT
SEQ2804	AAGGAGTAGACGTTGAGTCTTCCTTAGCGGGTTATCATCAACGATTTTCCTATTACT
SEQ2805	AAGGAGTAGACGTTGAGTCTTCCTTAGCGGGTTATCATCAACGATTTTCCTATTACT
SEQ2806	AAGGAGTAGACGTTGAGTCTTCCTTAGCGGGTTATCATCAACGATTTTCCTATTACT
SEQ2807	AAGGAGTAGACGTTGAGTCTTCCTTAGCGGGTTATCATCAACGATTTTCCTATTACT
SEQ2808	AAGGAGTAGACGTTGAGTCTTCCTTAGCGGGTTATCATCAACGATTTTCCTATTACT
SEQ2809	AAGGAGTAGACGTTGAGTCTTCCTTAGCGGGTTATCATCAACGATTTTCCTATTACT
SEQ2810	AAGGAGTAGACGTTGAGTCTTCCTTAGCGGGTTATCATCAACGATTTTCCTATTACT
SEQ2811	AAGGAGTAGACGTTGAGTCTTCCTTAGCGGGTTATCATCAACGATTTTCCTATTACT
SEQ2801	AAAAAACGTATCGTGAGTGGTTCCATTTAATTTCCAACATGGGGGCAAATACTGTAAGA
SEQ2802	-----
SEQ2803	AAAAAACGTATCGTGAGTGGTTCCATTTAATTTCCAACATGGGGGCAAATACTGTAAGA
SEQ2804	AAAAAACGTATCGTGAGTGGTTCCATTTAATTTCCAACATGGGGGCAAATACTGTAAGA
SEQ2805	AAAAAACGTATCGTGAGTGGTTCCATTTAATTTCCAACATGGGGGCAAATACTGTAAGA
SEQ2806	AAAAAACGTATCGTGAGTGGTTCCATTTAATTTCCAACATGGGGGCAAATACTGTAAGA
SEQ2807	AAAAAACGTATCGTGAGTGGTTCCATTTAATTTCCAACATGGGGGCAAATACTGTAAGA
SEQ2808	AAAAAACGTATCGTGAGTGGTTCCATTTAATTTCCAACATGGGGGCAAATACTGTAAGA
SEQ2809	AAAAAACGTATCGTGAGTGGTTCCATTTAATTTCCAACATGGGGGCAAATACTGTAAGA
SEQ2810	AAAAAACGTATCGTGAGTGGTTCCATTTAATTTCCAACATGGGGGCAAATACTGTAAGA
SEQ2811	AAAAAACGTATCGTGAGTGGTTCCATTTAATTTCCAACATGGGGGCAAATACTGTAAGA
SEQ2801	TCAAAGTACCGATGAATGTTGCATTTTACGATGCTTTATATCACCACAACAAAGCATCA
SEQ2802	-----
SEQ2803	TCAAAGTACCGATGAATGTTGCATTTTACGATGCTTTATATCACCACAACAAAGCATCA
SEQ2804	TCAAAGTACCGATGAATGTTGCATTTTACGATGCTTTATATCACCACAACAAAGCATCA
SEQ2805	TCAAAGTACCGATGAATGTTGCATTTTACGATGCTTTATATCACCACAACAAAGCATCA
SEQ2806	TCAAAGTACCGATGAATGTTGCATTTTACGATGCTTTATATCACCACAACAAAGCATCA
SEQ2807	TCAAAGTACCGATGAATGTTGCATTTTACGATGCTTTATATCACCACAACAAAGCATCA
SEQ2808	TCAAAGTACCGATGAATGTTGCATTTTACGATGCTTTATATCACCACAACAAAGCATCA
SEQ2809	TCAAAGTACCGATGAATGTTGCATTTTACGATGCTTTATATCACCACAACAAAGCATCA
SEQ2810	TCAAAGTACCGATGAATGTTGCATTTTACGATGCTTTATATCACCACAACAAAGCATCA
SEQ2811	TCAAAGTACCGATGAATGTTGCATTTTACGATGCTTTATATCACCACAACAAAGCATCA
SEQ2801	AGAGGCCACTGTATTTGTTGCAAGGAATACGTATAGATTCTTATCGCAATAATGCTTCT
SEQ2802	-----
SEQ2803	AGAGGCCACTGTATTTGTTGCAAGGAATACGTATAGATTCTTATCGCAATAATGCTTCT
SEQ2804	AGAGGCCACTGTATTTGTTGCAAGGAATACGTATAGATTCTTATCGCAATAATGCTTCT
SEQ2805	AGAGGCCACTGTATTTGTTGCAAGGAATACGTATAGATTCTTATCGCAATAATGCTTCT
SEQ2806	AGAGGCCACTGTATTTGTTGCAAGGAATACGTATAGATTCTTATCGCAATAATGCTTCT
SEQ2807	AGAGGCCACTGTATTTGTTGCAAGGAATACGTATAGATTCTTATCGCAATAATGCTTCT
SEQ2808	AGAGGCCACTGTATTTGTTGCAAGGAATACGTATAGATTCTTATCGCAATAATGCTTCT

**Table 28: Comparative Sequences relating to SAG1552
(conserved hypothetical protein)**

SEQ2809	AGAGGCCACTGTATTTGTTGCAAGGAATACGTATAGATTCTTATCGCAATAATGCTTCT
SEQ2810	AGAGGCCACTGTATTTGTTGCAAGGAATACGTATAGATTCTTATCGCAATAATGCTTCT
SEQ2811	AGAGGCCACTGTATTTGTTGCAAGGAATACGTATAGATTCTTATCGCAATAATGCTTCT
SEQ2801	TAACAGCTTTTAATGATAATTATAGGGGGTATTTAAACGAGAAGCAAAAGGCGTTGTG
SEQ2802	-----
SEQ2803	TAACAGCTTTTAATGATAATTATAGGGGGTATTTAAACGAGAAGCAAAAGGCGTTGTG
SEQ2804	TAACAGCTTTTAATGATAATTATAGGGGGTATTTAAACGAGAAGCAAAAGGCGTTGTG
SEQ2805	TAACAGCTTTTAATGATAATTATAGGGGGTATTTAAACGAGAAGCAAAAGGCGTTGTG
SEQ2806	TAACAGCTTTTAATGATAATTATAGGGGGTATTTAAACGAGAAGCAAAAGGCGTTGTG
SEQ2807	TAACAGCTTTTAATGATAATTATAGGGGGTATTTAAACGAGAAGCAAAAGGCGTTGTG
SEQ2808	TAACAGCTTTTAATGATAATTATAGGGGGTATTTAAACGAGAAGCAAAAGGCGTTGTG
SEQ2809	TAACAGCTTTTAATGATAATTATAGGGGGTATTTAAACGAGAAGCAAAAGGCGTTGTG
SEQ2810	TAACAGCTTTTAATGATAATTATAGGGGGTATTTAAACGAGAAGCAAAAGGCGTTGTG
SEQ2811	TAACAGCTTTTAATGATAATTATAGGGGGTATTTAAACGAGAAGCAAAAGGCGTTGTG
SEQ2801	ATATTCTCCATGGGCGTAAGCAAGTATGGAATACTGATTTTGGTAGCCGTCATTATCAT
SEQ2802	-----ATGACTA--GTGCAACAGGAGATGACTTATAT--GCTAGCAGTGATGAAAGC
SEQ2803	ATATTCTCCATGGGCGTAAGCAAGTATGGAATACTGATTTGGGTAGCCGTCATTATCAT
SEQ2804	ATATTCTCCATGGGCGTAAGCAAGTATGGAATACTGATTTGGGTAGCCGTCATTATCAT
SEQ2805	ATATTCTCCATGGGCGTAAGCAAGTATGGAATACTGATTTGGGTAGCCGTCATTATCAT
SEQ2806	ATATTCTCCATGGGCGTAAGCAAGTATGGAATACTGATTTGGGTAGCCGTCATTATCAT
SEQ2807	ATATTCTCCATGGGCGTAAGCAAGTATGGAATACTGATTTGGGTAGCCGTCATTATCAT
SEQ2808	ATATTCTCCATGGGCGTAAGCAAGTATGGAATACTGATTTGGGTAGCCGTCATTATCAT
SEQ2809	ATATTCTCCATGGGCGTAAGCAAGTATGGAATACTGATTTGGGTAGCCGTCATTATCAT
SEQ2810	ATATTCTCCATGGGCGTAAGCAAGTATGGAATACTGATTTGGGTAGCCGTCATTATCAT
SEQ2811	ATATTCTCCATGGGCGTAAGCAAGTATGGAATACTGATTTGGGTAGCCGTCATTATCAT
SEQ2801	TATGATCTTAGTCCTTGGGTACTTGGTTATGTCTAGGGGATGATTGGAATAGTGGT-AC
SEQ2802	TAT--CTCTA--CCTTGGC--ATTAAACAAACCTGAAAACTAAAGAAAAACGATTAT
SEQ2803	TATGATCTTAGTCCTTGGGTACTTGGTTATGTCTAGGGGATGATTGGAATAGTGGT-AC
SEQ2804	TATGATCTTAGTCCTTGGGTACTTGGTTATGTCTAGGGGATGATTGGAATAGTGGT-AC
SEQ2805	TATGATCTTAGTCCTTGGGTACTTGGTTATGTCTAGGGGATGATTGGAATAGTGGT-AC
SEQ2806	TATGATCTTAGTCCTTGGGTACTTGGTTATGTCTAGGGGATGATTGGAATAGTGGT-AC
SEQ2807	TATGATCTTAGTCCTTGGGTACTTGGTTATGTCTAGGGGATGATTGGAATAGTGGT-AC
SEQ2808	TATGATCTTAGTCCTTGGGTACTTGGTTATGTCTAGGGGATGATTGGAATAGTGGT-AC
SEQ2809	TATGATCTTAGTCCTTGGGTACTTGGTTATGTCTAGGGGATGATTGGAATAGTGGT-AC
SEQ2810	TATGATCTTAGTCCTTGGGTACTTGGTTATGTCTAGGGGATGATTGGAATAGTGGT-AC
SEQ2811	TATGATCTTAGTCCTTGGGTACTTGGTTATGTCTAGGGGATGATTGGAATAGTGGT-AC
SEQ2801	TGTCGCTT-ATACTAATCATCAAGAGAA-AAAAACGCAATATAAAGGAC-GTTATTTTAA
SEQ2802	TACCAATAGATATTA--CACCAAATCTGGTAGTAAAAATGAATGGTAGTAAGGTCAC
SEQ2803	TGTCGCTT-ATACTAATCATCAAGAGAA-AAAAACGCAATATAAAGGAC-GTTATTTTAA
SEQ2804	TGTCGCTT-ATACTAATCATCAAGAGAA-AAAAACGCAATATAAAGGAC-GTTATTTTAA
SEQ2805	TGTCGCTT-ATACTAATCATCAAGAGAA-AAAAACGCAATATAAAGGAC-GTTATTTTAA
SEQ2806	TGTCGCTT-ATACTAATCATCAAGAGAA-AAAAACGCAATATAAAGGAC-GTTATTTTAA
SEQ2807	TGTCGCTT-ATACTAATCATCAAGAGAA-AAAAACGCAATATAAAGGAC-GTTATTTTAA
SEQ2808	TGTCGCTT-ATACTAATCATCAAGAGAGAAAAACGCAATATAAAGGAC-GTTATTTTAA
SEQ2809	TGTCGCTT-ATACTAATCATCAAGAGAA-AAAAACGCAATATAAAGGAC-GTTATTTTAA
SEQ2810	TGTCGCTT-ATACTAATCATCAAGAGAA-AAAAACGCAATATAAAGGAC-GTTATTTTAA
SEQ2811	TGTCGCTT-ATACTAATCATCAAGAGAA-AAAAACGCAATATAAAGGAC-GTTATTTTAA
SEQ2801	AACTTCTGCGGAGCTAATCCATTGAGGTCATGCTAGCTCAAGTTATGGAT--GAATTG
SEQ2802	ATTTTCTAAATCTAGTGA-CTTTGTATTGTC-TATTGATCCAAATGGCAAGTCTGAATT-
SEQ2803	AACTTCTGTGGCAGCTAATCCATTGAGGTCATGCTAGCTCAAGTAATGGAT--GAATTG
SEQ2804	AACTTCTGTGGCAGCTAATCCATTGAGGTCATGCTAGCTCAAGTAATGGAT--GAATTG
SEQ2805	AACTTCTGTGGCAGCTAATCCATTGAGGTCATGCTAGCTCAAGTAATGGAT--GAATTG
SEQ2806	AACTTCTGTGGCAGCTAATCCATTGAGGTCATGCTAGCTCAAGTAATGGAT--GAATTG
SEQ2807	AACTTCTGTGGCAGCTAATCCATTGAGGTCATGCTAGCTCAAGTAATGGAT--GAATTG
SEQ2808	AACTTCTGTGGCAGCTAATCCATTGAGGTCATGCTAGCTCAAGTAATGGAT--GAATTG
SEQ2809	AACTTCTGTGGCAGCTAATCCATTGAGGTCATGCTAGCTCAAGTAATGGAT--GAATTG
SEQ2810	AACTTCTGTGGCAGCTAATCCATTGAGGTCATGCTAGCTCAAGTAATGGAT--GAATTG
SEQ2811	AACTTCTGTGGCAGCTAATCCATTGAGGTCATGCTAGCTCAAGTAATGGAT--GAATTG
SEQ2801	ACACATTATGAGACAGCTAAATATGGTTGGCAACATTTGATTAGTTTTTCAAACCTCACCA
SEQ2802	ATTTGTC-CAAGAGCGCTATA-ATGCCT--TAAAGCGAACTATCTTCGACAGCTTAACG
SEQ2803	ACACATTATGAGACAGCTAAATATGGTTGGCAACATTTGATTAGTTTTTCAAACCTCACCA
SEQ2804	ACACATTATGAGACAGCTAAATATGGTTGGCAACATTTGATTAGTTTTTCAAACCTCACCA

**Table 28: Comparative Sequences relating to SAG1552
(conserved hypothetical protein)**

SEQ2805	ACACATTATGAGACAGCTAAATATGGTTGGCAACATTGATTAGTTTTTCAAACCTCACCA
SEQ2806	ACACATTATGAGACAGCTAAATATGGTTGGCAACATTGATTAGTTTTTCAAACCTCACCA
SEQ2807	ACACATTATGAGACAGCTAAATATGGTTGGCAACATTGATTAGTTTTTCAAACCTCACCA
SEQ2808	ACACATTATGAGACAGCTAAATATGGTTGGCAACATTGATTAGTTTTTCAAACCTCACCA
SEQ2809	ACACATTATGAGACAGCTAAATATGGTTGGCAACATTGATTAGTTTTTCAAACCTCACCA
SEQ2810	ACACATTATGAGACAGCTAAATATGGTTGGCAACATTGATTAGTTTTTCAAACCTCACCA
SEQ2811	ACACATTATGAGACAGCTAAATATGGTTGGCAACATTGATTAGTTTTTCAAACCTCACCA
SEQ2801	CAACAGAC-----CCTTTTCGTTATCGAAAACCATTTG-AGGCACAGGCTCCTAAATA
SEQ2802	TAAAGATTTTTATGCTTTCCCAACAAAGAAGACAGTAGTAATTTTGAGCAGATCAATA
SEQ2803	CAACAGAC-----CCTTTTCATTATCGAAAACCATTTG-AGGCACAGGCTCCTAAATA
SEQ2804	CAACAGAC-----CCTTTTCATTATCGAAAACCATTTG-AGGCACAGGCTCCTAAATA
SEQ2805	CAACAGAC-----CCTTTTCATTATCGAAAACCATTTG-AGGCACAGGCTCCTAAATA
SEQ2806	CAACAGAC-----CCTTTTCATTATCGAAAACCATTTG-AGGCACAGGCTCCTAAATA
SEQ2807	CAACAGAC-----CCTTTTCATTATCGAAAACCATTTG-AGGCACAGGCTCCTAAATA
SEQ2808	CAACAGAC-----CCTTTTCATTATCGAAAACCATTTG-AGGCACAGGCTCCTAAATA
SEQ2809	CAACAGAC-----CCTTTTCATTATCGAAAACCATTTG-AGGCACAGGCTCCTAAATA
SEQ2810	CAACAGAC-----CCTTTTCATTATCGAAAACCATTTG-AGGCACAGGCTCCTAAATA
SEQ2811	CAACAGAC-----CCTTTTCATTATCGAAAACCATTTG-AGGCACAGGCTCCTAAATA
SEQ2801	G-TACAACTAAATGTAGAAAAATATTCAGCTAATTCGAATGTTAAAGCA---GGTATTT
SEQ2802	GGTATTGAGAAATACAAAGATTGTTGAAGACATGGAAGAAAGTAAAGCAACAGAGAGGT
SEQ2803	G-TACAACTAAATGTAGAAAAATATTCAGCTAATTCGAATGTTAAAGCA---GGTATGT
SEQ2804	G-TACAACTAAATGTAGAAAAATATTCAGCTAATTCGAATGTTAAAGCA---GGTATGT
SEQ2805	G-TACAACTAAATGTAGAAAAATATTCAGCTAATTCGAATGTTAAAGCA---GGTATGT
SEQ2806	G-TACAACTAAATGTAGAAAAATATTCAGCTAATTCGAATGTTAAAGCA---GGTATGT
SEQ2807	G-TACAACTAAATGTAGAAAAATATTCAGCTAATTCGAATGTTAAAGCA---GGTATGT
SEQ2808	G-TACAACTAAATGTAGAAAAATATTCAGCTAATTCGAATGTTAAAGCA---GGTATGT
SEQ2809	G-TACAACTAAATGTAGAAAAATATTCAGCTAATTCGAATGTTAAAGCA---GGTATGT
SEQ2810	G-TACAACTAAATGTAGAAAAATATTCAGCTAATTCGAATGTTAAAGCA---GGTATGT
SEQ2811	G-TACAACTAAATGTAGAAAAATATTCAGCTAATTCGAATGTTAAAGCA---GGTATGT
SEQ2801	TTGCAGCATATAAAGCTATTGATTTCCATCCTCGATACAAGGATTATCTATTATTTGATA
SEQ2802	TCTTACCAACTCATCTACTGGTCTT---CTCAAAACAGGAACAATTGAT-AGGCACCA
SEQ2803	TTGCAGCATATAAAGCTATTGATTTCCATCCTCGATACAAGGATTATCTATTATTTGATA
SEQ2804	TTGCAGCATATAAAGCTATTGATTTCCATCCTCGATACAAGGATTATCTATTATTTGATA
SEQ2805	TTGCAGCATATAAAGCTATTGATTTCCATCCTCGATACAAGGATTATCTATTATTTGATA
SEQ2806	TTGCAGCATATAAAGCTATTGATTTCCATCCTCGATACAAGGATTATCTATTATTTGATA
SEQ2807	TTGCAGCATATAAAGCTATTGATTTCCATCCTCGATACAAGGATTATCTATTATTTGATA
SEQ2808	TTGCAGCATATAAAGCTATTGATTTCCATCCTCGATACAAGGATTATCTATTATTTGATA
SEQ2809	TTGCAGCATATAAAGCTATTGATTTCCATCCTCGATACAAGGATTATCTATTATTTGATA
SEQ2810	TTGCAGCATATAAAGCTATTGATTTCCATCCTCGATACAAGGATTATCTATTATTTGATA
SEQ2811	TTGCAGCATATAAAGCTATTGATTTCCATCCTCGATACAAGGATTATCTATTATTTGATA
SEQ2801	AAGAGAATATCAGTAAAGAAGATAGACAAAAGATT-AAAGAACTTTCTTTGTCA CAGGGA
SEQ2802	AAAAACATTTGATTCAAAACAGATATTTTCGTTTGGAAGGACTTTATAGAGGTCAGAA
SEQ2803	AAGAGAATATCAGTAAAGAAGATAGACAAAAGATT-AAAGAACTTTCTTTGTCA CAGGGA
SEQ2804	AAGAGAATATCAGTAAAGAAGATAGACAAAAGATT-AAAGAACTTTCTTTGTCA CAGGGA
SEQ2805	AAGAGAATATCAGTAAAGAAGATAGACAAAAGATT-AAAGAACTTTCTTTGTCA CAGGGA
SEQ2806	AAGAGAATATCAGTAAAGAAGATAGACAAAAGATT-AAAGAACTTTCTTTGTCA CAGGGA
SEQ2807	AAGAGAATATCAGTAAAGAAGATAGACAAAAGATT-AAAGAACTTTCTTTGTCA CAGGGA
SEQ2808	AAGAGAATATCAGTAAAGAAGATAGACAAAAGATT-AAAGAACTTTCTTTGTCA CAGGGA
SEQ2809	AAGAGAATATCAGTAAAGAAGATAGACAAAAGATT-AAAGAACTTTCTTTGTCA CAGGGA
SEQ2810	AAGAGAATATCAGTAAAGAAGATAGACAAAAGATT-AAAGAACTTTCTTTGTCA CAGGGA
SEQ2811	AAGAGAATATCAGTAAAGAAGATAGACAAAAGATT-AAAGAACTTTCTTTGTCA CAGGGA
SEQ2801	TACGTTA-AACTGCTAAATGCTTATCAGAAAATCCCTGTTCTAGTCACGGGTTATGGCTA
SEQ2802	TCCGTGGCAGTTGTTGAATTTTCTGATCCA---TCATCTCAAAAAATTCAGATGATTA
SEQ2803	TACGTTA-AACTGCTAAATGCTTATCAGAAAATCCCTGTTCTAGTCACGGGTTATGGCTA
SEQ2804	TACGTTA-AACTGCTAAATGCTTATCAGAAAATCCCTGTTCTAGTCACGGGTTATGGCTA
SEQ2805	TACGTTA-AACTGCTAAATGCTTATCAGAAAATCCCTGTTCTAGTCACGGGTTATGGCTA
SEQ2806	TACGTTA-AACTGCTAAATGCTTATCAGAAAATCCCTGTTCTAGTCACGGGTTATGGCTA
SEQ2807	TACGTTA-AACTGCTAAATGCTTATCAGAAAATCCCTGTTCTAGTCACGGGTTATGGCTA
SEQ2808	TACGTTA-AACTGCTAAATGCTTATCAGAAAATCCCTGTTCTAGTCACGGGTTATGGCTA
SEQ2809	TACGTTA-AACTGCTAAATGCTTATCAGAAAATCCCTGTTCTAGTCACGGGTTATGGCTA
SEQ2810	TACGTTA-AACTGCTAAATGCTTATCAGAAAATCCCTGTTCTAGTCACGGGTTATGGCTA
SEQ2811	TACGTTA-AACTGCTAAATGCTTATCAGAAAATCCCTGTTCTAGTCACGGGTTATGGCTA

**Table 28: Comparative Sequences relating to SAG1552
(conserved hypothetical protein)**

SEQ2801	TCGACAGCGAGAGGTATTGCCCAAAAAGAAATTGATAAACGTCCTCTGCCGATTAATGA
SEQ2802	TTTAAACATTATGGTGTGAAGGAGTTAGAAATTGA - GAGCATGCTTTAGGATTAGGTG
SEQ2803	TCGACAGCGAGAGGTATTGCCCAAAAAGAAATTGATAAACGTCCTCTGCCGATTAATGA
SEQ2804	TCGACAGCGAGAGGTATTGCCCAAAAAGAAATTGATAAACGTCCTCTGCCGATTAATGA
SEQ2805	TCGACAGCGAGAGGTATTGCCCAAAAAGAAATTGATAAACGTCCTCTGCCGATTAATGA
SEQ2806	TCGACAGCGAGAGGTATTGCCCAAAAAGAAATTGATAAACGTCCTCTGCCGATTAATGA
SEQ2807	TCGACAGCGAGAGGTATTGCCCAAAAAGAAATTGATAAACGTCCTCTGCCGATTAATGA
SEQ2808	TCGACAGCGAGAGGTATTGCCCAAAAAGAAATTGATAAACGTCCTCTGCCGATTAATGA
SEQ2809	TCGACAGCGAGAGGTATTGCCCAAAAAGAAATTGATAAACGTCCTCTGCCGATTAATGA
SEQ2810	TCGACAGCGAGAGGTATTGCCCAAAAAGAAATTGATAAACGTCCTCTGCCGATTAATGA
SEQ2811	TCGACAGCGAGAGGTATTGCCCAAAAAGAAATTGATAAACGTCCTCTGCCGATTAATGA
SEQ2801	AAAGAACCAAGGTCAGCGTTTACTAGAAGATTATGAATCTTTTATATCATCCGGTAGTTT
SEQ2802	TAATAGCAAAGAAAACACACTGATAAAGATGGCAGAT - - - - - TATCGTTTGAAAAAAT
SEQ2803	AAAGAACCAAGGTCAGCGTTTACTAGAAGATTATGAATCTTTTATATCATCCGGTAGTTT
SEQ2804	AAAGAACCAAGGTCAGCGTTTACTAGAAGATTATGAATCTTTTATATCATCCGGTAGTTT
SEQ2805	AAAGAACCAAGGTCAGCGTTTACTAGAAGATTATGAATCTTTTATATCATCCGGTAGTTT
SEQ2806	AAAGAACCAAGGTCAGCGTTTACTAGAAGATTATGAATCTTTTATATCATCCGGTAGTTT
SEQ2807	AAAGAACCAAGGTCAGCGTTTACTAGAAGATTATGAATCTTTTATATCATCCGGTAGTTT
SEQ2808	AAAGAACCAAGGTCAGCGTTTACTAGAAGATTATGAATCTTTTATATCATCCGGTAGTTT
SEQ2809	AAAGAACCAAGGTCAGCGTTTACTAGAAGATTATGAATCTTTTATATCATCCGGTAGTTT
SEQ2810	AAAGAACCAAGGTCAGCGTTTACTAGAAGATTATGAATCTTTTATATCATCCGGTAGTTT
SEQ2811	AAAGAACCAAGGTCAGCGTTTACTAGAAGATTATGAATCTTTTATATCATCCGGTAGTTT
SEQ2801	GGAGCGACTATCAATGTCATGGCAAGACGATTGGAATGCAAGGGCGTGGAATACATCCTT
SEQ2802	GGAGAGAC - - CCGATAC - - - - CAAAACCTTTTAA - - - - AAGACTCCTATTATAGTATT
SEQ2803	GGAGCGACTATCAATGTCATGGCAAGACGATTGGAATGCAAGGGCGTGGAATACATCCTT
SEQ2804	GGAGCGACTATCAATGTCATGGCAAGACGATTGGAATGCAAGGGCGTGGAATACATCCTT
SEQ2805	GGAGCGACTATCAATGTCATGGCAAGACGATTGGAATGCAAGGGCGTGGAATACATCCTT
SEQ2806	GGAGCGACTATCAATGTCATGGCAAGACGATTGGAATGCAAGGGCGTGGAATACATCCTT
SEQ2807	GGAGCGACTATCAATGTCATGGCAAGACGATTGGAATGCAAGGGCGTGGAATACATCCTT
SEQ2808	GGAGCGACTATCAATGTCATGGCAAGACGATTGGAATGCAAGGGCGTGGAATACATCCTT
SEQ2809	GGAGCGACTATCAATGTCATGGCAAGACGATTGGAATGCAAGGGCGTGGAATACATCCTT
SEQ2810	GGAGCGACTATCAATGTCATGGCAAGACGATTGGAATGCAAGGGCGTGGAATACATCCTT
SEQ2811	GGAGCGACTATCAATGTCATGGCAAGACGATTGGAATGCAAGGGCGTGGAATACATCCTT
SEQ2801	GCCACAAATAAACATAGTCAATTCCCTATGGGGGGATGCACAAGTATTTAATCAAGGTTA
SEQ2802	A - - AGAAAGAA - - - - -
SEQ2803	GCCACAAATAAACATAGTCAATTCCCTATGGGGGGATGCACAAGTATTTAATCAAGGTTA
SEQ2804	GCCACAAATAAACATAGTCAATTCCCTATGGGGGGATGCACAAGTATTTAATCAAGGTTA
SEQ2805	GCCACAAATAAACATAGTCAATTCCCTATGGGGGGATGCACAAGTATTTAATCAAGGTTA
SEQ2806	GCCACAAATAAACATAGTCAATTCCCTATGGGGGGATGCACAAGTATTTAATCAAGGTTA
SEQ2807	GCCACAAATAAACATAGTCAATTCCCTATGGGGGGATGCACAAGTATTTAATCAAGGTTA
SEQ2808	GCCACAAATAAACATAGTCAATTCCCTATGGGGGGATGCACAAGTATTTAATCAAGGTTA
SEQ2809	GCCACAAATAAACATAGTCAATTCCCTATGGGGGGATGCACAAGTATTTAATCAAGGTTA
SEQ2810	GCCACAAATAAACATAGTCAATTCCCTATGGGGGGATGCACAAGTATTTAATCAAGGTTA
SEQ2811	GCCACAAATAAACATAGTCAATTCCCTATGGGGGGATGCACAAGTATTTAATCAAGGTTA
SEQ2801	GGTTTATTAGGCTTTAAAAACGCAAAACATCATTATCAAGTTGATGGTAAAAGAGGCCAA
SEQ2802	-----
SEQ2803	GGTTTATTAGGCTTTAAAAACGCAAAACATCATTATCAAGTTGATGGTAAAAGAGGCCAA
SEQ2804	GGTTTATTAGGCTTTAAAAACGCAAAACATCATTATCAAGTTGATGGTAAAAGAGGCCAA
SEQ2805	GGTTTATTAGGCTTTAAAAACGCAAAACATCATTATCAAGTTGATGGTAAAAGAGGCCAA
SEQ2806	GGTTTATTAGGCTTTAAAAACGCAAAACATCATTATCAAGTTGATGGTAAAAGAGGCCAA
SEQ2807	GGTTTATTAGGCTTTAAAAACGCAAAACATCATTATCAAGTTGATGGTAAAAGAGGCCAA
SEQ2808	GGTTTATTAGGCTTTAAAAACGCAAAACATCATTATCAAGTTGATGGTAAAAGAGGCCAA
SEQ2809	GGTTTATTAGGCTTTAAAAACGCAAAACATCATTATCAAGTTGATGGTAAAAGAGGCCAA
SEQ2810	GGTTTATTAGGCTTTAAAAACGCAAAACATCATTATCAAGTTGATGGTAAAAGAGGCCAA
SEQ2811	GGTTTATTAGGCTTTAAAAACGCAAAACATCATTATCAAGTTGATGGTAAAAGAGGCCAA
SEQ2801	GGAGAGTGGAACATCCTCTG-----
SEQ2802	-----
SEQ2803	GGAGAGTGGAACATCCTCTGATGACTAGTGCAACAGGAGATGACTTATATGCTAGCAG
SEQ2804	GGAGAGTGGAACATCCTCTGATGACTAGTGCAACAGGAGATGACTTATATGCTAGCAG
SEQ2805	GGAGAGTGGAACATCCTCTGATGACTAGTGCAACAGGAGATGACTTATATGCTAGCAG
SEQ2806	GGAGAGTGGAACATCCTCTGATGACTAGTGCAACAGGAGATGACTTATATGCTAGCAG
SEQ2807	GGAGAGTGGAACATCCTCTGATGACTAGTGCAACAGGAGATGACTTATATGCTAGCAG
SEQ2808	GAAGAGTGGAACATCCTCTGATGACTAGTGCAACAGGAGATGACTTATATGCTAGCAG

**Table 28: Comparative Sequences relating to SAG1552
(conserved hypothetical protein)**

SEQ2809	GAAGAGTGGAAACATCCTCTGATGACTAGTGCAACAGGAGATGACTTATATGCTAGCAG
SEQ2810	GGAGAGTGGAAACATCCTCTGATGACTAGTGCAACAGGAGATGACTTATATGCTAGCAG
SEQ2811	GGAGAGTGGAAACATCCTCTGATGACTAGTGCAACAGGAGATGACTTATATGCTAGCAG
SEQ2801	-----
SEQ2802	-----
SEQ2803	GATGAAAGCTATCTCTACCTTGCGATTAAAAACAAAACCTGAAAACTAAAAGAAAAACG
SEQ2804	GATGAAAGCTATCTCTACCTTGCGATTAAAAACAAAACCTGAAAACTAAAAGAAAAACG
SEQ2805	GATGAAAGCTATCTCTACCTTGCGATTAAAAACAAAACCTGAAAACTAAAAGAAAAACG
SEQ2806	GATGAAAGCTATCTCTACCTTGCGATTAAAAACAAAACCTGAAAACTAAAAGAAAAACG
SEQ2807	GATGAAAGCTATCTCTACCTTGCGATTAAAAACAAAACCTGAAAACTAAAAGAAAAACG
SEQ2808	GATGAAAGCTATCTCTACCTTGCGATTAAAAACAAAACCTGAAAACTAAAAGAAAAACG
SEQ2809	GATGAAAGCTATCTCTACCTTGCGATTAAAAACAAAACCTGAAAACTAAAAGAAAAACG
SEQ2810	GATGAAAGCTATCTCTACCTTGCGATTAAAAACAAAACCTGAAAACTAAAAGAAAAACG
SEQ2811	GATGAAAGCTATCTCTACCTTGCGATTAAAAACAAAACCTGAAAACTAAAAGAAAAACG
SEQ2801	-----
SEQ2802	-----
SEQ2803	TTATTACCAATAGATATTACACCAAAATCTGGTAGTAGAAAAATGAATGGTAGTAAGGT
SEQ2804	TTATTACCAATAGATATTACACCAAAATCTGGTAGTAGAAAAATGAATGGTAGTAAGGT
SEQ2805	TTATTACCAATAGATATTACACCAAAATCTGGTAGTAGAAAAATGAATGGTAGTAAGGT
SEQ2806	TTATTACCAATAGATATTACACCAAAATCTGGTAGTAGAAAAATGAATGGTAGTAAGGT
SEQ2807	TTATTACCAATAGATATTACACCAAAATCTGGTAGTAGAAAAATGAATGGTAGTAAGGT
SEQ2808	TTATTACCAATAGATATTACACCAAAATCTGGTAGTAGAAAAATGAATGGTAGTAAGGT
SEQ2809	TTATTACCAATAGATATTACACCAAAATCTGGTAGTAGAAAAATGAATGGTAGTAAGGT
SEQ2810	TTATTACCAATAGATATTACACCAAAATCTGGTAGTAGAAAAATGAATGGTAGTAAGGT
SEQ2811	TTATTACCAATAGATATTACACCAAAATCTGGTAGTAGAAAAATGAATGGTAGTAAGGT
SEQ2801	-----
SEQ2802	-----
SEQ2803	ACATTTTCTAAATCTAGTGACTTTGTATTGTCTATTGATCCAAATGGCAAGTCTGAATT
SEQ2804	ACATTTTCTAAATCTAGTGACTTTGTATTGTCTATTGATCCAAATGGCAAGTCTGAATT
SEQ2805	ACATTTTCTAAATCTAGTGACTTTGTATTGTCTATTGATCCAAATGGCAAGTCTGAATT
SEQ2806	ACATTTTCTAAATCTAGTGACTTTGTATTGTCTATTGATCCAAATGGCAAGTCTGAATT
SEQ2807	ACATTTTCTAAATCTAGTGACTTTGTATTGTCTATTGATCCAAATGGCAAGTCTGAATT
SEQ2808	ACATTTTCTAAATCTAGTGACTTTGTATTGTCTATTGATCCAAATGGCAAGTCTGAATT
SEQ2809	ACATTTTCTAAATCTAGTGACTTTGTATTGTCTATTGATCCAAATGGCAAGTCTGAATT
SEQ2810	ACATTTTCTAAATCTAGTGACTTTGTATTGTCTATTGATCCAAATGGCAAGTCTGAATT
SEQ2811	ACATTTTCTAAATCTAGTGACTTTGTATTGTCTATTGATCCAAATGGCAAGTCTGAATT
SEQ2801	-----
SEQ2802	-----
SEQ2803	TTTGTCCAAGAGCGCTATAATGCCTTAAAAGCGAACTATCTTCGACAGCTTAACGGTAA
SEQ2804	TTTGTCCAAGAGCGCTATAATGCCTTAAAAGCGAACTATCTTCGACAGCTTAACGGTAA
SEQ2805	TTTGTCCAAGAGCGCTATAATGCCTTAAAAGCGAACTATCTTCGACAGCTTAACGGTAA
SEQ2806	TTTGTCCAAGAGCGCTATAATGCCTTAAAAGCGAACTATCTTCGACAGCTTAACGGTAA
SEQ2807	TTTGTCCAAGAGCGCTATAATGCCTTAAAAGCGAACTATCTTCGACAGCTTAACGGTAA
SEQ2808	TTTGTCCAAGAGCGCTATAATGCCTTAAAAGCGAACTATCTTCGACAGCTTAACGGTAA
SEQ2809	TTTGTCCAAGAGCGCTATAATGCCTTAAAAGCGAACTATCTTCGACAGCTTAACGGTAA
SEQ2810	TTTGTCCAAGAGCGCTATAATGCCTTAAAAGCGAACTATCTTCGACAGCTTAACGGTAA
SEQ2811	TTTGTCCAAGAGCGCTATAATGCCTTAAAAGCGAACTATCTTCGACAGCTTAACGGTAA
SEQ2801	-----
SEQ2802	-----
SEQ2803	GATTTTTATGCTTTCCCAACCAAGAAGAAGACAGTAGTAATTTTGAGCAGATAAATATGGT
SEQ2804	GATTTTTATGCTTTCCCAACCAAGAAGAAGACAGTAGTAATTTTGAGCAGATAAATATGGT
SEQ2805	GATTTTTATGCTTTCCCAACCAAGAAGAAGACAGTAGTAATTTTGAGCAGATAAATATGGT
SEQ2806	GATTTTTATGCTTTCCCAACCAAGAAGAAGACAGTAGTAATTTTGAGCAGATAAATATGGT
SEQ2807	GATTTTTATGCTTTCCCAACCAAGAAGAAGACAGTAGTAATTTTGAGCAGATAAATATGGT
SEQ2808	GATTTTTATGCTTTCCCAACCAAGAAGAAGACAGTAGTAATTTTGAGCAGATAAATATGGT
SEQ2809	GATTTTTATGCTTTCCCAACCAAGAAGAAGACAGTAGTAATTTTGAGCAGATAAATATGGT
SEQ2810	GATTTTTATGCTTTCCCAACCAAGAAGAAGACAGTAGTAATTTTGAGCAGATAAATATGGT
SEQ2811	GATTTTTATGCTTTCCCAACCAAGAAGAAGACAGTAGTAATTTTGAGCAGATAAATATGGT
SEQ2801	-----
SEQ2802	-----
SEQ2803	TTGAGAAATACAAAGATTGTTGAAGACATGGAAAAAGTAAAAGCAACAGAGAGGTTCTT
SEQ2804	TTGAGAAATACAAAGATTGTTGAAGACATGGAAAAAGTAAAAGCAACAGAGAGGTTCTT

**Table 28: Comparative Sequences relating to SAG1552
(conserved hypothetical protein)**

SEQ2805	TTGAGAAATACAAAGATTGTTGAAGACATGGAAAAAGTAAAAGCAACAGAGAGGTTCTT
SEQ2806	TTGAGAAATACAAAGATTGTTGAAGACATGGAAAAAGTAAAAGCAACAGAGAGGTTCTT
SEQ2807	TTGAGAAATACAAAGATTGTTGAAGACATGGAAAAAGTAAAAGCAACAGAGAGGTTCTT
SEQ2808	TTGAGAAATACAAAGATTGTTGAAGACATGGAAAAAGTAAAAGCAACAGAGAGGTTCTT
SEQ2809	TTGAGAAATACAAAGATTGTTGAAGACATGGAAAAAGTAAAAGCAACAGAGAGGTTCTT
SEQ2810	TTGAGAAATACAAAGATTGTTGAAGACATGGAAAAAGTAAAAGCAACAGAGAGGTTCTT
SEQ2811	TTGAGAAATACAAAGATTGTTGAAGACATGGAAAAAGTAAAAGCAACAGAGAGGTTCTT
SEQ2801	-----
SEQ2802	-----
SEQ2803	CCAACTCATCCTACTGGTCTTCTCAAAACAGGAACAACATGATAGGCACCAAAAAACATT
SEQ2804	CCAACTCATCCTACTGGTCTTCTCAAAACAGGAACAACATGATAGGCACCAAAAAACATT
SEQ2805	CCAACTCATCCTACTGGTCTTCTCAAAACAGGAACAACATGATAGGCACCAAAAAACATT
SEQ2806	CCAACTCATCCTACTGGTCTTCTCAAAACAGGAACAACATGATAGGCACCAAAAAACATT
SEQ2807	CCAACTCATCCTACTGGTCTTCTCAAAACAGGAACAACATGATAGGCACCAAAAAACATT
SEQ2808	CCAACTCATCCTACTGGTCTTCTCAAAACAGGAACAACATGATAGGCACCAAAAAACATT
SEQ2809	CCAACTCATCCTACTGGTCTTCTCAAAACAGGAACAACATGATAGGCACCAAAAAACATT
SEQ2810	CCAACTCATCCTACTGGTCTTCTCAAAACAGGAACAACATGATAGGCACCAAAAAACATT
SEQ2811	CCAACTCATCCTACTGGTCTTCTCAAAACAGGAACAACATGATAGGCACCAAAAAACATT
SEQ2801	-----
SEQ2802	-----
SEQ2803	GATTCACAAACAGATATTTCGTTTGGAAAGGACTTTATAGAGGTCAGAATTCCTGGGCA
SEQ2804	GATTCACAAACAGATATTTCGTTTGGAAAGGACTTTATAGAGGTCAGAATTCCTGGGCA
SEQ2805	GATTCACAAACAGATATTTCGTTTGGAAAGGACTTTATAGAGGTCAGAATTCCTGGGCA
SEQ2806	GATTCACAAACAGATATTTCGTTTGGAAAGGACTTTATAGAGGTCAGAATTCCTGGGCA
SEQ2807	GATTCACAAACAGATATTTCGTTTGGAAAGGACTTTATAGAGGTCAGAATTCCTGGGCA
SEQ2808	GATTCACAAACAGATATTTCGTTTGGAAAGGACTTTATAGAGGTCAGAATTCCTGGGCA
SEQ2809	GATTCACAAACAGATATTTCGTTTGGAAAGGACTTTATAGAGGTCAGAATTCCTGGGCA
SEQ2810	GATTCACAAACAGATATTTCGTTTGGAAAGGACTTTATAGAGGTCAGAATTCCTGGGCA
SEQ2811	GATTCACAAACAGATATTTCGTTTGGAAAGGACTTTATAGAGGTCAGAATTCCTGGGCA
SEQ2801	-----
SEQ2802	-----
SEQ2803	TTGTTGAATTTTCTGATCCATCATCTCAAAAAATTACCGATGATTACTTTAAACATTA
SEQ2804	TTGTTGAATTTTCTGATCCATCATCTCAAAAAATTACCGATGATTACTTTAAACATTA
SEQ2805	TTGTTGAATTTTCTGATCCATCATCTCAAAAAATTACCGATGATTACTTTAAACATTA
SEQ2806	TTGTTGAATTTTCTGATCCATCATCTCAAAAAATTACCGATGATTACTTTAAACATTA
SEQ2807	TTGTTGAATTTTCTGATCCATCATCTCAAAAAATTACCGATGATTACTTTAAACATTA
SEQ2808	TTGTTGAATTTTCTGATCCATCATCTCAAAAAATTACCGATGATTACTTTAAACATTA
SEQ2809	TTGTTGAATTTTCTGATCCATCATCTCAAAAAATTACCGATGATTACTTTAAACATTA
SEQ2810	TTGTTGAATTTTCTGATCCATCATCTCAAAAAATTACCGATGATTACTTTAAACATTA
SEQ2811	TTGTTGAATTTTCTGATCCATCATCTCAAAAAATTACCGATGATTACTTTAAACATTA
SEQ2801	-----
SEQ2802	-----
SEQ2803	GGTGTGAAGGAGTTAGAAATTGAGAG--CATTGCTTTAGGATTAGGTGCTAATAGCAAA
SEQ2804	GGTGTGAAGGAGTTAGAAATTGAGAG--CATTGCTTTAGGATTAGGTGCTAATAGCAAA
SEQ2805	GGTGTGAAGGAGTTAGAAATTGAGAGCCATTGCTTTAGGATTAGGTGCTAATAGCAAA
SEQ2806	GGTGTGAAGGAGTTAGAAATTGAGAG--CATTGCTTTAGGATTAGGTGCTAATAGCAAA
SEQ2807	GGTGTGAAGGAGTTAGAAATTGAGAG--CATTGCTTTAGGATTAGGTGCTAATAGCAAA
SEQ2808	GGTGTGAAGGAGTTAGAAATTGAGAG--CATTGCTTTAGGATTAGGTGCTAATAGCAAA
SEQ2809	GGTGTGAAGGAGTTAGAAATTGAGAG--CATTGCTTTAGGATTAGGTGCTAATAGCAAA
SEQ2810	GGTGTGAAGGAGTTAGAAATTGAGAG--CATTGCTTTAGGATTAGGTGCTAATAGCAAA
SEQ2811	GGTGTGAAGGAGTTAGAAATTGAGAG--CATTGCTTTAGGATTAGGTGCTAATAGCAAA
SEQ2801	-----
SEQ2802	-----
SEQ2803	AAAACACACTGATAAAGATGGCAGATTATCGTTTGAAAAATTGGGAGAGACCCGATACC
SEQ2804	AAAACACACTGATAAAGATGGCAGATTATCGTTTGAAAAATTGGGAGAGACCCGATACC
SEQ2805	AAAACACACTGATAAAGATGGCAGATTATCGTTTGAAAAATTGGGAGAGACCCGATACC
SEQ2806	AAAACACACTGATAAAGATGGCAGATTATCGTTTGAAAAATTGGGAGAGACCCGATACC
SEQ2807	AAAACACACTGATAAAGATGGCAGATTATCGTTTGAAAAATTGGGAGAGACCCGATACC
SEQ2808	AAAACACACTGATAAAGATGGCAGATTATCGTTTGAAAAATTGGGAGAGACCCGATACC
SEQ2809	AAAACACACTGATAAAGATGGCAGATTATCGTTTGAAAAATTGGGAGAGACCCGATACC
SEQ2810	AAAACACACTGATAAAGATGGCAGATTATCGTTTGAAAAATTGGGAGAGACCCGATACC
SEQ2811	AAAACACACTGATAAAGATGGCAGATTATCGTTTGAAAAATTGGGAGAGACCCGATACC

**Table 28: Comparative Sequences relating to SAG1552
(conserved hypothetical protein)**

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SEQ2801 -----
SEQ2802 -----
SEQ2803 AAACCTTTTAAAAGACTCCTATTATGTATTAGAAAGAA-----
SEQ2804 AAACCTTTTAAAAGACTCCTATTATAGTATTAGAAAGAAATGGTCTAAAGAAAGAGAG
SEQ2805 AAACCTTTTAAAAGAA-----
SEQ2806 AAACCTTTTAAAAGACTCCTATTATGTATTAGAAAGA-----
SEQ2807 AAACCTTTTAAAAGACT-----
SEQ2808 AAACCTTTTAAAAGACTCCTATTATAGT-----
SEQ2809 AAACCTTTTAAAAGACTCCTATTATAGTATTAGAAAG-----
SEQ2810 AAACCTTTTAAAAGACTCCTATTATAGTATTAG-----
SEQ2811 AAACCTTTTAAAAGACTCCTATTATAGTATTAGAAAGAAATGG-----

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SEQ2801 -----
SEQ2802 -----
SEQ2803 -----
SEQ2804 GAACATATGGTCCA
SEQ2805 -----
SEQ2806 -----
SEQ2807 -----
SEQ2808 -----
SEQ2809 -----
SEQ2810 -----
SEQ2811 -----

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>SEQ ID NO 2850:62_1169NT frame: 1

FVVKGDTVLHKPTNKPFVVKGVDESSLAGYHHNDFPITQKTYREWFHLISNMGANTVRV
KVP MNVAFYDALYHHNKASKRPLYLQIGIRIDSYRNNASITAFNDNYRGYLKREAGVVD
ILHGRKQVWNTDFGSRHYHYDLSPWVLGYVVGDDWNSGTVAAYTNHQEKKQYKGRYFKTS
AAANPFVEMLAQVMDLTHYETAKYGWQHLISFSNSPTTDPFRYRKPFEAQAPKYVQLNV
ENIQANSNVKAGIFAAYKAIDFHPRYKDYLLFDKENISKEDRQKIKELSLSQGYVKLLNA
YHKIPVLVTGYGYSTARGIAQKEIDKRPLPINEKEQGQRLLEDYESFISGSGFGATINAW
QDDWNARAWNTSFATNKHSQFLWGDAQVFNQGYGLLGFKNAKHHYQVDGKRGKGWKP
MTSATGDDLYASDESILYLAIKTKPEKLKEKRLLPIDITPKSGSRKMNGSKVTFKSSD
FVLSIDPNGKSELVQERYNALKANYLRQLNGKDFYAFPPKKNSSNFEQINMVLNRTKIV
EDMEKVKATERFLPHTPTGLLKTGTIDRHQKTFDSQTDISFGKDFIEVRIPWQLNFS
SSQKIHHDDYFKHYGVKELEIESIALGLGANSKENTLIKMDYRLKNWERPDTKTKLKDSY
YSI.ER

>SEQ ID NO 2851:62_18RS21 frame: 1

KGLLKENTRTNFVVKGDTVLHKPTNKPFVVKGVDESSLAGYHHNDFPITQKTYREWFHL
ISNMGANTVRVVKPMNVAFYDALYHHNKASKRPLYLQIGIRIDSYRNNASITAFNDNYRG
YLKREAGVVDILHGRKQVWNTDLGSRHYHYDLSPWVLGYVVGDDWNSGTVAAYTNHQEKK
QYKGRYFKTSVAANPFVEMLAQVMDLTHYETAKYGWQHLISFSNSPTTDPFHYRKPFE
AQAPKYVQLNVENIQANSNVKAGMFAAYKAIDFHPRYKDYLLFDKENISKEDRQKIKELS
LSQGYVKLLNAYYHKIPVLVTGYGYSTARGIAQKEIDKRPLPINEKEQGQRLLEDYESFIS
SGSGFGATINAWQDDWNARAWNTSFATNKHSQFLWGDAQVFNQGYGLLGFKNAKHHYQVDG
KRGKGWKPMTSATGDDLYASDESILYLAIKTKPEKLKEKRLLPIDITPKSGSRKMNGSK
GSKVTFKSSDFVLSIDPNGKSELVQERYNALKANYLRQLNGKDFYAFPPKKNSSNFEQ
INMVLNRTKIVEDMEKVKATERFLPHTPTGLLKTGTIDRHQKTFDSQTDISFGKDFIEVR
IPWQLNFSDPSSQKIHHDDYFKHYGVKELEIESIALGLGANSKENTLIKMDYRLKNWER
PDTKTKFLKDSYYVLRK

>SEQ ID NO 2852:62_2603 frame: 3

LKENTRTNFVVKGDTVLHKPTNKPFVVKGVDESSLAGYHHNDFPITQKTYREWFHLISN
MGANTVRVVKPMNVAFYDALYHHNKASKRPLYLQIGIRIDSYRNNASITAFNDNYRGYLK
REAGVVDILHGRKQVWNTDLGSRHYHYDLSPWVLGYVVGDDWNSGTVAAYTNHQEKKQY
KGRYFKTSVAANPFVEMLAQVMDLTHYETAKYGWQHLISFSNSPTTDPFHYRKPFEAQ
PKYVQLNVENIQANSNVKAGMFAAYKAIDFHPRYKDYLLFDKENISKEDRQKIKELSLSQ
GYVKLLNAYYHKIPVLVTGYGYSTARGIAQKEIDKRPLPINEKEQGQRLLEDYESFISGSG
FGATINAWQDDWNARAWNTSFATNKHSQFLWGDAQVFNQGYGLLGFKNAKHHYQVDGKRG
KGEWKHPLMTSATGDDLYASDESILYLAIKTKPEKLKEKRLLPIDITPKSGSRKMNGSK
VTFKSSDFVLSIDPNGKSELVQERYNALKANYLRQLNGKDFYAFPPKKNSSNFEQINM
VLNRTKIVEDMEKVKATERFLPHTPTGLLKTGTIDRHQKTFDSQTDISFGKDFIEVRIPW
QLNFSDPSSQKIHHDDYFKHYGVKELEIESIALGLGANSKENTLIKMDYRLKNWERPDT
KTKFLKDSYYSIKKEWSKERERTYGP

**Table 28: Comparative Sequences relating to SAG1552
(conserved hypothetical protein)**

>SEQ ID NO 2853:62_A909 frame: 1
KGLLKENTRTNFVVKGDTVLHKPTNKPFFVVKGVDEVSSLAGYHHNDFPITQKTYREWFHL
ISNMGANTVRVKVPMNVAFYDALYHHNKASKRPLYLLQGIRIDSYRNNASITAFNDNYRG
YLKREAKGVVDILHGRKQVWNTDLGSRHYHYDLSPWVLGYVVGDDWNSGTVAAYTNHQEKK
TQYKGRYFKTSVAANPFEVMLAQVMDELTHYETAKYGWQHLSFSNSPTTDPFHYRKPFE
AQAPKYVQLNVENIQANSNVKAGMFAAYKAIDFHPRYKDYLLFDKENISKEDRQKIKELS
LSQGYVKLLNAYHKIPVLVTGYGYSTARGIAQKEIDKRPLPINEKEQGQRLLLEDYESFIS
SGSFGATINAWQDDWNARAWNTSFATNKHSQFLWGDAQVFNQGYGLLGFKNAKHHYQVDG
KRGKGWKHPLMTSATGDDLYASSDESILYLAIKTKPEKLKEKRLLPIDITPKSGSRKMN
GSKVTFSKSSDFVLSIDPNGKSELVQERYNALKANYLRQLNGKDFYAFPPKKNSSNFEQ
INMVLNRTKIVEDMEKVKATERFLPTHPTGLLKTGTDRHQKTFDSQTDISFGKDFIEVR
IPWQLLNFSDDPSSQRIHDDYFKHYGVKELEN.EPLL.D.VLIAKKTTH..RWQIIV.KIGR
DPIPKPF.K

>SEQ ID NO 2854:62_A909 frame: 1
KGLLKENTRTNFVVKGDTVLHKPTNKPFFVVKGVDEVSSLAGYHHNDFPITQKTYREWFHL
ISNMGANTVRVKVPMNVAFYDALYHHNKASKRPLYLLQGIRIDSYRNNASITAFNDNYRG
YLKREAKGVVDILHGRKQVWNTDLGSRHYHYDLSPWVLGYVVGDDWNSGTVAAYTNHQEKK
TQYKGRYFKTSVAANPFEVMLAQVMDELTHYETAKYGWQHLSFSNSPTTDPFHYRKPFE
AQAPKYVQLNVENIQANSNVKAGMFAAYKAIDFHPRYKDYLLFDKENISKEDRQKIKELS
LSQGYVKLLNAYHKIPVLVTGYGYSTARGIAQKEIDKRPLPINEKEQGQRLLLEDYESFIS
SGSFGATINAWQDDWNARAWNTSFATNKHSQFLWGDAQVFNQGYGLLGFKNAKHHYQVDG
KRGKGWKHPLMTSATGDDLYASSDESILYLAIKTKPEKLKEKRLLPIDITPKSGSRKMN
GSKVTFSKSSDFVLSIDPNGKSELVQERYNALKANYLRQLNGKDFYAFPPKKNSSNFEQ
INMVLNRTKIVEDMEKVKATERFLPTHPTGLLKTGTDRHQKTFDSQTDISFGKDFIEVR
IPWQLLNFSDDPSSQRIHDDYFKHYGVKELEN.EPLL.D.VLIAKKTTH..RWQIIV.KIGR
DPIPKPF.K

>SEQ ID NO 2855:62_CJB110 frame: 1
YYFDGSLYLPKGLLKENTRTNFVVKGDTVLHKPTNKPFFVVKGVDEVSSLAGYHHNDFPIT
QKTYREWFHLISNMGANTVRVKVPMNVAFYDALYHHNKASKRPLYLLQGIRIDSYRNNAS
ITAFNDNYRGYLKREAKGVVDILHGRKQVWNTDFGSRHYHYDLSPWVLGYVVGDDWNSGT
VAYTNHQEKKTQYKGRYFKTSVAANPFEVMLAQVMDELTHYETAKYGWQHLSFSNSPTT
DPFHYRKPFEAQAPKYVQLNVENIQANSNVKAGMFAAYKAIDFHPRYKDYLLFDKENISK
EDRQKIKELSLSQGYVKLLNAYHKIPVLVTGYGYSTARGIAQKEIDKRPLPINEKEQGQR
LLEDYESFISSGSFGATINAWQDDWNARAWNTSFATNKHSQFLWGDAQVFNQGYGLLGFK
NAKHHYQVDGKRGKGWKHPLMTSATGDDLYASSDESILYLAIKTKPEKLKEKRLLPIDI
TPKSGSRKMNNGSKVTFSKSSDFVLSIDPNGKSELVQERYNALKANYLRQLNGKDFYAF
PKKNSSNFEQINMVLNRTKIVEDMEKVKATERFLPTHPTGLLKTGTDRHQKTFDSQTDI
SFGKDFIEVRIPWQLLNFSDDPSSQRIHDDYFKHYGVKELEIESIALGLGANSKENTLIK
MADYRLKNWERPDTKTFLKDSYVYLRK

>SEQ ID NO 2856:62_COH1 frame: 2
LPQGLLKENTRTNFVVKGDTVLHKPTNKPFFVVKGVDEVSSLAGYHHNDFPITQKTYREWF
HLISNMGANTVRVKVPMNVAFYDALYHHNKASKRPLYLLQGIRIDSYRNNASITAFNDNY
RGYLKREAKGVVDILHGRKQVWNTDFGSRHYHYDLSPWVLGYVVGDDWNSGTVAAYTNHQ
KKTQYKGRYFKTSVAANPFEVMLAQVMDELTHYETAKYGWQHLSFSNSPTTDPFHYRKP
FEAQAPKYVQLNVENIQANSNVKAGMFAAYKAIDFHPRYKDYLLFDKENISKEDRQKIKE
LSLSQGYVKLLNAYHKIPVLVTGYGYSTARGIAQKEIDKRPLPINEKEQGQRLLLEDYESF
ISSGSFGATINAWQDDWNARAWNTSFATNKHSQFLWGDAQVFNQGYGLLGFKNAKHHYQV
DGKRGKGWKHPLMTSATGDDLYASSDESILYLAIKTKPEKLKEKRLLPIDITPKSGSRK
MNGSKVTFSKSSDFVLSIDPNGKSELVQERYNALKANYLRQLNGKDFYAFPPKKNSSNF
EQINMVLNRTKIVEDMEKVKATERFLPTHPTGLLKTGTDRHQKTFDSQDPDISFGKDFIE
VRIPWQLLNFSDDPSSQRIHDDYFKHYGVKELEIESIALGLGANSKENTLIKMDYRLKNW
ERPDTKTFLKD

>SEQ ID NO 2857:62_H36B frame: 2
RGLLKENTRTNFVVKGDTVLHKPTNKPFFVVKGVDEVSSLAGYHHNDFPITQKTYREWFHL
ISNMGANTVRVKVPMNVAFYDALYHHNKASKRPLYLLQGIRIDSYRNNASITAFNDNYRG
YLKREAKGVVDILHGRKQVWNTDFGSSHYHYDLSPWVLGYVVGDDGHS GTVALY

>SEQ ID NO 2858:62_JM9130013 frame: 3
FVVKGDTVLHKPTNKPFFVVKGVDEVSSLAGYHHNDFPITQKTYREWFHLISNMGANTVRV
KVPNMVAFYDALYHHNKASKRPLYLLQGIRIDSYRNNASITAFNDNYRGYLKREAKGVVD
ILHGRKQVWNTDFGSSHYHYDLSPWVLGYVVGDDWNSGTVAAYTNHQEKKTQYKGRYFKTS
VAANPFEVMLAQVMDELTHYETAKYGWQHLSFSNSPTTDPFHYRKPFEAQAPKYVQLNV
ENIQANSNVKAGMFAAYKAIDFHPRYKDYLLFDKENISKEDRQKIKELSLSQGYVKLLNAY
HKIPVLVTGYGYSTARGIAQKEIDKRPLPINEKEQGQRLLLEDYESFISSGSFGATINAW

**Table 28: Comparative Sequences relating to SAG1552
(conserved hypothetical protein)**

QDDWNARVWNTSFATNKHSQFLWGDAQVFNQGYGLLGFKNAKHHYQVDGKRGKEEWKHP
MTSATGDDLYASSDESILYLAIKTKPEKLKEKRLLPIDITPKSGSRKMNGSKVTFSSKSSD
FVLSIDPNGKSELFVQERYNALKANYLRQLNGKDFYAFPPKKNSSNFEQINMVLNRTKIV
EDMEKVKATERFLPHTPTGLLKTGTDRHQKTFSQTDISFGKDFIEVRIPWQLLNFS
SSQKIHHDDYFKHYGVKELEIESIALGLGANSKENTLIKMDYRLKNWERPDTKTFLKDSY
YSIKK

>SEQ ID NO 2859:62_M732 frame: 2
TRTNFVVKGDTVLHKTNPFFVVKGVDESSLAGYHHNDFPITQKTYREWFHLISNMGAN
TVRVKVPNMVAFYDALYHHNKESKRPLYLLQGIRIDSYRNNASITAFNDNYRGYLKREAK
GVVDILHGRKQVWNTDFGSRHYHYDLSPWVLGYVVGDDCNSGTVAITNHQEKKTQYKGRY
FKTSVAANPFEVMLAQVMDDELTHYETAKYGWQHLISFSNSPTTDPFHYRKPFQAPKPYV
QLNVENIQANSNVKAGMFAAYKAIDFHPRYKDYLLFDKENISKEDRQKIKELSLSQGYVK
LLNAYHKI PVLVTGYGYSTARGIAQKEIDKRPLPINEKEQGQRLLEDYESFISSGSFGAT
INAWQDDWNARAWNTSFATNKHSQFLWGDAQVFNQGYGLLGFKNAKHHYQVDGKRGKEW
KHPMTSATGDDLYASSDESILYLAIKTKPEKLKEKRLLPIDITPKSGSRKMNGSKVTFSS
KSSDFVLSIDPNGKSELFVQERYNALKANYLRQLNGKDFYAFPPKKNSSNFEQINMVLN
TKIVEDMEKVKATERFLPHTPTGLLKTGTDRHQKTFSQTDISFGKDFIEVRIPWQLLN
FSDPSSQKIHHDDYFKHYGVKELEIESIALGLGANSKENTLIKMDYRLKNWERPDTKTFL
KDSYYSIK

>SEQ ID NO 2860:62_M781 frame: 1
FDGSLYLPQGLLKENTRTNFVVKGDTVLHKTNPFFVVKGVDESSLAGYHHNDFPITQK
TYREWFHLISNMGANTVRVKVPMNVAFYDALYHHNKESKRPLYLLQGIRIDSYRNNASIT
AFNDNYRGYLKREAKGVVDILHGRKQVWNTDFGSRHYHYDLSPWVLGYVVGDDWNSGTVA
YTNHQEKKTQYKGRYFKTSVAANPFEVMLAQVMDDELTHYETAKYGWQHLISFSNSPTTDP
FHYRKPFQAPKPYVQLNVENIQANSNVKAGMFAAYKAIDFHPRYKDYLLFDKENISKED
RQKIKELSLSQGYVKLLNAYHKI PVLVTGYGYSTARGIAQKEIDKRPLPINEKEQGQRL
EDYESFISSGSFGATINAWQDDWNARAWNTSFATNKHSQFLWGDAQVFNQGYGLLGFKNA
KHHYQVDGKRGKEWHPMTSATGDDLYASSDESILYLAIKTKPEKLKEKRLLPIDITP
KSGSRKMNGSKVTFSSKSSDFVLSIDPNGKSELFVQERYNALKANYLRQLNGKDFYAFPPK
KNSSNFEQINMVLNRTKIVEDMEKVKATERFLPHTPTGLLKTGTDRHQKTFSQTDISF
GKDFIEVRIPWQLLNFSQKIHHDDYFKHYGVKELEIESIALGLGANSKENTLIKMD
YRLKNWERPDTKTFLKDSYYSIKKEW

SEQ2850 -----FVVKGDTVLHKTNPFFVVKGVDESSLAGYHHNDFPIT
SEQ2851 -----KGLLKENTRTNFVVKGDTVLHKTNPFFVVKGVDESSLAGYHHNDFPIT
SEQ2852 -----LKENTRTNFVVKGDTVLHKTNPFFVVKGVDESSLAGYHHNDFPIT
SEQ2853 -----KGLLKENTRTNFVVKGDTVLHKTNPFFVVKGVDESSLAGYHHNDFPIT
SEQ2854 -----KGLLKENTRTNFVVKGDTVLHKTNPFFVVKGVDESSLAGYHHNDFPIT
SEQ2855 YFDGSLYLPQGLLKENTRTNFVVKGDTVLHKTNPFFVVKGVDESSLAGYHHNDFPIT
SEQ2856 -----LPQGLLKENTRTNFVVKGDTVLHKTNPFFVVKGVDESSLAGYHHNDFPIT
SEQ2857 -----RGLLKENTRTNFVVKGDTVLHKTNPFFVVKGVDESSLAGYHHNDFPIT
SEQ2858 -----FVVKGDTVLHKTNPFFVVKGVDESSLAGYHHNDFPIT
SEQ2859 -----TRTNFVVKGDTVLHKTNPFFVVKGVDESSLAGYHHNDFPIT
SEQ2860 -FDGSLYLPQGLLKENTRTNFVVKGDTVLHKTNPFFVVKGVDESSLAGYHHNDFPIT

SEQ2850 QKTYREWFHLISNMGANTVRVKVPMNVAFYDALYHHNKASKRPLYLLQGIRIDSYRNNAS
SEQ2851 QKTYREWFHLISNMGANTVRVKVPMNVAFYDALYHHNKASKRPLYLLQGIRIDSYRNNAS
SEQ2852 QKTYREWFHLISNMGANTVRVKVPMNVAFYDALYHHNKASKRPLYLLQGIRIDSYRNNAS
SEQ2853 QKTYREWFHLISNMGANTVRVKVPMNVAFYDALYHHNKASKRPLYLLQGIRIDSYRNNAS
SEQ2854 QKTYREWFHLISNMGANTVRVKVPMNVAFYDALYHHNKASKRPLYLLQGIRIDSYRNNAS
SEQ2855 QKTYREWFHLISNMGANTVRVKVPMNVAFYDALYHHNKASKRPLYLLQGIRIDSYRNNAS
SEQ2856 QKTYREWFHLISNMGANTVRVKVPMNVAFYDALYHHNKASKRPLYLLQGIRIDSYRNNAS
SEQ2857 QKTYREWFHLISNMGANTVRVKVPMNVAFYDALYHHNKASKRPLYLLQGIRIDSYRNNAS
SEQ2858 QKTYREWFHLISNMGANTVRVKVPMNVAFYDALYHHNKASKRPLYLLQGIRIDSYRNNAS
SEQ2859 QKTYREWFHLISNMGANTVRVKVPMNVAFYDALYHHNKASKRPLYLLQGIRIDSYRNNAS
SEQ2860 QKTYREWFHLISNMGANTVRVKVPMNVAFYDALYHHNKASKRPLYLLQGIRIDSYRNNAS

SEQ2850 ITAFNDNYRGYLKREAKGVVDILHGRKQVWNTDFGSRHYHYDLSPWVLGYVVGDDWNSGT
SEQ2851 ITAFNDNYRGYLKREAKGVVDILHGRKQVWNTDLGSRHYHYDLSPWVLGYVVGDDWNSGT
SEQ2852 ITAFNDNYRGYLKREAKGVVDILHGRKQVWNTDLGSRHYHYDLSPWVLGYVVGDDWNSGT
SEQ2853 ITAFNDNYRGYLKREAKGVVDILHGRKQVWNTDLGSRHYHYDLSPWVLGYVVGDDWNSGT
SEQ2854 ITAFNDNYRGYLKREAKGVVDILHGRKQVWNTDLGSRHYHYDLSPWVLGYVVGDDWNSGT
SEQ2855 ITAFNDNYRGYLKREAKGVVDILHGRKQVWNTDFGSRHYHYDLSPWVLGYVVGDDWNSGT
SEQ2856 ITAFNDNYRGYLKREAKGVVDILHGRKQVWNTDFGSRHYHYDLSPWVLGYVVGDDWNSGT
SEQ2857 ITAFNDNYRGYLKREAKGVVDILHGRKQVWNTDFGSSHYHYDLSPWVLGYVVGDDGHS
SEQ2858 ITAFNDNYRGYLKREAKGVVDILHGRKQVWNTDFGSSHYHYDLSPWVLGYVVGDDWNSGT

**Table 28: Comparative Sequences relating to SAG1552
(conserved hypothetical protein)**

SEQ2859	ITAFNDNYRGYLGKREAGVVDILHGRKQVWNTDFGSRHYHYDLSPWVLGYVVGDDCNSGT
SEQ2860	ITAFNDNYRGYLGKREAGVVDILHGRKQVWNTDFGSRHYHYDLSPWVLGYVVGDDWNSGT
SEQ2850	VAYTNHQEKKTOYKGRYFKTSAAANPFVMLAQVMDELTHYETAKYGWQHLLISFSNSPTT
SEQ2851	VAYTNHQEKKTOYKGRYFKTSVAANPFVMLAQVMDELTHYETAKYGWQHLLISFSNSPTT
SEQ2852	VAYTNHQEKKTOYKGRYFKTSVAANPFVMLAQVMDELTHYETAKYGWQHLLISFSNSPTT
SEQ2853	VAYTNHQEKKTOYKGRYFKTSVAANPFVMLAQVMDELTHYETAKYGWQHLLISFSNSPTT
SEQ2854	VAYTNHQEKKTOYKGRYFKTSVAANPFVMLAQVMDELTHYETAKYGWQHLLISFSNSPTT
SEQ2855	VAYTNHQEKKTOYKGRYFKTSVAANPFVMLAQVMDELTHYETAKYGWQHLLISFSNSPTT
SEQ2856	VAYTNHQEKKTOYKGRYFKTSVAANPFVMLAQVMDELTHYETAKYGWQHLLISFSNSPTT
SEQ2857	VALY-----
SEQ2858	VAYTNHQEKKTOYKGRYFKTSVAANPFVMLAQVMDELTHYETAKYGWQHLLISFSNSPTT
SEQ2859	VAYTNHQEKKTOYKGRYFKTSVAANPFVMLAQVMDELTHYETAKYGWQHLLISFSNSPTT
SEQ2860	VAYTNHQEKKTOYKGRYFKTSVAANPFVMLAQVMDELTHYETAKYGWQHLLISFSNSPTT
SEQ2850	PFHYRKPFEAQAPKYVQLNVENIQANSNVKAGIFAAYKAIDFHPRYKYDYLDFDENISK
SEQ2851	PFHYRKPFEAQAPKYVQLNVENIQANSNVKAGMFAAYKAIDFHPRYKYDYLDFDENISK
SEQ2852	PFHYRKPFEAQAPKYVQLNVENIQANSNVKAGMFAAYKAIDFHPRYKYDYLDFDENISK
SEQ2853	PFHYRKPFEAQAPKYVQLNVENIQANSNVKAGMFAAYKAIDFHPRYKYDYLDFDENISK
SEQ2854	PFHYRKPFEAQAPKYVQLNVENIQANSNVKAGMFAAYKAIDFHPRYKYDYLDFDENISK
SEQ2855	PFHYRKPFEAQAPKYVQLNVENIQANSNVKAGMFAAYKAIDFHPRYKYDYLDFDENISK
SEQ2856	PFHYRKPFEAQAPKYVQLNVENIQANSNVKAGMFAAYKAIDFHPRYKYDYLDFDENISK
SEQ2857	-----
SEQ2858	PFHYRKPFEAQAPKYVQLNVENIQANSNVKAGMFAAYKAIDFHPRYKYDYLDFDENISK
SEQ2859	PFHYRKPFEAQAPKYVQLNVENIQANSNVKAGMFAAYKAIDFHPRYKYDYLDFDENISK
SEQ2860	PFHYRKPFEAQAPKYVQLNVENIQANSNVKAGMFAAYKAIDFHPRYKYDYLDFDENISK
SEQ2850	DRQKIKELSLSQGYVKLLNAYHKIPVLVTGYGYSTARGIAQKEIDKRPLPINEKEQQQR
SEQ2851	DRQKIKELSLSQGYVKLLNAYHKIPVLVTGYGYSTARGIAQKEIDKRPLPINEKEQQQR
SEQ2852	DRQKIKELSLSQGYVKLLNAYHKIPVLVTGYGYSTARGIAQKEIDKRPLPINEKEQQQR
SEQ2853	DRQKIKELSLSQGYVKLLNAYHKIPVLVTGYGYSTARGIAQKEIDKRPLPINEKEQQQR
SEQ2854	DRQKIKELSLSQGYVKLLNAYHKIPVLVTGYGYSTARGIAQKEIDKRPLPINEKEQQQR
SEQ2855	DRQKIKELSLSQGYVKLLNAYHKIPVLVTGYGYSTARGIAQKEIDKRPLPINEKEQQQR
SEQ2856	DRQKIKELSLSQGYVKLLNAYHKIPVLVTGYGYSTARGIAQKEIDKRPLPINEKEQQQR
SEQ2857	-----
SEQ2858	DRQKIKELSLSQGYVKLLNAYHKIPVLVTGYGYSTARGIAQKEIDKRPLPINEKEQQQR
SEQ2859	DRQKIKELSLSQGYVKLLNAYHKIPVLVTGYGYSTARGIAQKEIDKRPLPINEKEQQQR
SEQ2860	DRQKIKELSLSQGYVKLLNAYHKIPVLVTGYGYSTARGIAQKEIDKRPLPINEKEQQQR
SEQ2850	LEDYESFISSGSFGATINAWQDDWNARAWNTSFATNKHSQFLWGDAQVFNQGYGLLGFK
SEQ2851	LEDYESFISSGSFGATINAWQDDWNARAWNTSFATNKHSQFLWGDAQVFNQGYGLLGFK
SEQ2852	LEDYESFISSGSFGATINAWQDDWNARAWNTSFATNKHSQFLWGDAQVFNQGYGLLGFK
SEQ2853	LEDYESFISSGSFGATINAWQDDWNARAWNTSFATNKHSQFLWGDAQVFNQGYGLLGFK
SEQ2854	LEDYESFISSGSFGATINAWQDDWNARAWNTSFATNKHSQFLWGDAQVFNQGYGLLGFK
SEQ2855	LEDYESFISSGSFGATINAWQDDWNARAWNTSFATNKHSQFLWGDAQVFNQGYGLLGFK
SEQ2856	LEDYESFISSGSFGATINAWQDDWNARAWNTSFATNKHSQFLWGDAQVFNQGYGLLGFK
SEQ2857	-----
SEQ2858	LEDYESFISSGSFGATINAWQDDWNARAWNTSFATNKHSQFLWGDAQVFNQGYGLLGFK
SEQ2859	LEDYESFISSGSFGATINAWQDDWNARAWNTSFATNKHSQFLWGDAQVFNQGYGLLGFK
SEQ2860	LEDYESFISSGSFGATINAWQDDWNARAWNTSFATNKHSQFLWGDAQVFNQGYGLLGFK
SEQ2850	AKHHYQVDGKRKGGEWKHPLMTSATGDDLYASSDESILYLAIKTKPEKLKEKRLLPIDI
SEQ2851	AKHHYQVDGKRKGGEWKHPLMTSATGDDLYASSDESILYLAIKTKPEKLKEKRLLPIDI
SEQ2852	AKHHYQVDGKRKGGEWKHPLMTSATGDDLYASSDESILYLAIKTKPEKLKEKRLLPIDI
SEQ2853	AKHHYQVDGKRKGGEWKHPLMTSATGDDLYASSDESILYLAIKTKPEKLKEKRLLPIDI
SEQ2854	AKHHYQVDGKRKGGEWKHPLMTSATGDDLYASSDESILYLAIKTKPEKLKEKRLLPIDI
SEQ2855	AKHHYQVDGKRKGGEWKHPLMTSATGDDLYASSDESILYLAIKTKPEKLKEKRLLPIDI
SEQ2856	AKHHYQVDGKRKGGEWKHPLMTSATGDDLYASSDESILYLAIKTKPEKLKEKRLLPIDI
SEQ2857	-----
SEQ2858	AKHHYQVDGKRKGGEWKHPLMTSATGDDLYASSDESILYLAIKTKPEKLKEKRLLPIDI
SEQ2859	AKHHYQVDGKRKGGEWKHPLMTSATGDDLYASSDESILYLAIKTKPEKLKEKRLLPIDI
SEQ2860	AKHHYQVDGKRKGGEWKHPLMTSATGDDLYASSDESILYLAIKTKPEKLKEKRLLPIDI
SEQ2850	PKSGSRKMNGSKVTFSSDFVLSIDPNGKSELFVQERYNALKANYLRQLNGKDFYAFP
SEQ2851	PKSGSRKMNGSKVTFSSDFVLSIDPNGKSELFVQERYNALKANYLRQLNGKDFYAFP
SEQ2852	PKSGSRKMNGSKVTFSSDFVLSIDPNGKSELFVQERYNALKANYLRQLNGKDFYAFP
SEQ2853	PKSGSRKMNGSKVTFSSDFVLSIDPNGKSELFVQERYNALKANYLRQLNGKDFYAFP
SEQ2854	PKSGSRKMNGSKVTFSSDFVLSIDPNGKSELFVQERYNALKANYLRQLNGKDFYAFP
SEQ2855	PKSGSRKMNGSKVTFSSDFVLSIDPNGKSELFVQERYNALKANYLRQLNGKDFYAFP

**Table 28: Comparative Sequences relating to SAG1552
(conserved hypothetical protein)**

SEQ2856	PKSGSRKMNGSKVTFSKSSDFVLSIDPNGKSELFVQERYNALKANYLRQLNGKDFYAFP
SEQ2857	-----
SEQ2858	PKSGSRKMNGSKVTFSKSSDFVLSIDPNGKSELFVQERYNALKANYLRQLNGKDFYAFP
SEQ2859	PKSGSRKMNGSKVTFSKSSDFVLSIDPNGKSELFVQERYNALKANYLRQLNGKDFYAFP
SEQ2860	PKSGSRKMNGSKVTFSKSSDFVLSIDPNGKSELFVQERYNALKANYLRQLNGKDFYAFP
SEQ2850	KNSSNFEQINMVLNRTKIVEDMEKVKATERFLPTHPTGLLKTGTIDRHQKTFDSQTDI
SEQ2851	KNSSNFEQINMVLNRTKIVEDMEKVKATERFLPTHPTGLLKTGTIDRHQKTFDSQTDI
SEQ2852	KNSSNFEQINMVLNRTKIVEDMEKVKATERFLPTHPTGLLKTGTIDRHQKTFDSQTDI
SEQ2853	KNSSNFEQINMVLNRTKIVEDMEKVKATERFLPTHPTGLLKTGTIDRHQKTFDSQTDI
SEQ2854	KNSSNFEQINMVLNRTKIVEDMEKVKATERFLPTHPTGLLKTGTIDRHQKTFDSQTDI
SEQ2855	KNSSNFEQINMVLNRTKIVEDMEKVKATERFLPTHPTGLLKTGTIDRHQKTFDSQTDI
SEQ2856	KNSSNFEQINMVLNRTKIVEDMEKVKATERFLPTHPTGLLKTGTIDRHQKTFDSQTDI
SEQ2857	-----
SEQ2858	KNSSNFEQINMVLNRTKIVEDMEKVKATERFLPTHPTGLLKTGTIDRHQKTFDSQTDI
SEQ2859	KNSSNFEQINMVLNRTKIVEDMEKVKATERFLPTHPTGLLKTGTIDRHQKTFDSQTDI
SEQ2860	KNSSNFEQINMVLNRTKIVEDMEKVKATERFLPTHPTGLLKTGTIDRHQKTFDSQTDI
SEQ2850	FGKDFIEVRIPWQLLNFSDPSSQKIHDDYFKHYGVKELEIESIALGLGANSKENTLIK
SEQ2851	FGKDFIEVRIPWQLLNFSDPSSQKIHDDYFKHYGVKELEIESIALGLGANSKENTLIK
SEQ2852	FGKDFIEVRIPWQLLNFSDPSSQKIHDDYFKHYGVKELEIESIALGLGANSKENTLIK
SEQ2853	FGKDFIEVRIPWQLLNFSDPSSQRIHDDYFKHYGVKELENEPLLDVLI AKKTHRWQIIIV
SEQ2854	FGKDFIEVRIPWQLLNFSDPSSQRIHDDYFKHYGVKELENEPLLDVLI AKKTHRWQIIIV
SEQ2855	FGKDFIEVRIPWQLLNFSDPSSQKIHDDYFKHYGVKELEIESIALGLGANSKENTLIK
SEQ2856	FGKDFIEVRIPWQLLNFSDPSSQKIHDDYFKHYGVKELEIESIALGLGANSKENTLIK
SEQ2857	-----
SEQ2858	FGKDFIEVRIPWQLLNFSDPSSQKIHDDYFKHYGVKELEIESIALGLGANSKENTLIK
SEQ2859	FGKDFIEVRIPWQLLNFSDPSSQKIHDDYFKHYGVKELEIESIALGLGANSKENTLIK
SEQ2860	FGKDFIEVRIPWQLLNFSDPSSQKIHDDYFKHYGVKELEIESIALGLGANSKENTLIK
SEQ2850	DYRLKNWERPDTKTFLKDSYYSIER-----
SEQ2851	DYRLKNWERPDTKTFLKDSYYVLRK-----
SEQ2852	DYRLKNWERPDTKTFLKDSYYSIKKEWSKERERTYGP
SEQ2853	IGRDPIPKPFK-----
SEQ2854	IGRDPIPKPFK-----
SEQ2855	DYRLKNWERPDTKTFLKDSYYVLRK-----
SEQ2856	DYRLKNWERPDTKTFLKD-----
SEQ2857	-----
SEQ2858	DYRLKNWERPDTKTFLKDSYYSIKK-----
SEQ2859	DYRLKNWERPDTKTFLKDSYYSIK-----
SEQ2860	DYRLKNWERPDTKTFLKDSYYSIKKEW-----

Table 29: Comparative Sequences relating to SAG1641 (YaeC family protein)**SEQ ID NO. 2901: SAG1641 FROM THE 090 GBS TYPE Ia STRAIN**

AATCAAGAAGTTTCAGCAAGCTCAACTTCAAGTAAAGTTGTTAAAGTTGGTGTATGACCTTTTCTGACACTGAAAAA
 GCACGTTGGGATAAAATTGAAAAGCTAGTAGGCGATAAAGCTAAAATCAAATTCACAGAATTTACAGATTATACACAA
 CCAAATCAAGCGACAGCCAATAAGGATGTGGATATTAATGCCTTTCAACATTACAATTTCTTAGAAAACTGGAATAAG
 GAAAAAAGAAAACTTAATTCCTTGAAGAGCTTACTTAGCCCCAATTCGTATCTATTCTGAGAAGGTAAAAATCT
 CTTAAAAAATTGAAAAAAGGAGCCACTATTGCAATTCCAATGATGCAACAAATGGTAGCCGTGCATTGTATGTCCTT
 CAGTCAGCAGGTTTAATCAAATTGAATGTTTCTGGTAAGAAGGTTGCAACAGTTGCTAATATCACATCTAATAAAAAA
 GATATTAATATTCAAGAGTTAGATGCGAGTCAAACACCACGTGCACTCAAAGATGTAGATGCAGCTATTATTATAAT
 ACATACATTGAGCAAGCTAATTTAAAACCTTCAGATGCTATCTTTGTTGAGAAATCAGATAAAAAATTCAAAACAATGG
 ATTAATATCATTTGCGGGACGTAAAAATTGAAAAAGCAAAAGAACGCTAAAGCTATCCAAGCTATCTTGGATGCTTAT
 CACACAGATGAAGTGAAAAAAGTTATCAAAGATACTTCAGCTGATATTCCACAATGGAACCCAGCTTTCTGTACAA

**SEQ ID NO. 2902: SAG1641 FROM THE 1169NT1 GBS TYPE V STRAIN
(REVERSE COMPLEMENT)**

ATCAAGAAGTTTCAGCAAGCTCAACTTCAAGTAAAGTTGTTAAAGTTGGTGTATGACCTTTTCTGACACTGAAAAA
 CACGTTGGGATAAAATTGAAAAGCTAGTAGGTGATAAAGCTAAAATCAAATTTACAGAATTTACAGATTATACACAAC
 CAAATCAAGCGACAGCCAATAAGGATGTGGATATTAATGCCTTTCAACATTACAATTTCTTAGAAAACTGGAATAAGG
 AAAATAAGAAAACTTAATTCCTTGAAGAGCTTACTTAGCTCCAATTCGTATCTATTCTGAGAAGGTAAAAATCTC
 TTAATAAATTGAAAAAAGGAGCCACTATTGCAATTCCAATGATGCAACAAATGGTAGCCGTGCATTGTATGTCCTT
 AGTCAGCAGGTTTAATCAAATTGAATGTTTCTGGTAAGAAGGTTGCAACAGTTGCTAATATCACATCTAATAAAAAAGG
 ATATTAATATTCAAGAGTTAGATGCGAGTCAAACACCACGTGCACTCAAAGATGTAGATGCAGCTATTATTATAATA
 CATACATTGAGCAAGCTAATTTAAAACCTTCAGATGCTATCTTTGTTGAGAAATCAGATAAAAAATTCAAAACAATGGA
 TTAATATCATTTGCGGGACGTAAAAATTGAAAAAGCAAAAGAACGCTAAAGCTATCCAAGCTATCTTGGATGCTTATC
 ACACAGATGAAGTGAAAAAAGTTATCAAAGATACTTCAGCTGATATTCCACAATGG

SEQ ID NO. 2903: SAG1641 FROM THE 18RS21 GBS TYPE II STRAIN

AATCAAGAAGTTTCAGCAAGCTCAACTTCAAGTAAAGTTGTTAAAGTTGGTGTATGACCTTTTCTGACACTGAAAAA
 GCACGTTGGGATAAAATTGAAAAGCTAGTAGGTGATAAAGCTAAAATCAAATTTACAGAATTTACAGATTATACACAA
 CCAAATCAAGCGACAGCCAATAAGGATGTGGATATTAATGCCTTTCAACATTACAATTTCTTAGAAAACTGGAATAAG
 GAAAAAAGAAAACTTAATTCCTTGAAGAGCTTACTTAGCTCCAATTCGTATCTATTCTGAGAAGGTAAAAATCT
 CTTAAAAAATTGAAAAAAGGAGCCACTATTGCAATTCCAATGATGCAACAAATGGTAGCCGTGCATTGTATGTCCTT
 CAGTCAGCAGGTTTAATCAAATTGAATGTTTCTGGTAAGAAGGTTGCAACAGTTGCTAATATCACATCTAATAAAAAA
 GATATTAATATTCAAGAGTTAGATGCGAGTCAAACACCACGTGCACTCAAAGATGTAGATGCAGCTATTATTATAAAT
 ACATACATTGAGCAAGCTAATTTAAAACCTTCAGATGCTATCTTTGTTGAGAAATCAGATAAAAAATTCAAAACAATGG
 ATTAATATCATTTGCGGGACGTAAAAATTGAAAAAGCAAAAGAACGCTAAAGCTATCCAAGCTATCTTGGATGCTTAT
 CACACAGATGAAGTGAAAAAAGTTATCAAAGATACTTCAGCTGATATTCCAC

SEQ ID NO. 2904: SAG1641 FROM THE 2603 V/R GBS TYPE V STRAIN

AATCAAGAAGTTTCAGCAAGCTCAACTTCAAGTAAAGTTGTTAAAGTTGGTGTATGACCTTTTCTGACACTGAAAAA
 GCACGTTGGGATAAAATTGAAAAGCTAGTAGGTGATAAAGCTAAAATCAAATTTACAGAATTTACAGATTATACACAA
 CCAAATCAAGCGACAGCCAATAAGGATGTGGATATTAATGCCTTTCAACATTACAATTTCTTAGAAAACTGGAATAAG
 GAAAAAAGAAAACTTAATTCCTTGAAGAGCTTACTTAGCTCCAATTCGTATCTATTCTGAGAAGGTAAAAATCT
 CTTAAAAAATTGAAAAAAGGAGCCACTATTGCAATTCCAATGATGCAACAAATGGTAGCCGTGCATTGTATGTCCTT
 CAGTCAGCAGGTTTAATCAAATTGAATGTTTCTGGTAAGAAGGTTGCAACAGTTGCTAATATCACATCTAATAAAAAA
 GATATTAATATTCAAGAGTTAGATGCCAGTCAAACACCACGTGCACTCAAAGATGTAGATGCAGCTATTATTATAAAT
 ACATACATTGAGCAAGCTAATTTAAAACCTTCAGATGCTATCTTTGTTGAGAAATCAGATAAAAAATTCAAAACAATGG
 ATTAATATCATTTGCGGGACGTAAAAATTGAAAAAGCAAAAGAACGCTAAAGCTATCCAAGCTATCTTGGATGCTTAT
 CACACAGATGAAGTGAAAAAAGTTATCAAAGATACTTCAGCTGATATTCCACAATGG

SEQ ID NO. 2905: SAG1641 FROM THE A909 GBS TYPE Ia STRAIN

AATCAAGAAGTTTCAGCAAGCTCAACTTCAAGTAAAGTTGTTAAAGTTGGTGTATGACCTTTTCTGACACTGAAAAA
 GCACGTTGGGATAAAATTGAAAAGCTAGTAGGTGATAAAGCTAAAATCAAATTTACAGAATTTACAGATTATACACAA
 CCAAATCAAGCGACAGCCAATAAGGATGTGGATATTAATGCCTTTCAACATTACAATTTCTTAGAAAACTGGAATAAG
 GAAAAAAGAAAACTTAATTCCTTGAAGAGCTTACTTAGCTCCAATTCGTATCTATTCTGAGAAGGTAAAAATCT
 CTTAAAAAATTGAAAAAAGGAGCCACTATTGCAATTCCAATGATGCAACAAATGGTAGCCGTGCATTGTATGTCCTT
 CAGTCAGCAGGTTTAATCAAATTGAATGTTTCTGGTAAGAAGGTTGCAACAGTTGCTAATATCACATCTAATAAAAAA
 GATATTAATATTCAAGAGTTAGATGCGAGTCAAACACCACGTGCACTCAAAGATGTAGATGCAGCTATTATTATAAAT
 ACATACATTGAGCAAGCTAATTTAAAACCTTCAGATGCTATCTTTGTTGAGAAATCAGATAAAAAATTCAAAACAATGG
 ATTAATATCATTTGCGGGACGTAAAAATTGAAAAAGCAAAAGAACGCTAAAGCTATCCAAGCTATCTTGGATGCTTAT
 CACACAGATGAAGTGAAAAAAGTTATCAAAGATACTTCAGCTGATATTCCACAATGG

Table 29: Comparative Sequences relating to SAG1641 (YaeC family protein)**SEQ ID NO. 2906: SAG1641 FROM THE CJB110 GBS NONTYPEABLE STRAIN**

AAGTAAAGTTGTTAAAGTTGGTGTATGACCTTTTCTGACACTGAAAAAGCACGTTGGGATAAAATTGAAAAGCTAGT
 AGCGGATAAAGCTAAATCAAAATTCACAGAATTTACAGATTATACACAACCAAATCAAGCGACAGCCAATAAGGATGT
 GGATATTAATGCCTTTCAACATTACAATTTCTTAGAAAACCTGGAATAAGGAAAAATAAGAAAACTTAATTCCACTTGA
 AAAGACTTACTTAGCCCCAATTCGTATCTATTCTGAGAAGGTAAATCTCTTAAAAAATTGAAAAAGGAGCCACTAT
 TGCAATTCAAATGATGCAACAAATGGTAGCCGTGCATTGTATGTCCTTCAGTCAGCAGGTTTAATCAAATTTGAATGT
 TTCTGGTAAGAAGGTTGCAACAGTTGCTAATATCACATCTAATAAAAAAGATATTAATATTCAGGAGTTAGATGCGAG
 TCAAACACCACGTGCACTCAAAGATGTAGATGCAGCTATTATTAATAATACATACATTGAGCAAGCTAATTTAAAACC
 TTCAGATGCTATCTTTGTTGAGAAATCAGATAAAAAATTCAAAACAATGGATTAATATCATTGCGGGACGTAAAAATTG
 GAAAAAGCAAAAGACGCTAAAGCTATCCAAGCTATCTTGGATGCTTATCACACAGATGAAGTGAAAAAGTTATCAA
 AGATACTTCAGCTGATATTCCACAATGGAA

**SEQ ID NO. 2907: SAG1641 FROM THE COH1 GBS TYPE III STRAIN
(REVERSE COMPLEMENT)**

AGTTTCAGCAAGCTCAACTTCAAGTAAAGTTGTTAAAGTTGGTGTATGACCTTTTCTGACACTGAAAAAGCACGTTG
 GGATAAAATTGAAAAGCTAGTAGGTGATAAAGCTAAATCAAATTTACAGAATTTACAGATTATACACAACCAAATCA
 AGCGACAGCCAATAAGGATGTGGATATTAATGCCTTTCAACATTACAATTTCTTAGAAAACCTGGAATAAGGAAAAATA
 GAAAAACTTAATTCACCTTGAAAAGACTTACTTAGCTCCAATTCGTATCTATTCTGAGAAGGTAAATCTCTTAAAAA
 ATTGAAAAAAGGAGCCACTATTGCAATTCAAATGATGCAACAAATGGTAGCCGTGCATTGTATGTACTTCAGTCAGC
 AGGTTTAATCAAATTTGAATGTTTCTGGTAAGAAGGTTGCAACAGTTGCTAATATCACATCTAATAAAAAAGGATATTA
 TATTTCAGGAGTTAGATGCGAGTCAAACACCACGTGCACTCAAAGATGTAGATGCAGCTATTATTAATAATACATACAT
 TGAGCAAGCTAATTTAAAACCTTCAGATGCTATCTTTGTTGAGAAATCAGATAAAAAATTCAAAACAATGGATTAATAT
 CATTCGCGGACGTAAAAATTGAAAAAGCAAAAGACGCTAAAGCTATCCAAGCTATCTTGGATGCTTATCACACAGA
 TGAAGTGAAAAAGTTATCAAAGATACTTCAGCTGATATTCCACAATGG

SEQ ID NO. 2908: SAG1641 FROM THE H36b GBS TYPE Ib STRAIN

AAGAAGTTTCAGCAAGCTCAACTTCAAGTAAAGTTGTTAAAGTTGGTGTATGACCTTTTCTGACACTGAAAAAGCAC
 GTTGGGATAAAATTGAAAAGCTAGTAGGTGATAAAGCTAAATCAAATTTACAGAATTTACAGATTATACACAACCAA
 ATCAAGCGACAGCCAATAAGGATGTGGATATTAATGCCTTTCAACATTACAATTTCTTAGAAAACCTGGAATAAGGAAA
 ATAAAGAAAACTTAATTCACCTTGAAAAGACTTACTTAGCTCCAATTCGTATCTATTCTGAGAAGGTAAATCTCTTA
 AAAAATTGAAAAAAGGAGCCACTATTGCAATTCCAAATGATGCAACAAATGGTAGCCGTGCATTGTATGTCTTCAGT
 CAGCAGGTTTAAATCAAATTTGAATGTTTCTGGTAAGAAGGTTGCAACAGTTGCTAATATCACATCTAATAAAAAAGGATA
 TTAATATTTCAGGAGTTAGATGCGAGTCAAACACCACGTGCACTCAAAGATGTAGATGCAGCTATTATTAATAATACAT
 ACATTGAGCAAGCTAATTTAAAACCTTCAGATGCTATCTTTGTTGAGAAATCAGATAAAAAATTCAAAACAATGGATTA
 ATATCATTGCGGGACGTAAAAATTGAAAAAGCAAAAGACGCTAAAGCTATCCAAGCTATCTTGGATGCTTATCACA
 CAGATGAAGTGAAAAAGTTATCAAAGATACTTCAGCTGATATTCCACAATGG

SEQ ID NO. 2909: SAG1641 FROM THE JM3190013 GBS TYPE VIII STRAIN

TTCAGCAAGCTCAACTTCAAGTAAAGTTGTTAAAGTTGGTGTATGACCTTTTCTGACACTGAAAAAGCACGTTGGGA
 TAAATTTGAAAAGCTAGTAGGTGATAAAGCTAAATCAAATTTACAGAATTTACAGATTATACACAACCAAATCAAGC
 GACGCCAATAAGGATGTGGATATTAATGCCTTTCAACATTACAATTTCTTAGAAAACCTGGAATAAGGAAAAATAAGAA
 AAATTAATTCACCTTGAAAAGACTTACTTAGCTCCAATTCGTATCTATTCTGAGAAGGTAAATCTCTTAAAAAATT
 GAAAAAAGGAGCCACTATTGCAATTCCAAATGATGCAACAAATGGTAGCCGTGCATTGTATGTCCTTCAGTCAGCAGG
 TTTAATCAAATTTGAATGTTTCTGGTAAGAAGGTTGCAACAGTTGCTAATATCACATCTAATAAAAAAGGATATTAATAT
 TCAGGAGTTAGATGCGAGTCAAACACCACGTGCACTCAAAGATGTAGATGCAGCTATTATTAATAATACATACATTGA
 GCAAGCTAATTTAAAACCTTCAGATGCTATCTTTGTTGAGAAATCAGATAAAAAATTCAAAACAATGGATTAATATCAT
 TGCGGGACGTAAAAATTGAAAAAGCAAAAGACGCTAAAGCTATCCAAGCTATCTTGGATGCTTATCACACAGATGA
 AGTGAAAAAAGTTATCAAAGATACTTCAGCTGATATTCCACAATGG

SEQ ID NO. 2910: SAG1641 FROM THE M732 GBS TYPE III STRAIN

AATCAAGAAGTTTCAGCAAGCTCAACTTCAAGTAAAGTTGTTAAAGTTGGTGTATGACCTTTTCTGACACTGAAAAA
 GCACGTTGGGATAAAATTGAAAAGCTAGTAGGTGATAAAGCTAAATCAAATTTACAGAATTTACAGATTATACACAA
 CCAATCAAGCGACAGCCAATAAGGATGTGGATATTAATGCCTTTCAACATTACAATTTCTTAGAAAACCTGGAATAAG
 GAAAAATAAGAAAACTTAATTCACCTTGAAAAGACTTACTTAGCTCCAATTCGTATCTATTCTGAGAAGGTAAATCTCTTAAAAAATT
 CTTAAAAAATTGAAAAAAGGAGCCACTATTGCAATTCCAAATGATGCAACAAATGGTAGCCGTGCATTGTATGTCCTT
 CAGTCAGCAGGTTTAATCAAATTTGAATGTTTCTGGTAAGAAGGTTGCAACAGTTGCTAATATCACATCTAATAAAAAAG
 GATATTAATATTCAGGAGTTAGATGCGAGTCAAACACCACGTGCACTCAAAGATGTAGATGCAGCTATTATTAATAAT
 ACATACATTGAGCAAGCTAATTTAAAACCTTCAGATGCTATCTTTGTTGAGAAATCAGATAAAAAATTCAAAACAATGG
 ATTAATATCATTGCGGGACGTAAAAATTGAAAAAGCAAAAGACGCTAAAGCTATCCAAGCTATCTTGGATGCTTATCACACAGATGA
 CACACAGATGAAGTGAAAAAAGTTATCAAAGATACTTCAGCTGATATTCCACAATGG

Table 29: Comparative Sequences relating to SAG1641 (YaeC family protein)

SEQ ID NO. 2911: SAG1641 FROM THE M781 GBS TYPE III STRAIN

AGTTTCAGCAAGCTCAACTTCAAGTAAAGTTGTTAAAGTTGGTGTATGACCTTTCTGACACTGAAAAAGCACGTTG
GGATAAAATTGAAAAGCTAGTAGGTGATAAAGCTAAAAATCAAATTTACAGAATTTACAGATTATACACAACCAATCA
AGCGACAGCCAATAAGGATGTGGATATTAATGCCTTTCAACATTACAATTTCTTAGAAAACTGGAATAAGGAAAAATAA
GAAAAACTTAATTCACCTTGAAAAGACTTTACTTAGCTCCAATTCGTATCTATTCTGAGAAGGTAAAAATCTCTTAAAAA
ATTGAAAAAAGGAGCCACTATTGCAATTCCAAATGATGCAACAAATGGTAGCCGTGCATTGTATGTCCTTCAGTCAGC
AGGTTTAATCAAATTGAATGTTTCTGGTAAGAAGGTTGCAACAGTTGCTAATATCACATCTAATAAAAAAGGATATTA
TATTCAGGAGTTAGATGCGAGTCAAACACCAGTGCCTCAAGATGTAGATGCAGCTATTATTAATAATACATACAT
TGAGCAAGCTAATTTAAACCTTCAGATGCTATCTTTGTTGAGAAATCAGATAAAAAATTCAAAACAATGGATTAATAT
CATTCGCGGACGTAAAAAATTGGAAAAAGCAAAAGAACGCTAAAGCTATCCAAGCTATCTGGGATGCTTATCACACAGA
TGAAGTGAAAAAGTTATCAAAGATACTTCAGCTGATATTCCACAATGG

SEQ2901 ATCAAGAAGTTTCAGCAAGCTCAACTTCAAGTAAAGTTGTTAAAGTTGGTGTATGACC
SEQ2902 ATCAAGAAGTTTCAGCAAGCTCAACTTCAAGTAAAGTTGTTAAAGTTGGTGTATGACC
SEQ2903 ATCAAGAAGTTTCAGCAAGCTCAACTTCAAGTAAAGTTGTTAAAGTTGGTGTATGACC
SEQ2904 ATCAAGAAGTTTCAGCAAGCTCAACTTCAAGTAAAGTTGTTAAAGTTGGTGTATGACC
SEQ2905 ATCAAGAAGTTTCAGCAAGCTCAACTTCAAGTAAAGTTGTTAAAGTTGGTGTATGACC
SEQ2906 -----AAGTAAAGTTGTTAAAGTTGGTGTATGACC
SEQ2907 -----AGTTTCAGCAAGCTCAACTTCAAGTAAAGTTGTTAAAGTTGGTGTATGACC
SEQ2908 ---AAGAAGTTTCAGCAAGCTCAACTTCAAGTAAAGTTGTTAAAGTTGGTGTATGACC
SEQ2909 -----TTCAGCAAGCTCAACTTCAAGTAAAGTTGTTAAAGTTGGTGTATGACC
SEQ2910 ATCAAGAAGTTTCAGCAAGCTCAACTTCAAGTAAAGTTGTTAAAGTTGGTGTATGACC
SEQ2911 -----AGTTTCAGCAAGCTCAACTTCAAGTAAAGTTGTTAAAGTTGGTGTATGACC

SEQ2901 TTTTCTGACACTGAAAAAGCACGTTGGGATAAAATTGAAAAGCTAGTAGGCGATAAAAGCT
SEQ2902 TTTTCTGACACTGAAAAAGCACGTTGGGATAAAATTGAAAAGCTAGTAGGTGATAAAGCT
SEQ2903 TTTTCTGACACTGAAAAAGCACGTTGGGATAAAATTGAAAAGCTAGTAGGTGATAAAGCT
SEQ2904 TTTTCTGACACTGAAAAAGCACGTTGGGATAAAATTGAAAAGCTAGTAGGTGATAAAGCT
SEQ2905 TTTTCTGACACTGAAAAAGCACGTTGGGATAAAATTGAAAAGCTAGTAGGTGATAAAGCT
SEQ2906 TTTTCTGACACTGAAAAAGCACGTTGGGATAAAATTGAAAAGCTAGTAGGCGATAAAGCT
SEQ2907 TTTTCTGACACTGAAAAAGCACGTTGGGATAAAATTGAAAAGCTAGTAGGTGATAAAGCT
SEQ2908 TTTTCTGACACTGAAAAAGCACGTTGGGATAAAATTGAAAAGCTAGTAGGTGATAAAGCT
SEQ2909 TTTTCTGACACTGAAAAAGCACGTTGGGATAAAATTGAAAAGCTAGTAGGTGATAAAGCT
SEQ2910 TTTTCTGACACTGAAAAAGCACGTTGGGATAAAATTGAAAAGCTAGTAGGTGATAAAGCT
SEQ2911 TTTTCTGACACTGAAAAAGCACGTTGGGATAAAATTGAAAAGCTAGTAGGTGATAAAGCT

SEQ2901 AAAATCAAATTTACAGAATTTACAGATTATACACAACCAATCAAGCGACAGCCAATAAG
SEQ2902 AAAATCAAATTTACAGAATTTACAGATTATACACAACCAATCAAGCGACAGCCAATAAG
SEQ2903 AAAATCAAATTTACAGAATTTACAGATTATACACAACCAATCAAGCGACAGCCAATAAG
SEQ2904 AAAATCAAATTTACAGAATTTACAGATTATACACAACCAATCAAGCGACAGCCAATAAG
SEQ2905 AAAATCAAATTTACAGAATTTACAGATTATACACAACCAATCAAGCGACAGCCAATAAG
SEQ2906 AAAATCAAATTTACAGAATTTACAGATTATACACAACCAATCAAGCGACAGCCAATAAG
SEQ2907 AAAATCAAATTTACAGAATTTACAGATTATACACAACCAATCAAGCGACAGCCAATAAG
SEQ2908 AAAATCAAATTTACAGAATTTACAGATTATACACAACCAATCAAGCGACAGCCAATAAG
SEQ2909 AAAATCAAATTTACAGAATTTACAGATTATACACAACCAATCAAGCGACAGCCAATAAG
SEQ2910 AAAATCAAATTTACAGAATTTACAGATTATACACAACCAATCAAGCGACAGCCAATAAG
SEQ2911 AAAATCAAATTTACAGAATTTACAGATTATACACAACCAATCAAGCGACAGCCAATAAG

SEQ2901 GATGTGGATATTAATGCCTTTCAACATTACAATTTCTTAGAAAACTGGAATAAGGAAAAAT
SEQ2902 GATGTGGATATTAATGCCTTTCAACATTACAATTTCTTAGAAAACTGGAATAAGGAAAAAT
SEQ2903 GATGTGGATATTAATGCCTTTCAACATTACAATTTCTTAGAAAACTGGAATAAGGAAAAAT
SEQ2904 GATGTGGATATTAATGCCTTTCAACATTACAATTTCTTAGAAAACTGGAATAAGGAAAAAT
SEQ2905 GATGTGGATATTAATGCCTTTCAACATTACAATTTCTTAGAAAACTGGAATAAGGAAAAAT
SEQ2906 GATGTGGATATTAATGCCTTTCAACATTACAATTTCTTAGAAAACTGGAATAAGGAAAAAT
SEQ2907 GATGTGGATATTAATGCCTTTCAACATTACAATTTCTTAGAAAACTGGAATAAGGAAAAAT
SEQ2908 GATGTGGATATTAATGCCTTTCAACATTACAATTTCTTAGAAAACTGGAATAAGGAAAAAT
SEQ2909 GATGTGGATATTAATGCCTTTCAACATTACAATTTCTTAGAAAACTGGAATAAGGAAAAAT
SEQ2910 GATGTGGATATTAATGCCTTTCAACATTACAATTTCTTAGAAAACTGGAATAAGGAAAAAT
SEQ2911 GATGTGGATATTAATGCCTTTCAACATTACAATTTCTTAGAAAACTGGAATAAGGAAAAAT

SEQ2901 AAGAAAACTTAATTCACCTTGAAAAGACTTACTTAGCCCCAATTCGTATCTATTCTGAG
SEQ2902 AAGAAAACTTAATTCACCTTGAAAAGACTTACTTAGCTCCAATTCGTATCTATTCTGAG
SEQ2903 AAGAAAACTTAATTCACCTTGAAAAGACTTACTTAGCTCCAATTCGTATCTATTCTGAG
SEQ2904 AAGAAAACTTAATTCACCTTGAAAAGACTTACTTAGCTCCAATTCGTATCTATTCTGAG
SEQ2905 AAGAAAACTTAATTCACCTTGAAAAGACTTACTTAGCTCCAATTCGTATCTATTCTGAG
SEQ2906 AAGAAAACTTAATTCACCTTGAAAAGACTTACTTAGCCCCAATTCGTATCTATTCTGAG
SEQ2907 AAGAAAACTTAATTCACCTTGAAAAGACTTACTTAGCTCCAATTCGTATCTATTCTGAG
SEQ2908 AAGAAAACTTAATTCACCTTGAAAAGACTTACTTAGCTCCAATTCGTATCTATTCTGAG

Table 29: Comparative Sequences relating to SAG1641 (YaeC family protein)

SEQ2909	AAGAAAACTTAATTCACCTTGAAAAGACTTACTTAGCTCCAATTCGTATCTATTCTGAG
SEQ2910	AAGAAAACTTAATTCACCTTGAAAAGACTTACTTAGCTCCAATTCGTATCTATTCTGAG
SEQ2911	AAGAAAACTTAATTCACCTTGAAAAGACTTACTTAGCTCCAATTCGTATCTATTCTGAG
SEQ2901	AAGGTAAATCTCTTAAAAAATTGAAAAAGGAGCCACTATTGCAATTCCAAATGATGCA
SEQ2902	AAGGTAAATCTCTTAAAAAATTGAAAAAGGAGCCACTATTGCAATTCCAAATGATGCA
SEQ2903	AAGGTAAATCTCTTAAAAAATTGAAAAAGGAGCCACTATTGCAATTCCAAATGATGCA
SEQ2904	AAGGTAAATCTCTTAAAAAATTGAAAAAGGAGCCACTATTGCAATTCCAAATGATGCA
SEQ2905	AAGGTAAATCTCTTAAAAAATTGAAAAAGGAGCCACTATTGCAATTCCAAATGATGCA
SEQ2906	AAGGTAAATCTCTTAAAAAATTGAAAAAGGAGCCACTATTGCAATTCCAAATGATGCA
SEQ2907	AAGGTAAATCTCTTAAAAAATTGAAAAAGGAGCCACTATTGCAATTCCAAATGATGCA
SEQ2908	AAGGTAAATCTCTTAAAAAATTGAAAAAGGAGCCACTATTGCAATTCCAAATGATGCA
SEQ2909	AAGGTAAATCTCTTAAAAAATTGAAAAAGGAGCCACTATTGCAATTCCAAATGATGCA
SEQ2910	AAGGTAAATCTCTTAAAAAATTGAAAAAGGAGCCACTATTGCAATTCCAAATGATGCA
SEQ2911	AAGGTAAATCTCTTAAAAAATTGAAAAAGGAGCCACTATTGCAATTCCAAATGATGCA
SEQ2901	ACAAATGGTAGCCGTGCATTGTATGTCCTTCAGTCAGCAGGTTTAAATCAAATTGAATGTT
SEQ2902	ACAAATGGTAGCCGTGCATTGTATGTCCTTCAGTCAGCAGGTTTAAATCAAATTGAATGTT
SEQ2903	ACAAATGGTAGCCGTGCATTGTATGTCCTTCAGTCAGCAGGTTTAAATCAAATTGAATGTT
SEQ2904	ACAAATGGTAGCCGTGCATTGTATGTCCTTCAGTCAGCAGGTTTAAATCAAATTGAATGTT
SEQ2905	ACAAATGGTAGCCGTGCATTGTATGTCCTTCAGTCAGCAGGTTTAAATCAAATTGAATGTT
SEQ2906	ACAAATGGTAGCCGTGCATTGTATGTCCTTCAGTCAGCAGGTTTAAATCAAATTGAATGTT
SEQ2907	ACAAATGGTAGCCGTGCATTGTATGTCCTTCAGTCAGCAGGTTTAAATCAAATTGAATGTT
SEQ2908	ACAAATGGTAGCCGTGCATTGTATGTCCTTCAGTCAGCAGGTTTAAATCAAATTGAATGTT
SEQ2909	ACAAATGGTAGCCGTGCATTGTATGTCCTTCAGTCAGCAGGTTTAAATCAAATTGAATGTT
SEQ2910	ACAAATGGTAGCCGTGCATTGTATGTCCTTCAGTCAGCAGGTTTAAATCAAATTGAATGTT
SEQ2911	ACAAATGGTAGCCGTGCATTGTATGTCCTTCAGTCAGCAGGTTTAAATCAAATTGAATGTT
SEQ2901	TCTGGTAAGAAGGTTGCAACAGTTGCTAATATCACATCTAATAAAAAAGATATTAATATT
SEQ2902	TCTGGTAAGAAGGTTGCAACAGTTGCTAATATCACATCTAATAAAAAAGGATATTAATATT
SEQ2903	TCTGGTAAGAAGGTTGCAACAGTTGCTAATATCACATCTAATAAAAAAGGATATTAATATT
SEQ2904	TCTGGTAAGAAGGTTGCAACAGTTGCTAATATCACATCTAATAAAAAAGGATATTAATATT
SEQ2905	TCTGGTAAGAAGGTTGCAACAGTTGCTAATATCACATCTAATAAAAAAGGATATTAATATT
SEQ2906	TCTGGTAAGAAGGTTGCAACAGTTGCTAATATCACATCTAATAAAAAAGGATATTAATATT
SEQ2907	TCTGGTAAGAAGGTTGCAACAGTTGCTAATATCACATCTAATAAAAAAGGATATTAATATT
SEQ2908	TCTGGTAAGAAGGTTGCAACAGTTGCTAATATCACATCTAATAAAAAAGGATATTAATATT
SEQ2909	TCTGGTAAGAAGGTTGCAACAGTTGCTAATATCACATCTAATAAAAAAGGATATTAATATT
SEQ2910	TCTGGTAAGAAGGTTGCAACAGTTGCTAATATCACATCTAATAAAAAAGGATATTAATATT
SEQ2911	TCTGGTAAGAAGGTTGCAACAGTTGCTAATATCACATCTAATAAAAAAGGATATTAATATT
SEQ2901	CAGGAGTTAGATGCGAGTCAAAACCCACGTGCACTCAAAGATGTAGATGCAGCTATTATT
SEQ2902	CAGGAGTTAGATGCGAGTCAAAACCCACGTGCACTCAAAGATGTAGATGCAGCTATTATT
SEQ2903	CAGGAGTTAGATGCGAGTCAAAACCCACGTGCACTCAAAGATGTAGATGCAGCTATTATT
SEQ2904	CAGGAGTTAGATGCGAGTCAAAACCCACGTGCACTCAAAGATGTAGATGCAGCTATTATT
SEQ2905	CAGGAGTTAGATGCGAGTCAAAACCCACGTGCACTCAAAGATGTAGATGCAGCTATTATT
SEQ2906	CAGGAGTTAGATGCGAGTCAAAACCCACGTGCACTCAAAGATGTAGATGCAGCTATTATT
SEQ2907	CAGGAGTTAGATGCGAGTCAAAACCCACGTGCACTCAAAGATGTAGATGCAGCTATTATT
SEQ2908	CAGGAGTTAGATGCGAGTCAAAACCCACGTGCACTCAAAGATGTAGATGCAGCTATTATT
SEQ2909	CAGGAGTTAGATGCGAGTCAAAACCCACGTGCACTCAAAGATGTAGATGCAGCTATTATT
SEQ2910	CAGGAGTTAGATGCGAGTCAAAACCCACGTGCACTCAAAGATGTAGATGCAGCTATTATT
SEQ2911	CAGGAGTTAGATGCGAGTCAAAACCCACGTGCACTCAAAGATGTAGATGCAGCTATTATT
SEQ2901	AATAATACATACATTGAGCAAGCTAATTTAAAACCTTCAGATGCTATCTTTGTTGAGAAA
SEQ2902	AATAATACATACATTGAGCAAGCTAATTTAAAACCTTCAGATGCTATCTTTGTTGAGAAA
SEQ2903	AATAATACATACATTGAGCAAGCTAATTTAAAACCTTCAGATGCTATCTTTGTTGAGAAA
SEQ2904	AATAATACATACATTGAGCAAGCTAATTTAAAACCTTCAGATGCTATCTTTGTTGAGAAA
SEQ2905	AATAATACATACATTGAGCAAGCTAATTTAAAACCTTCAGATGCTATCTTTGTTGAGAAA
SEQ2906	AATAATACATACATTGAGCAAGCTAATTTAAAACCTTCAGATGCTATCTTTGTTGAGAAA
SEQ2907	AATAATACATACATTGAGCAAGCTAATTTAAAACCTTCAGATGCTATCTTTGTTGAGAAA
SEQ2908	AATAATACATACATTGAGCAAGCTAATTTAAAACCTTCAGATGCTATCTTTGTTGAGAAA
SEQ2909	AATAATACATACATTGAGCAAGCTAATTTAAAACCTTCAGATGCTATCTTTGTTGAGAAA
SEQ2910	AATAATACATACATTGAGCAAGCTAATTTAAAACCTTCAGATGCTATCTTTGTTGAGAAA
SEQ2911	AATAATACATACATTGAGCAAGCTAATTTAAAACCTTCAGATGCTATCTTTGTTGAGAAA

Table 29: Comparative Sequences relating to SAG1641 (YaeC family protein)

SEQ2901	TCAGATAAAAAATTCAAAACAATGGATTAATATCATTGCGGGACGTAAAAATTGGAAAAAG
SEQ2902	TCAGATAAAAAATTCAAAACAATGGATTAATATCATTGCGGGACGTAAAAATTGGAAAAAG
SEQ2903	TCAGATAAAAAATTCAAAACAATGGATTAATATCATTGCGGGACGTAAAAATTGGAAAAAG
SEQ2904	TCAGATAAAAAATTCAAAACAATGGATTAATATCATTGCGGGACGTAAAAATTGGAAAAAG
SEQ2905	TCAGATAAAAAATTCAAAACAATGGATTAATATCATTGCGGGACGTAAAAATTGGAAAAAG
SEQ2906	TCAGATAAAAAATTCAAAACAATGGATTAATATCATTGCGGGACGTAAAAATTGGAAAAAG
SEQ2907	TCAGATAAAAAATTCAAAACAATGGATTAATATCATTGCGGGACGTAAAAATTGGAAAAAG
SEQ2908	TCAGATAAAAAATTCAAAACAATGGATTAATATCATTGCGGGACGTAAAAATTGGAAAAAG
SEQ2909	TCAGATAAAAAATTCAAAACAATGGATTAATATCATTGCGGGACGTAAAAATTGGAAAAAG
SEQ2910	TCAGATAAAAAATTCAAAACAATGGATTAATATCATTGCGGGACGTAAAAATTGGAAAAAG
SEQ2911	TCAGATAAAAAATTCAAAACAATGGATTAATATCATTGCGGGACGTAAAAATTGGAAAAAG
SEQ2901	CAAAGAAGCGCTAAAGCTATCCAAGCTATCTTGGATGCTTATCACACAGATGAAGTGAAA
SEQ2902	CAAAGAAGCGCTAAAGCTATCCAAGCTATCTTGGATGCTTATCACACAGATGAAGTGAAA
SEQ2903	CAAAGAAGCGCTAAAGCTATCCAAGCTATCTTGGATGCTTATCACACAGATGAAGTGAAA
SEQ2904	CAAAGAAGCGCTAAAGCTATCCAAGCTATCTTGGATGCTTATCACACAGATGAAGTGAAA
SEQ2905	CAAAGAAGCGCTAAAGCTATCCAAGCTATCTTGGATGCTTATCACACAGATGAAGTGAAA
SEQ2906	CAAAGAAGCGCTAAAGCTATCCAAGCTATCTTGGATGCTTATCACACAGATGAAGTGAAA
SEQ2907	CAAAGAAGCGCTAAAGCTATCCAAGCTATCTTGGATGCTTATCACACAGATGAAGTGAAA
SEQ2908	CAAAGAAGCGCTAAAGCTATCCAAGCTATCTTGGATGCTTATCACACAGATGAAGTGAAA
SEQ2909	CAAAGAAGCGCTAAAGCTATCCAAGCTATCTTGGATGCTTATCACACAGATGAAGTGAAA
SEQ2910	CAAAGAAGCGCTAAAGCTATCCAAGCTATCTTGGATGCTTATCACACAGATGAAGTGAAA
SEQ2911	CAAAGAAGCGCTAAAGCTATCCAAGCTATCTTGGATGCTTATCACACAGATGAAGTGAAA
SEQ2901	AAAGTTATCAAAGATACTTCAGCTGATATTCACAATGGAACCCAGCTTTCTTGTACAA
SEQ2902	AAAGTTATCAAAGATACTTCAGCTGATATTCACAATGG-----
SEQ2903	AAAGTTATCAAAGATACTTCAGCTGATATTCAC-----
SEQ2904	AAAGTTATCAAAGATACTTCAGCTGATATTCACAATGG-----
SEQ2905	AAAGTTATCAAAGATACTTCAGCTGATATTCACAATGG-----
SEQ2906	AAAGTTATCAAAGATACTTCAGCTGATATTCACAATGGA-----
SEQ2907	AAAGTTATCAAAGATACTTCAGCTGATATTCACAATGG-----
SEQ2908	AAAGTTATCAAAGATACTTCAGCTGATATTCACAATGG-----
SEQ2909	AAAGTTATCAAAGATACTTCAGCTGATATTCACAATGG-----
SEQ2910	AAAGTTATCAAAGATAC-----
SEQ2911	AAAGTTATCAAAGATACTTCAGCTGATATTCACAATGG-----
>SEQ ID NO 2950: 35_090 frame: 1	
NQEVSASSTSSKVVKGVMTFSDTEKARWDKIEKLVGDKAKIKFTEFTDYTPNQATANK	
DVDINAFQHYNFLENWKNENKKNLI PLEKTYLAPIRIYSEKVKSLKLLKKGATIAIPNDA	
TNGSRALYVLQSAGLIKLVNKGKVVATVANITSNKKDINIQLDASQTPRALKDVDAAII	
NNTYIEQANLKPDAIFVEKSDKNSKQWINI IAGRKNWKKQKNAKAIQAILDAYHTDEVK	
KVIKDTADIPQWNPFLY	
>SEQ ID NO 2951: 35_1169NT frame: 3	
QEVSASSTSSKVVKGVMTFSDTEKARWDKIEKLVGDKAKIKFTEFTDYTPNQATANKD	
VDINAFQHYNFLENWKNENKKNLI PLEKTYLAPIRIYSEKVKSLKLLKKGATIAIPNDAT	
NGSRALYVLQSAGLIKLVNKGKVVATVANITSNKKDINIQLDASQTPRALKDVDAAII	
NNTYIEQANLKPDAIFVEKSDKNSKQWINI IAGRKNWKKQKNAKAIQAILDAYHTDEVK	
VIKDTADIPQW	
>SEQ ID NO 2952: 35_18RS21 frame: 1	
NQEVSASSTSSKVVKGVMTFSDTEKARWDKIEKLVGDKAKIKFTEFTDYTPNQATANK	
DVDINAFQHYNFLENWKNENKKNLI PLEKTYLAPIRIYSEKVKSLKLLKKGATIAIPNDA	
TNGSRALYVLQSAGLIKLVNKGKVVATVANITSNKKDINIQLDASQTPRALKDVDAAII	
NNTYIEQANLKPDAIFVEKSDKNSKQWINI IAGRKNWKKQKNAKAIQAILDAYHTDEVK	
KVIKDTADIP	
>SEQ ID NO 2953:35_2603 frame: 1	
NQEVSASSTSSKVVKGVMTFSDTEKARWDKIEKLVGDKAKIKFTEFTDYTPNQATANK	
DVDINAFQHYNFLENWKNENKKNLI PLEKTYLAPIRIYSEKVKSLKLLKKGATIAIPNDA	
TNGSRALYVLQSAGLIKLVNKGKVVATVANITSNKKDINIQLDASQTPRALKDVDAAII	
NNTYIEQANLKPDAIFVEKSDKNSKQWINI IAGRKNWKKQKNAKAIQAILDAYHTDEVK	
KVIKDTADIPQW	

Table 29: Comparative Sequences relating to SAG1641 (YaeC family protein)

>SEQ ID NO 2954:35_A909 frame: 1
 NQEVASSTSSKVVKGVMFTFSDTEKARWDKIEKLVGDKAKIKFTEFTDYTPNQATANK
 DVDINAFQHYNFLENWKNENKKNLIPEKTYLAPIRIYSEKVKSLKKLKKGATIAIPNDA
 TNGSRALYVLQASAGLIKLVSGKKVATVANITSNKKDINIQLDASQTPRALKDVDAAII
 NNITYIEQANLKPSDAIFVEKSDKNSKQWINIIAGRKNWKKQKNAKAIQAILDAYHTDEVK
 KVIKDTADIPQW

>SEQ ID NO 2955:35_CJB110 frame: 2
 SKVVKGVMFTFSDTEKARWDKIEKLVGDKAKIKFTEFTDYTPNQATANKDVDINAFQHY
 NFLENWKNENKKNLIPEKTYLAPIRIYSEKVKSLKKLKKGATIAIPNDATNGSRALYVL
 QSAGLIKLVSGKKVATVANITSNKKDINIQLDASQTPRALKDVDAAIINNITYIEQANL
 KPSDAIFVEKSDKNSKQWINIIAGRKNWKKQKNAKAIQAILDAYHTDEVKKVIKDTSDI
 PQW

>SEQ ID NO 2956:35_COH1 frame: 2
 VSASSTSSKVVKGVMFTFSDTEKARWDKIEKLVGDKAKIKFTEFTDYTPNQATANKDVD
 INAFQHYNFLENWKNENKKNLIPEKTYLAPIRIYSEKVKSLKKLKKGATIAIPNDATNG
 SRALYVLQASAGLIKLVSGKKVATVANITSNKKDINIQLDASQTPRALKDVDAAIINN
 YIEQANLKPSDAIFVEKSDKNSKQWINIIAGRKNWKKQKNAKAIQAILDAYHTDEVKKVI
 KDTSDADIPQW

>SEQ ID NO 2957:35_H36B frame: 3
 EVASSTSSKVVKGVMFTFSDTEKARWDKIEKLVGDKAKIKFTEFTDYTPNQATANKDV
 DINAFQHYNFLENWKNENKKNLIPEKTYLAPIRIYSEKVKSLKKLKKGATIAIPNDATN
 GSRALYVLQASAGLIKLVSGKKVATVANITSNKKDINIQLDASQTPRALKDVDAAIINN
 TYIEQANLKPSDAIFVEKSDKNSKQWINIIAGRKNWKKQKNAKAIQAILDAYHTDEVKKV
 IKDTSDADIPQW

>SEQ ID NO 2958:35_JM9130013 frame: 2
 SASSTSSKVVKGVMFTFSDTEKARWDKIEKLVGDKAKIKFTEFTDYTPNQATANKDVDI
 NAFQHYNFLENWKNENKKNLIPEKTYLAPIRIYSEKVKSLKKLKKGATIAIPNDATNGS
 RALYVLQASAGLIKLVSGKKVATVANITSNKKDINIQLDASQTPRALKDVDAAIINN
 YIEQANLKPSDAIFVEKSDKNSKQWINIIAGRKNWKKQKNAKAIQAILDAYHTDEVKKVI
 KDTSDADIPQW

>SEQ ID NO 2959:35_M732 frame: 1
 NQEVASSTSSKVVKGVMFTFSDTEKARWDKIEKLVGDKAKIKFTEFTDYTPNQATANK
 DVDINAFQHYNFLENWKNENKKNLIPEKTYLAPIRIYSEKVKSLKKLKKGATIAIPNDA
 TNGSRALYVLQASAGLIKLVSGKKVATVANITSNKKDINIQLDASQTPRALKDVDAAII
 NNITYIEQANLKPSDAIFVEKSDKNSKQWINIIAGRKNWKKQKNAKAIQAILDAYHTDEVK
 KVIKD

>SEQ ID NO 2960:35_M781 frame: 2
 VSASSTSSKVVKGVMFTFSDTEKARWDKIEKLVGDKAKIKFTEFTDYTPNQATANKDVD
 INAFQHYNFLENWKNENKKNLIPEKTYLAPIRIYSEKVKSLKKLKKGATIAIPNDATNG
 SRALYVLQASAGLIKLVSGKKVATVANITSNKKDINIQLDASQTPRALKDVDAAIINN
 YIEQANLKPSDAIFVEKSDKNSKQWINIIAGRKNWKKQKNAKAIQAILDAYHTDEVKKVI
 KDTSDADIPQW

SEQ2950 QEVASSTSSKVVKGVMFTFSDTEKARWDKIEKLVGDKAKIKFTEFTDYTPNQATANK
 SEQ2951 QEVASSTSSKVVKGVMFTFSDTEKARWDKIEKLVGDKAKIKFTEFTDYTPNQATANK
 SEQ2952 QEVASSTSSKVVKGVMFTFSDTEKARWDKIEKLVGDKAKIKFTEFTDYTPNQATANK
 SEQ2953 QEVASSTSSKVVKGVMFTFSDTEKARWDKIEKLVGDKAKIKFTEFTDYTPNQATANK
 SEQ2954 QEVASSTSSKVVKGVMFTFSDTEKARWDKIEKLVGDKAKIKFTEFTDYTPNQATANK
 SEQ2955 -----SKVVKGVMFTFSDTEKARWDKIEKLVGDKAKIKFTEFTDYTPNQATANK
 SEQ2956 --VSASSTSSKVVKGVMFTFSDTEKARWDKIEKLVGDKAKIKFTEFTDYTPNQATANK
 SEQ2957 --EVSASSTSSKVVKGVMFTFSDTEKARWDKIEKLVGDKAKIKFTEFTDYTPNQATANK
 SEQ2958 ---SASSTSSKVVKGVMFTFSDTEKARWDKIEKLVGDKAKIKFTEFTDYTPNQATANK
 SEQ2959 QEVASSTSSKVVKGVMFTFSDTEKARWDKIEKLVGDKAKIKFTEFTDYTPNQATANK
 SEQ2960 --VSASSTSSKVVKGVMFTFSDTEKARWDKIEKLVGDKAKIKFTEFTDYTPNQATANK

SEQ2950 DVDINAFQHYNFLENWKNENKKNLIPEKTYLAPIRIYSEKVKSLKKLKKGATIAIPNDA
 SEQ2951 DVDINAFQHYNFLENWKNENKKNLIPEKTYLAPIRIYSEKVKSLKKLKKGATIAIPNDA
 SEQ2952 DVDINAFQHYNFLENWKNENKKNLIPEKTYLAPIRIYSEKVKSLKKLKKGATIAIPNDA
 SEQ2953 DVDINAFQHYNFLENWKNENKKNLIPEKTYLAPIRIYSEKVKSLKKLKKGATIAIPNDA
 SEQ2954 DVDINAFQHYNFLENWKNENKKNLIPEKTYLAPIRIYSEKVKSLKKLKKGATIAIPNDA
 SEQ2955 DVDINAFQHYNFLENWKNENKKNLIPEKTYLAPIRIYSEKVKSLKKLKKGATIAIPNDA
 SEQ2956 DVDINAFQHYNFLENWKNENKKNLIPEKTYLAPIRIYSEKVKSLKKLKKGATIAIPNDA
 SEQ2957 DVDINAFQHYNFLENWKNENKKNLIPEKTYLAPIRIYSEKVKSLKKLKKGATIAIPNDA
 SEQ2958 DVDINAFQHYNFLENWKNENKKNLIPEKTYLAPIRIYSEKVKSLKKLKKGATIAIPNDA

Table 29: Comparative Sequences relating to SAG1641 (YaeC family protein)

SEQ2959	DVDINAFQHYNFLENWKNENKKNLIPIRYSEKVKSLKKLKKGATIAIPNDA
SEQ2960	DVDINAFQHYNFLENWKNENKKNLIPIRYSEKVKSLKKLKKGATIAIPNDA
SEQ2950	TNGSRALYVLQSAGLIKLVSGKKVATVANITSNKKDINIQLDASQTPRALKDVDAAII
SEQ2951	TNGSRALYVLQSAGLIKLVSGKKVATVANITSNKKDINIQLDASQTPRALKDVDAAII
SEQ2952	TNGSRALYVLQSAGLIKLVSGKKVATVANITSNKKDINIQLDASQTPRALKDVDAAII
SEQ2953	TNGSRALYVLQSAGLIKLVSGKKVATVANITSNKKDINIQLDASQTPRALKDVDAAII
SEQ2954	TNGSRALYVLQSAGLIKLVSGKKVATVANITSNKKDINIQLDASQTPRALKDVDAAII
SEQ2955	TNGSRALYVLQSAGLIKLVSGKKVATVANITSNKKDINIQLDASQTPRALKDVDAAII
SEQ2956	TNGSRALYVLQSAGLIKLVSGKKVATVANITSNKKDINIQLDASQTPRALKDVDAAII
SEQ2957	TNGSRALYVLQSAGLIKLVSGKKVATVANITSNKKDINIQLDASQTPRALKDVDAAII
SEQ2958	TNGSRALYVLQSAGLIKLVSGKKVATVANITSNKKDINIQLDASQTPRALKDVDAAII
SEQ2959	TNGSRALYVLQSAGLIKLVSGKKVATVANITSNKKDINIQLDASQTPRALKDVDAAII
SEQ2960	TNGSRALYVLQSAGLIKLVSGKKVATVANITSNKKDINIQLDASQTPRALKDVDAAII
SEQ2950	NNTYIEQANLKPSDAIFVEKSDKNSKQWINIIAGRKNWKKQKNAKAIQAILDAYHTDEVK
SEQ2951	NNTYIEQANLKPSDAIFVEKSDKNSKQWINIIAGRKNWKKQKNAKAIQAILDAYHTDEVK
SEQ2952	NNTYIEQANLKPSDAIFVEKSDKNSKQWINIIAGRKNWKKQKNAKAIQAILDAYHTDEVK
SEQ2953	NNTYIEQANLKPSDAIFVEKSDKNSKQWINIIAGRKNWKKQKNAKAIQAILDAYHTDEVK
SEQ2954	NNTYIEQANLKPSDAIFVEKSDKNSKQWINIIAGRKNWKKQKNAKAIQAILDAYHTDEVK
SEQ2955	NNTYIEQANLKPSDAIFVEKSDKNSKQWINIIAGRKNWKKQKNAKAIQAILDAYHTDEVK
SEQ2956	NNTYIEQANLKPSDAIFVEKSDKNSKQWINIIAGRKNWKKQKNAKAIQAILDAYHTDEVK
SEQ2957	NNTYIEQANLKPSDAIFVEKSDKNSKQWINIIAGRKNWKKQKNAKAIQAILDAYHTDEVK
SEQ2958	NNTYIEQANLKPSDAIFVEKSDKNSKQWINIIAGRKNWKKQKNAKAIQAILDAYHTDEVK
SEQ2959	NNTYIEQANLKPSDAIFVEKSDKNSKQWINIIAGRKNWKKQKNAKAIQAILDAYHTDEVK
SEQ2960	NNTYIEQANLKPSDAIFVEKSDKNSKQWINIIAGRKNWKKQKNAKAIQAILDAYHTDEVK
SEQ2950	KVIKDT SADIPQWNPAPFLY
SEQ2951	KVIKDT SADIPQW-----
SEQ2952	KVIKDT SADIP-----
SEQ2953	KVIKDT SADIPQW-----
SEQ2954	KVIKDT SADIPQW-----
SEQ2955	KVIKDT SADIPQW-----
SEQ2956	KVIKDT SADIPQW-----
SEQ2957	KVIKDT SADIPQW-----
SEQ2958	KVIKDT SADIPQW-----
SEQ2959	KVIKDT SADIPQW-----
SEQ2960	KVIKDT SADIPQW-----

**Table 30: Comparative Sequences relating to SAG2147
(protein of unknown function / lipoprotein, putative)**

**SEQ ID NO. 3001: SAG2147 FROM THE 1169NT1 GBS TYPE V STRAIN
(REVERSE COMPLEMENT)**

AAAAGTTTCAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAAGTTTCGCGTAGCC
AAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAAACAGGCT
CCAAAACCTTCTCAGGCATCTAATGAAGTCCCAAAATCAAGTTCTCAATCTACAGAAGCT
AATTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACAAGCAGTTGTAACA
GAAAATACCCCTGCTACCAGTCAGGCACAACAACTTATGCTGTTACTGAGACAACCTTAC
AAACCTGCTCAACACCAGACAAGTGGCCAAGTATTGAGCAATGGAATACTGCAGGGGCG
GTCGGATCTGCTGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGG
GAACATATTATTGCCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAGGAGCT
TCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGATCAAGTT
AATTCAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTAC

**SEQ ID NO. 3002: SAG2147 FROM THE 18RS21 GBS TYPE II STRAIN
(REVERSE COMPLEMENT)**

AAAAGTTTCAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAAGTTTC
GCGTAGCCAAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAA
AACAGGCTCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAAATCAAGTTCTCAATCTA
CAGAAGCTAATTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCAGCTGTAGAACAAGCAG
TTGTAACAGAAAAACCCCTGCTACCAGTCAGGCACAACAGCTTATGCTGTTACTGAGA
CAACTTATAGACCTGCTCAACACCAGACGAGTGGCCAAGTATTGAGTAATGGAATACTG
CAGGGGCTATTGGCTCAGCAGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCCTCAGT
CTACTTGGGAACATATTATTGCCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCT
CAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGG
ATCAAGTTAATTCAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTAC

**SEQ ID NO. 3003: SAG2147 FROM THE 2603 V/R GBS TYPE V STRAIN
(REVERSE COMPLEMENT)**

AAAAGTTTCAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAAGT
TCGCGTAGCCAAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGT
AAAAACAGGCTCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAAATCAAGTTCTCAATC
TACAGAAGCTAATTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCAGCTGTAGAACAAGC
AGTTGTAACAGAAAAACCCCTGCTACCAGTCAGGCACAACAGCTTATGCTGTTACTGA
GACAACCTTATAGACCTGCTCAACACCAGACGAGTGGCCAAGTATTGAGTAATGGAATACT
TGCAGGGGCTATTGGCTCAGCAGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCCTCA
GTCTACTTGGGAACATATTATTGCCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGC
CTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAG
GGATCAAGTTAATTCAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTA
C

**SEQ ID NO. 3004: SAG2147 FROM THE 090 GBS TYPE Ia STRAIN
(REVERSE COMPLEMENT)**

TAGCCAAAAAATCAAAAATGATTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAAAC
AGGCTCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAAATCAAGTTCTCAATCTACAG
AAGCTAATTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCAGCTGTAGAACAAGCAGTTG
TAACAGAAAAACCCCTGCTACCAGTCAGGCACAACAGCTTATGCTGTTACTGAGACAA
CTTATAGACCTGCTCAACACCAGACGAGTGGCCAAGTATTGAGTAATGGAATACTGCAG
GGGCTATTGGCTCAGCAGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTA
CTTGGGAACATATTATTGCCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAG
GAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGA

**SEQ ID NO. 3005: SAG2147 FROM THE A909 GBS TYPE Ia STRAIN
(REVERSE COMPLEMENT)**

AAGGCGACATCTAAATCAAAAGTAGAAGATGTAAAACAGGCTCCAAAACCTTCTCAGGCA
TCTAATGAAGCCCCAAAATCAAGTTCTCAATCTACAGAAGCTAATTCTCAGCAACAAGTT
ACTGCGAGTGAAGAGGCAGCTGTAGAACAAGCAGTTGTAACAGAAAAACCCCTGCTACC
AGTCAGGCACAACAAGCTTATGCTGTTACTGAGACAACCTTATAGACCTGCTCAACACCAG
ACAAGTGGCCAAGTATTGAGTAATGGAATACTGCAGGGGCTATTGGCTCAGCAGCTGCA
GCACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATTATTGCCCCGT
GAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAACG
ATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGAATCAAGTTAATTCAGCTATTAAAGCT
TATCGTGCTCAAGGTTTATCA

**Table 30: Comparative Sequences relating to SAG2147
(protein of unknown function / lipoprotein, putative)**

**SEQ ID NO. 3006: SAG2147 FROM THE CJB110 GBS NONTYPEABLE STRAIN
(REVERSE COMPLEMENT)**

AAATCTTTGTCAAAAGCAGATAAAGTTCGCGTAGCCAAAAATCAAAAATGACTAAGGCGA
CATCTAAATCAAAAGTAGAAGATGTAAACAGGCTCCAAAACCTTCTCAGGCATCTAATG
AAGCCCCAAAATCAAGTTCTCAATCTACAGAAGCTAATTCTCAGCAACAAGTTACTGCGA
GTGAAGAGGCAGCTGTAGAACAAGCAGTTGTAAACAGAAAACACCCCTGCTACCAGTCAGG
CACAACAAGCTTATGCTGTTACTGAGACAACTTATAGACCTGCTCAACACCAGACGAGTG
GCCAAGTATTGAGTAATGGAAATACTGCAGGGGCTATTGGCTCAGCAGCTGCAGCACAAA
TGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAA
ATGGTAATCCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAG
GTTGGGGTTCAACAGCTACAGTTCAGGATCAAGTTAATTCAGCTATTAAAGCTTATCCTG
CTCAAGGTTTATCAGCTTGGGGTTAC

**SEQ ID NO. 3007: SAG2147 FROM THE COH1 GBS TYPE III STRAIN
(REVERSE COMPLEMENT)**

AAAAGTTCACAAGTTACTACTGAATCTTTGTCAAAAGCAGATAA
AGTTTCGCGTAGCCAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGA
TGTAAAACAGGCTCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAAATCAAGTTCTCA
ATCTACAGAAGCTAATTTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACA
AGCAGTTGTAAACAGAAAATACCCCTGCTACCAGTCAGGCACAACAACTTATGCTGTTAC
TGAGACAACTTACAAACCTGCTCAACACCAGACAAGTGGCCAAGTATTGAGCAATGGAAA
TACTGCAGGGGCGGTCGGATCTGCTGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCC
TCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAA
TGCCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGT
TCAGGATCAAGTTAATTCAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGG
TTAC

**SEQ ID NO. 3008: SAG2147 FROM THE H36b GBS TYPE Ib STRAIN
(REVERSE COMPLEMENT)**

AAAAGTTCACAAGTTACTACTGAATCTTTGTCAAAAGC
AGATAAAGTTTCGCGTAGCCAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGT
AGAAGATGTAAACAGGCTCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAAATCAAG
TTCTCAATCTACAGAAGCTAATTTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCAGCTGT
AGAACAAGCAGTTGTAAACAGAAAACACCCCTGCTACCAGTCAGGCACAACAAGCTTATGC
TGTTACTGAGACAACTTATAGACCTGCTCAACACCAGACAAGTGGCCAAGTATTGAGTAA
TGGAATACTGCAGGGGCTATTGGCTCAGCAGCTGCAGCACAAATGGCTGCTGCAACAGG
AGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGT
TGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGC
TACAGTTCAGGATCAAGTTAATTCAGCTATTAAAGCTT

**SEQ ID NO. 3009: SAG2147 FROM THE M732 GBS TYPE III STRAIN
(REVERSE COMPLEMENT)**

AAAAGTTCACAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTCGCGTAGC
CAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAACAGGC
TCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAAATCAAGTTCTCAATCTACAGAAGC
TAATTTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACAAGCAGTTGTAAAC
AGAAAATACCCCTGCTACCAGTCAGGCACAACAACTTATGCTGTTACTGAGACAACTTA
CAAACCTGCTCAACACCAGACAAGTGGCCAAGTATTGAGCAATGGAAATACTGCAGGGGC
GGTCGGATCTGCTGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTG
GGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAGGAGC
TTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGATCAAGT
TAATTCAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTA

**Table 30: Comparative Sequences relating to SAG2147
(protein of unknown function / lipoprotein, putative)**

SEQ ID NO. 3010: SAG2147 FROM THE M781 GBS TYPE III STRAIN
(REVERSE COMPLEMENT)

GTAACCCCAAGCTGATAAACCTTGAGCACGATAAGCTTTAATAGCTGAATTAACTTGATC
CTGAAGTGTAGCTGTTGAACCCCAACCTGGCATCGTTTGGAAAAGTCCTGAAGCTCCTGA
GGCATTAGCAACATTAGGATTACCATTTGATTACAGGGCAATAATATGTTCCCAAGTAGA
CTGAGGGACTCCTGTTGCAGCAGCCATTTGTGCTGCAGCAGCAGATCCGACCGCCCCCTGC
AGTATTTCCATTGCTCAATACTTGGCCACTTGTCTGGTGTGAGCAGGTTTGTAAAGTTGT
CTCAGTAACAGCATAAGTTTGTGTGCTGACTGGTAGCAGGGGTATTTCTGTTACAAC
TGCTTGTTCTACAGCCGCCTCTTCACTCGCAGTAACTTGTGCTGAGAATTAGCTTCTGT
AGATTGAGAACTTGATTTTGGGGCTTCATTAGATGCCTGAGAAGGTTTGGAGCCTGTTT
TACATCTTCTACTTTTGATTAGATGTCGCCTTAGTCATTTTGTATTTTGGCTACGCG
AACTTTATCTGCTTTTGACAAAGA

SEQ3001 -----
SEQ3002 -----
SEQ3003 -----
SEQ3004 -----
SEQ3005 AGGCGACATCTAAATCAAAAGTAGAAGATGTAAAACAGGCTCCAAAACCTTCTCAGGCA
SEQ3007 -----
SEQ3008 -----
SEQ3009 -----
SEQ3010 -----

SEQ3001 -----
SEQ3002 -----
SEQ3003 -----
SEQ3004 -----
SEQ3005 CTAATGAAGCCCCAAATCAAGTTCTCAATCTACAGAAGCTAATTCTCAGCAACAAGTT
SEQ3007 -----
SEQ3008 -----
SEQ3009 -----
SEQ3010 -----

SEQ3001 -----
SEQ3002 -----
SEQ3003 -----
SEQ3004 -----
SEQ3005 CTGCGAGTGAAGAGGCAGCTGTAGAACAAGCAGTTGTAACAGAAAAACCCCCTGCTACC
SEQ3007 -----
SEQ3008 -----
SEQ3009 -----
SEQ3010 -----

SEQ3001 -----
SEQ3002 -----
SEQ3003 -----
SEQ3004 -----
SEQ3005 GTCAGGCACAACAAGCTTATGCTGTTACTGAGACAACCTTATAGACCTGCTCAACACCAG
SEQ3007 -----
SEQ3008 -----
SEQ3009 -----
SEQ3010 -----

SEQ3001 -----
SEQ3002 -----
SEQ3003 -----
SEQ3004 -----
SEQ3005 CAAGTGCCCAAGTATTGAGTAATGGAATACTGCAGGGGCTATGGCTCAGCAGCTGCA
SEQ3007 -----
SEQ3008 -----
SEQ3009 -----
SEQ3010 -----

**Table 30: Comparative Sequences relating to SAG2147
(protein of unknown function / lipoprotein, putative)**

SEQ3001	-----
SEQ3002	-----
SEQ3003	-----
SEQ3004	-----
SEQ3005	CACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGT
SEQ3007	-----
SEQ3008	-----
SEQ3009	-----
SEQ3010	-----
SEQ3001	-----
SEQ3002	-----
SEQ3003	-----
SEQ3004	-----
SEQ3005	AATCAAATGGTAATCCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAACG
SEQ3007	-----
SEQ3008	-----
SEQ3009	-----
SEQ3010	-----
SEQ3001	-----
SEQ3002	-----
SEQ3003	-----
SEQ3004	-----
SEQ3005	TGCCAGGTTGGGGTTCAACAGCTACAGTTCAGAATCAAGTTAATTAGCTATTAAAGCT
SEQ3007	-----
SEQ3008	-----
SEQ3009	-----
SEQ3010	-----
SEQ3001	AAAGTTCACAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTCGCGTAGCCAAA
SEQ3002	AAAGTTCACAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTCGCGTAGCCAAA
SEQ3003	AAAGTTCACAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTCGCGTAGCCAAA
SEQ3004	-----TAGCCAAA
SEQ3005	ATCGTGCTCAAGGTTTATCASAATCTTTGTCAAAAGCAGATAAAGTTCGCGTAGCCAAA
SEQ3007	AAAGTTCACAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTCGCGTAGCCAAA
SEQ3008	AAAGTTCACAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTCGCGTAGCCAAA
SEQ3009	AAAGTTCACAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTCGCGTAGCCAAA
SEQ3010	-----GTAACCCCAAGCTGA---TAAACCTTGAGCACGATAAGCTTTAATAGCTGAA
SEQ3001	AATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAACAGGCTCCA
SEQ3002	AATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAACAGGCTCCA
SEQ3003	AATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAACAGGCTCCA
SEQ3004	AATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAACAGGCTCCA
SEQ3005	AATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAACAGGCTCCA
SEQ3007	AATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAACAGGCTCCA
SEQ3008	AATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAACAGGCTCCA
SEQ3009	AATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAACAGGCTCCA
SEQ3010	TAACCTTGATCCTGAACTGTAGCTGTTGAACCCCAACCTGGCATCGTTTGAAAAGTCTCT
SEQ3001	AACCTTCTCAGGCATCTAATGAAGTCCCAAAATCAAGTTCTCAATCTACAGAAGCTAAT
SEQ3002	AACCTTCTCAGGCATCTAATGAAGTCCCAAAATCAAGTTCTCAATCTACAGAAGCTAAT
SEQ3003	AACCTTCTCAGGCATCTAATGAAGTCCCAAAATCAAGTTCTCAATCTACAGAAGCTAAT
SEQ3004	AACCTTCTCAGGCATCTAATGAAGTCCCAAAATCAAGTTCTCAATCTACAGAAGCTAAT
SEQ3005	AACCTTCTCAGGCATCTAATGAAGTCCCAAAATCAAGTTCTCAATCTACAGAAGCTAAT
SEQ3007	AACCTTCTCAGGCATCTAATGAAGTCCCAAAATCAAGTTCTCAATCTACAGAAGCTAAT
SEQ3008	AACCTTCTCAGGCATCTAATGAAGTCCCAAAATCAAGTTCTCAATCTACAGAAGCTAAT
SEQ3009	AACCTTCTCAGGCATCTAATGAAGTCCCAAAATCAAGTTCTCAATCTACAGAAGCTAAT
SEQ3010	AAGCTCCTGAGGCATT---AGCAACATTAGGATTAC-CATTTGATTACCGGCAATAAT
SEQ3001	TCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACAAGCAGTTGTAACAGA
SEQ3002	TCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACAAGCAGTTGTAACAGA
SEQ3003	TCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACAAGCAGTTGTAACAGA
SEQ3004	TCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACAAGCAGTTGTAACAGA
SEQ3005	TCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACAAGCAGTTGTAACAGA
SEQ3007	TCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACAAGCAGTTGTAACAGA
SEQ3008	TCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACAAGCAGTTGTAACAGA
SEQ3009	TCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACAAGCAGTTGTAACAGA
SEQ3010	TGTTCCCAAGTAGACTGAGGGACTCTGTTGCAGCAGCCATTGTGCTGCAGCAGCAGA

**Table 30: Comparative Sequences relating to SAG2147
(protein of known function / lipoprotein, putative)**

SEQ3001	--AAATACCCCTGCTACCAAGTCAGGCACAACAACTTATGCTGTTACTGAGACAACCTTA
SEQ3002	--AAACACCCCTGCTACCAAGTCAGGCACAACAACTTATGCTGTTACTGAGACAACCTTA
SEQ3003	--AAACACCCCTGCTACCAAGTCAGGCACAACAACTTATGCTGTTACTGAGACAACCTTA
SEQ3004	--AAACACCCCTGCTACCAAGTCAGGCACAACAACTTATGCTGTTACTGAGACAACCTTA
SEQ3005	--AAACACCCCTGCTACCAAGTCAGGCACAACAACTTATGCTGTTACTGAGACAACCTTA
SEQ3007	--AAATACCCCTGCTACCAAGTCAGGCACAACAACTTATGCTGTTACTGAGACAACCTTA
SEQ3008	--AAACACCCCTGCTACCAAGTCAGGCACAACAACTTATGCTGTTACTGAGACAACCTTA
SEQ3009	--AAATACCCCTGCTACCAAGTCAGGCACAACAACTTATGCTGTTACTGAGACAACCTTA
SEQ3010	CCGACCGCCCTGCAGTATTTCCATTGCTCAATACTTG-GCCACTTGTCTGGTGTGAG
SEQ3001	AAACCTGCTCAACACCAGACAAGTGGC-CAAGTATTGAGCAATGGAAATACTGCAGGGG
SEQ3002	AGACCTGCTCAACACCAGACGAGTGGC-CAAGTATTGAGTAATGGAAATACTGCAGGGG
SEQ3003	AGACCTGCTCAACACCAGACGAGTGGC-CAAGTATTGAGTAATGGAAATACTGCAGGGG
SEQ3004	AGACCTGCTCAACACCAGACGAGTGGC-CAAGTATTGAGTAATGGAAATACTGCAGGGG
SEQ3005	AGACCTGCTCAACACCAGACGAGTGGC-CAAGTATTGAGTAATGGAAATACTGCAGGGG
SEQ3007	AAACCTGCTCAACACCAGACAAGTGGC-CAAGTATTGAGCAATGGAAATACTGCAGGGG
SEQ3008	AGACCTGCTCAACACCAGACAAGTGGC-CAAGTATTGAGTAATGGAAATACTGCAGGGG
SEQ3009	AAACCTGCTCAACACCAGACAAGTGGC-CAAGTATTGAGCAATGGAAATACTGCAGGGG
SEQ3010	AGGTTTGTAAAGTTGTCTCAGTAACAGCATAAGTTTGTGTGCTGACTGGTAGCAGGGG
SEQ3001	GGTCGGATCTGCTGCTGCAGCACAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTT
SEQ3002	TATTGGCTCAGCAGCTGCAGCACAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTT
SEQ3003	TATTGGCTCAGCAGCTGCAGCACAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTT
SEQ3004	TATTGGCTCAGCAGCTGCAGCACAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTT
SEQ3005	TATTGGCTCAGCAGCTGCAGCACAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTT
SEQ3007	GGTCGGATCTGCTGCTGCAGCACAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTT
SEQ3008	TATTGGCTCAGCAGCTGCAGCACAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTT
SEQ3009	GGTCGGATCTGCTGCTGCAGCACAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTT
SEQ3010	A-TTT--TCTGTTACAACCTGCTTGTCTACAGCCGCTCTTCACTCGCAGTAACCTTGT
SEQ3001	GGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAGGAG
SEQ3002	GGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAGGAG
SEQ3003	GGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAGGAG
SEQ3004	GGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAGGAG
SEQ3005	GGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAGGAG
SEQ3007	GGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAGGAG
SEQ3008	GGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAGGAG
SEQ3009	GGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCTCAGGAG
SEQ3010	GCTGAGA-ATTAGCTTCTGTAGATTGAG---AA--CTTGATTGTTGGGGCTTCATTAGATG
SEQ3001	CTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGATCAAG
SEQ3002	CTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGATCAAG
SEQ3003	CTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGATCAAG
SEQ3004	CTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGA-----
SEQ3005	CTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGATCAAG
SEQ3007	CTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGATCAAG
SEQ3008	CTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGATCAAG
SEQ3009	CTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGATCAAG
SEQ3010	CCTGAGAAGGTTTT-----GGAGCCTGTTTTACATCTTCTACTTTTGATTTAGATGTGCG
SEQ3001	TAATTCAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTAC--
SEQ3002	TAATTCAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTAC--
SEQ3003	TAATTCAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTAC--
SEQ3004	-----
SEQ3005	TAATTCAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTAC--
SEQ3007	TAATTCAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTAC--
SEQ3008	TAATTCAGCTATTAAAGCTT-----
SEQ3009	TAATTCAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTA---
SEQ3010	TTAGTCA-TTTTGATTTTTTGGCTACGCGAATTTTATCTGCTTTTGACAAAGA

**Table 30: Comparative Sequences relating to SAG2147
(protein of unknown function / lipoprotein, putative)**

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>SEQ ID NO 3050: 25_1169NT frame: 1
KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEVPKSSSQSTEAN
SQQQVTASEEAAVEQAVVTENTPATSAQQQTYAVTETTYKPAQHQTSGQVLSNGNTAGAV
GSAAAAQMAAATGVPQSTWEHIIARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SAIKAYRAQGLSAWGY

>SEQ ID NO 3051:25_18RS21 frame: 1
KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SQQQVTASEEAAVEQAVVTENTPATSAQQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI
GSAAAAQMAAATGVPQSTWEHIIARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SAIKAYRAQGLSAWGY

>SEQ ID NO 3052:25_2603 frame: 1
KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SQQQVTASEEAAVEQAVVTENTPATSAQQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI
GSAAAAQMAAATGVPQSTWEHIIARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SAIKAYRAQGLSAWGY

>SEQ ID NO 3053:25_090 frame: 3
AKKSKMIKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTASEEAAVEQAVV
TENTPATSAQQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI GSAAAAQMAAATGVPQST
WEHIIARESNNGNPNVANASGASGLFQTMPGWGSTATVQ

>SEQ ID NO 3054:25_A909 frame: 1
KATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTASEEAAVEQAVVTENTPAT
SAQQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI GSAAAAQMAAATGVPQSTWEHIIAR
ESNNGNPNVANASGASGLFQTMPGWGSTATVQNVNSAIKAYRAQGLS

>SEQ ID NO 3055:25_CJB110 frame: 3
SLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTAS
EEAAVEQAVVTENTPATSAQQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI GSAAAAQM
AAATGVPQSTWEHIIARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAIKAYRA
QGLSAWGY

>SEQ ID NO 3056:25_COH1 frame: 1
KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SQQQVTASEEAAVEQAVVTENTPATSAQQQTYAVTETTYKPAQHQTSGQVLSNGNTAGAV
GSAAAAQMAAATGVPQSTWEHIIARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SAIKAYRAQGLSAWGY

>SEQ ID NO 3057:25_H36B frame: 1
KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SQQQVTASEEAAVEQAVVTENTPATSAQQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI
GSAAAAQMAAATGVPQSTWEHIIARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SAIKA

>SEQ ID NO 3058:25_M732 frame: 1
KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SQQQVTASEEAAVEQAVVTENTPATSAQQQTYAVTETTYKPAQHQTSGQVLSNGNTAGAV
GSAAAAQMAAATGVPQSTWEHIIARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SAIKAYRAQGLSAWG

>SEQ ID NO 3059:25_M781 frame: 4
SLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTAS
EEAAVEQAVVTENTPATSAQQQTYAVTETTYKPAQHQTSGQVLSNGNTAGAVGSAAAAQM
AAATGVPQSTWEHIIARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAIKAYRA
QGLSAWGY

SEQ3050      SSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEVPKSSSQSTEAN
SEQ3051      SSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SEQ3052      SSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SEQ3053      -----AKKSKMIKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SEQ3054      -----KATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SEQ3055      -----SLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SEQ3056      SSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SEQ3057      SSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SEQ3058      SSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SEQ3059      -----SLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN

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**Table 30: Comparative Sequences relating to SAG2147
(protein of unknown function / lipoprotein, putative)**

SEQ3050	SQQQVTASEEAAVEQAVVTENTPATSSQAQQTAYAVTETTYKPAQHQTSGQVLSNGNTAGAV
SEQ3051	SQQQVTASEEAAVEQAVVTENTPATSSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI
SEQ3052	SQQQVTASEEAAVEQAVVTENTPATSSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI
SEQ3053	SQQQVTASEEAAVEQAVVTENTPATSSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI
SEQ3054	SQQQVTASEEAAVEQAVVTENTPATSSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI
SEQ3055	SQQQVTASEEAAVEQAVVTENTPATSSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI
SEQ3056	SQQQVTASEEAAVEQAVVTENTPATSSQAQQTAYAVTETTYKPAQHQTSGQVLSNGNTAGAV
SEQ3057	SQQQVTASEEAAVEQAVVTENTPATSSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI
SEQ3058	SQQQVTASEEAAVEQAVVTENTPATSSQAQQTAYAVTETTYKPAQHQTSGQVLSNGNTAGAV
SEQ3059	SQQQVTASEEAAVEQAVVTENTPATSSQAQQTAYAVTETTYKPAQHQTSGQVLSNGNTAGAV
SEQ3050	GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SEQ3051	GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SEQ3052	GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SEQ3053	GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQ----
SEQ3054	GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQNQVN
SEQ3055	GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SEQ3056	GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SEQ3057	GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SEQ3058	GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SEQ3059	GSAAAAQMAAATGVPQSTWEHI IARESNNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
SEQ3050	AIKAYRAQGLSAWGY
SEQ3051	AIKAYRAQGLSAWGY
SEQ3052	AIKAYRAQGLSAWGY
SEQ3053	-----
SEQ3054	AIKAYRAQGLS----
SEQ3055	AIKAYRAQGLSAWGY
SEQ3056	AIKAYRAQGLSAWGY
SEQ3057	AIKA-----
SEQ3058	AIKAYRAQGLSAWG-
SEQ3059	AIKAYRAQGLSAWGY

**Table 31: Comparative Sequences relating to SAG2148
(LysM domain protein)**

SEQ ID NO. 3101: SAG2148 FROM THE 1169NT1 GBS TYPE V STRAIN

GCATCTTATACCGTGAAATCAGGTGATACCTTATCAGCTATTGCTAAAAATCATAAACTACGGTACAAGAGTTAGTG
TCTCTCAATAGTATCAGTAACGCTGATGTCATCAGTATAGGTGATGTTTTAAATTTGGATAATTCTACAGCTAGTCAA
GCAGAAGCAAAATCTCAACCAACAATTGAAAATTCAATGAATTCCTCATCAAATTTGAGTTCAAGTGATTGAGCTGCA
AAAGAAGAAATAGCTCGTCGTGAATCAAATGGTAGTTATACTGCACAGAATGGACAATATTATGGAAGATATCAACTG
TCTCAATCTTACCTAAATGGCGACTTATCTCCTGAAAATCAAGAAAAAGTAGCGGACAATTATGTGGCTTCTCGTTAC
GGATCTTGGTCGGCAGCGCTATCATTTTGAATAGTAACGGCTGGTAT

SEQ ID NO. 3102: SAG2148 FROM THE 18RS21 GBS TYPE II STRAIN

GCATCTTATACCGTGAAATCAGGTGATACCTTATCAGCTATTGCTAAAAATCATAAACTACGGTACAAGAGTTAGTG
TCTCTCAATAGTATCAGTAACGCTGATGTCATCAGTATAGGTGATGTTTTAAATTTGGATAATTCTACAGCTAGTCAA
GCAGAAGCAAAATCTCAACCAACAATTGAAAATTCAATGAATTCCTCATCAAATTTGAGTTCAAGTGATTGAGCCGCA
AAAGAAGAAATAGCTCGTCGTGAATCAAATGGTAGTTATACTGCACAGAATGGACAATATTATGGAAGATATCAACTG
TCTCAATCTTACCTAAATGGCGACTTATCTCCTGAAAATCAAGAAAAAGTAGCGGACAATTATGTGGTTTCTCGTTAC
GGATCTTGGTCGGCAGCGCTATCATTTTGAATAGTAACGGCTGGTAT

SEQ ID NO. 3103: SAG2148 FROM THE 2603 V/R GBS TYPE V STRAIN

GCATCTTATACCGTGAAATCAGGTGATACCTTATCAGCTATTGCTAAAAATCATAAACTACGGTACAAGAGTTAGTG
TCTCTCAATAGTATCAGTAACGCTGATGTCATCAGTATAGGTGATGTTTTAAATTTGGATAATTCTACAGCTAGTCAA
GCAGAAGCAAAATCTCAACCAACAATTGAAAATTCAATGAATTCCTCATCAAATTTGAGTTCAAGTGATTGAGCCGCA
AAAGAAGAAATAGCTCGTCGTGAATCAAATGGTAGTTATACTGCACAGAATGGACAATATTATGGAAGATATCAACTG
TCTCAATCTTACCTAAATGGCGACTTATCTCCTGAAAATCAAGAAAAAGTAGCGGACAATTATGTGGTTTCTCGTTAC
GGATCTTGGTCGGCAGCGCTATCATTTTGAATAGTAACGGCTGGTAT

SEQ ID NO. 3104: SAG2148 FROM THE 090 GBS TYPE Ia STRAIN

GCATCTTATACCGTGAAATCAGGTGATACCTTATCAGCTATTGCTAAAAATCATAAACTACGGTACAAGAGTTAGTG
TCTCTCAATAGTATCAGTAACGCTGATGTCATCAGTATAGGTGATGTTTTAAATTTGGATAATTCTAAAGCTAGTCAA
GCAGAAGCAAAATCTCAACCAACAATTGAAAATTCAATGAATTCCTCATCAAATTTGAGTTCAAGTGATTGAGCCGCA
AAAGAAGAAATAGCTCGTCGTGAATCAAATGGTAGTTATACTGCACAGAATGGACAATATTATGGAAGATATCAACTG
TCTCAATCTTACCTAAATGGCGACTTATCTCCTGAAAATCAAGAAAAAGTAGCGGACAATTATGTGGTTTCTCGTTAC
GGATCTTGGTCGGCAGCGCTATCATTTTGAATAGTAACGGCTGGTAT

SEQ ID NO. 3105: SAG2148 FROM THE A909 GBS TYPE Ia STRAIN

GCATCTTATACCGTGAAATCAGGTGATACCTTATCAGCTATTGCTAAAAATCATAAACTACGGTACAAGAGTTAGTG
TCTCTCAATAGTATCAGTAACGCTGATGTCATCAGTATAGGTGATGTTTTAAATTTGGATAATTCTACAGCTAGTCAA
GCAGAAGCAAAATCTCAACCAACAATTGAAAATTCAATGAATTCCTCATCAAATTTGAGTTCAAGTGATTGAGCCGCA
AAAGAAGAAATAGCTCGTCGTGAATCAAATGGTAGTTATACTGCACAGAATGGACAATATTATGGAAGATATCAACTG
TCTCAATCTTACCTAAATGGCGACTTATCTCCTGAAAATCAAGAAAAAGTAGCGGACAATTATGTGGCTTCTCGTTAC
GGATCTTGGTCGGCAGCGCTATCATTTTGAATAGTAACGGCTGGTAT

SEQ ID NO. 3106: SAG2148 FROM THE CJB110 GBS NONTYPEABLE STRAIN

GCATCTTATACCGTGAAATCAGGTGATACCTTATCAGCTATTGCTAAAAATCATAAACTACGGTACAAGAGTTAGTG
TCTCTCAATAGTATCAGTAACGCTGATGTCATCAGTATAGGTGATGTTTTAAATTTGGATAATTCTAAAGCTAGTCAA
GCAGAAGCAAAATCTCAACCAACAATTGAAAATTCAATGAATTCCTCATCAAATTTGAGTTCAAGTGATTGAGCCGCA
AAAGAAGAAATAGCTCGTCGTGAATCAAATGGTAGTTATACTGCACAGAATGGACAATATTATGGAAGATATCAACTG
TCTCAATCTTACCTAAATGGCGACTTATCTCCTGAAAATCAAGAAAAAGTAGCGGACAATTATGTGGTTTCTCGTTAC
GGATCTTGGTCGGCAGCGCTATCATTTTGAATAGTAACGGCTGGTAT

SEQ ID NO. 3107: SAG2148 FROM THE COH1 GBS TYPE III STRAIN

GCATCTTATACCGTGAAATCAGGTGATACCTTATCAGCTATTGCTAAAAATCATAAACTACGGTACAATAGTTAGTG
TCTCTCAATAGTATCAGTAACGCTGATGTCATCAGTATAGGTGATGTTTTAAATTTGGATAATTCTACAGCTAGTCAA
GCAGAAGCAAAATCTCAACCAACAATTGAAAATTCAATGAATTCCTCATCAAATTTGAGTTCAAGTGATTGAGCTGCA
AAAGAAGAAATAGCTCGTCGTGAATCAAATGGTAGTTATACTGCACAGAATGGACAATATTATGGAAGATATCAACTG
TCTCAATCTTACCTAAATGGCGACTTATCTCCTGAAAATCAAGAAAAAGTAGCGGACAATTATGTGGCTTCTCGTTAC
GGATCTTGGTCGGCAGCGCTATCATTTTGAATAGTAACGGCTGGTAT

**Table 31: Comparative Sequences relating to SAG2148
(LysM domain protein)**

SEQ ID NO. 3108: SAG2148 FROM THE H36b GBS TYPE Ib STRAIN
(REVERSE COMPLEMENT)

GCATCTTATACCGTGAAATCAGGTGATACCTTATCAGCTATTGCTAAAAATCATAAACTACGGTACAAGAGTTAGTG
TCTCTCAATAGTATCAGTAACGCTGATGTCATCAGTATAGGTGATGTTTTAAAAATTGGATAATTCTACAGCTAGTCAA
GCAGAAGCAAAATCTCAACCAACAATTGAAAATTCAATGAATTCTTCATCAAATTGAGTTCAAGTGATTACAGCCGCA
AAAGAAGAAAATAGCTCGTGTGAATCAAATGGTAGTTATACTGCACAGAATGGACAATATTATGGAAGATATCAACTG
TCTCAATCTTACCTAAATGGCGACTTATCTCCTGAAAATCAAGAAAAAGTAGCGGACAATTATGTGGCTTCTCGTTAC
GGATCTTGGTCGGCAGCGCTATCATTTTGAATAGTAACGGCTGGTAT

SEQ ID NO. 3109: SAG2148 FROM THE JM9130013 GBS TYPE VIII STRAIN
(REVERSE COMPLEMENT)

GCATCTTATACCGTGAAATCAGGTGATACCTTATCAGCTATTGCTAAAAATCATAAACTACGGTACAAGAGTTAGTG
TCTCTCAATAGTATCAGTAACGCTGACGTGATGTCATCAGTATAGGTGATGTTTTAAAAATTGGATAATTCTACAAGTATGCAA
GCAGAAGCAAAATCTCAACCAACAATTGAAAATTCAATGAATTCTTCATCAAATTGAGTTCAAGTGATTACAGCCGCA
AAAGAAGAAAATAGCTCGTGTGAATCAAATGGTAGTTATACTGCACAGAATGGACAATATTATGGAAGATATCAACTG
TCTCAATCTTACCTAAATGGCGACTTATCTCCTGAAAATCAAGAAAAAGTAGCGGACAATTATGTGGCTTCTCGTTAC
GGATCTTGGTCGGCAGCGCTATCATTTTGAATAGTAACGGCTGGTAT

SEQ ID NO. 3110: SAG2148 FROM THE M732 GBS TYPE III STRAIN

GCATCTTATACCGTGAAATCAGGTGATACCTTATCAGCTATTGCTAAAAATCATAAACTACGGTACAATAGTTAGTG
TCTCTCAATAGTATCAGTAACGCTGATGTCATCAGTATAGGTGATGTTTTAAAAATTGGATAATTCTACAGCTAGTCAA
GCAGAAGCAAAATCTCAACCAACAATTGAAAATTCAATGAATTCTTCATCAAATTGAGTTCAAGTGATTACAGCTGCA
AAAGAAGAAAATAGCTCGTGTGAATCAAATGGTAGTTATACTGCACAGAATGGACAATATTATGGAAGATATCAACTG
TCTCAATCTTACCTAAATGGCGACTTATCTCCTGAAAATCAAGAAAAAGTAGCGGACAATTATGTGGCTTCTCGTTAC
GGATCTTGGTCGGCAGCGCTATCATTTTGAATAGTAACGGCTGGTAT

SEQ ID NO. 3111: SAG2148 FROM THE M781 GBS TYPE III STRAIN
(REVERSE COMPLEMENT)

GCATCTTATACCGTGAAATCAGGTGATACCTTATCAGCTATTGCTAAAAATCATAAACTACGGTACAATAGTTAGTG
TCTCTCAATAGTATCAGTAACGCTGATGTCATCAGTATAGGTGATGTTTTAAAAATTGGATAATTCTACAGCTAGTCAA
GCAGAAGCAAAATCTCAACCAACAATTGAAAATTCAATGAATTCTTCATCAAATTGAGTTCAAGTGATTACAGCTGCA
AAAGAAGAAAATAGCTCGTGTGAATCAAATGGTAGTTATACTGCACAGAATGGACAATATTATGGAAGATATCAACTG
TCTCAATCTTACCTAAATGGCGACTTATCTCCTGAAAATCAAGAAAAAGTAGCGGACAATTATGTGGCTTCTCGTTAC
GGATCTTGGTCGGCAGCGCTATCATTTTGAATAGTAACGGCTGGTAT

SEQ3101	GCATCTTATACCGTGAAATCAGGTGATACCTTATCAGCTATTGCTAAAAATCATAAACT
SEQ3102	GCATCTTATACCGTGAAATCAGGTGATACCTTATCAGCTATTGCTAAAAATCATAAACT
SEQ3103	GCATCTTATACCGTGAAATCAGGTGATACCTTATCAGCTATTGCTAAAAATCATAAACT
SEQ3104	GCATCTTATACCGTGAAATCAGGTGATACCTTATCAGCTATTGCTAAAAATCATAAACT
SEQ3105	GCATCTTATACCGTGAAATCAGGTGATACCTTATCAGCTATTGCTAAAAATCATAAACT
SEQ3106	GCATCTTATACCGTGAAATCAGGTGATACCTTATCAGCTATTGCTAAAAATCATAAACT
SEQ3107	GCATCTTATACCGTGAAATCAGGTGATACCTTATCAGCTATTGCTAAAAATCATAAACT
SEQ3108	GCATCTTATACCGTGAAATCAGGTGATACCTTATCAGCTATTGCTAAAAATCATAAACT
SEQ3109	GCATCTTATACCGTGAAATCAGGTGATACCTTATCAGCTATTGCTAAAAATCATAAACT
SEQ3110	GCATCTTATACCGTGAAATCAGGTGATACCTTATCAGCTATTGCTAAAAATCATAAACT
SEQ3111	GCATCTTATACCGTGAAATCAGGTGATACCTTATCAGCTATTGCTAAAAATCATAAACT

SEQ3101	ACGGTACAAGAGTTAGTGTCTCTCAATAGTATCAGTAACGCTGATGTCATCAGTATAGGT
SEQ3102	ACGGTACAAGAGTTAGTGTCTCTCAATAGTATCAGTAACGCTGATGTCATCAGTATAGGT
SEQ3103	ACGGTACAAGAGTTAGTGTCTCTCAATAGTATCAGTAACGCTGATGTCATCAGTATAGGT
SEQ3104	ACGGTACAAGAGTTAGTGTCTCTCAATAGTATCAGTAACGCTGATGTCATCAGTATAGGT
SEQ3105	ACGGTACAAGAGTTAGTGTCTCTCAATAGTATCAGTAACGCTGATGTCATCAGTATAGGT
SEQ3106	ACGGTACAAGAGTTAGTGTCTCTCAATAGTATCAGTAACGCTGATGTCATCAGTATAGGT
SEQ3107	ACGGTACAATAGTTAGTGTCTCTCAATAGTATCAGTAACGCTGATGTCATCAGTATAGGT
SEQ3108	ACGGTACAAGAGTTAGTGTCTCTCAATAGTATCAGTAACGCTGATGTCATCAGTATAGGT
SEQ3109	ACGGTACAAGAGTTAGTGTCTCTCAATAGTATCAGTAACGCTGACGTCATCAGTATAGGT
SEQ3110	ACGGTACAATAGTTAGTGTCTCTCAATAGTATCAGTAACGCTGATGTCATCAGTATAGGT
SEQ3111	ACGGTACAATAGTTAGTGTCTCTCAATAGTATCAGTAACGCTGATGTCATCAGTATAGGT

**Table 31: Comparative Sequences relating to SAG2148
(LysM domain protein)**

SEQ3101	GATGTTTTAAATTTGGATAAATCTACAGCTAGTCAAGCAGAAGCAAAATCTCAACCAACA
SEQ3102	GATGTTTTAAATTTGGATAAATCTACAGCTAGTCAAGCAGAAGCAAAATCTCAACCAACA
SEQ3103	GATGTTTTAAATTTGGATAAATCTACAGCTAGTCAAGCAGAAGCAAAATCTCAACCAACA
SEQ3104	GATGTTTTAAATTTGGATAAATCTAAAGCTAGTCAAGCAGAAGCAAAATCTCAACCAACA
SEQ3105	GATGTTTTAAATTTGGATAAATCTACAGCTAGTCAAGCAGAAGCAAAATCTCAACCAACA
SEQ3106	GATGTTTTAAATTTGGATAAATCTAAAGCTAGTCAAGCAGAAGCAAAATCTCAACCAACA
SEQ3107	GATGTTTTAAATTTGGATAAATCTACAGCTAGTCAAGCAGAAGCAAAATCTCAACCAACA
SEQ3108	GATGTTTTAAATTTGGATAAATCTACAGCTAGTCAAGCAGAAGCAAAATCTCAACCAACA
SEQ3109	GATGTTTTAAATTTGGATAAATCTCAACTAGTCAAGCAGAAGCAAAATCTCAACCAACA
SEQ3110	GATGTTTTAAATTTGGATAAATCTACAGCTAGTCAAGCAGAAGCAAAATCTCAACCAACA
SEQ3111	GATGTTTTAAATTTGGATAAATCTACAGCTAGTCAAGCAGAAGCAAAATCTCAACCAACA
SEQ3101	ATTGAAAATTCAATGAATTCCTCATCAAATTTGAGTTCAAGTGATTGAGCTGCAAAAGAA
SEQ3102	ATTGAAAATTCAATGAATTCCTCATCAAATTTGAGTTCAAGTGATTGAGCTGCAAAAGAA
SEQ3103	ATTGAAAATTCAATGAATTCCTCATCAAATTTGAGTTCAAGTGATTGAGCTGCAAAAGAA
SEQ3104	ATTGAAAATTCAATGAATTCCTCATCAAATTTGAGTTCAAGTGATTGAGCTGCAAAAGAA
SEQ3105	ATTGAAAATTCAATGAATTCCTCATCAAATTTGAGTTCAAGTGATTGAGCTGCAAAAGAA
SEQ3106	ATTGAAAATTCAATGAATTCCTCATCAAATTTGAGTTCAAGTGATTGAGCTGCAAAAGAA
SEQ3107	ATTGAAAATTCAATGAATTCCTCATCAAATTTGAGTTCAAGTGATTGAGCTGCAAAAGAA
SEQ3108	ATTGAAAATTCAATGAATTCCTCATCAAATTTGAGTTCAAGTGATTGAGCTGCAAAAGAA
SEQ3109	ATTGAAAATTCAATGAATTCCTCATCAAATTTGAGTTCAAGTGATTGAGCTGCAAAAGAA
SEQ3110	ATTGAAAATTCAATGAATTCCTCATCAAATTTGAGTTCAAGTGATTGAGCTGCAAAAGAA
SEQ3111	ATTGAAAATTCAATGAATTCCTCATCAAATTTGAGTTCAAGTGATTGAGCTGCAAAAGAA
SEQ3101	GAAATAGCTCGTCGTGAATCAAATGGTAGTTTATACTGCACAGAATGGACAATATTATGGA
SEQ3102	GAAATAGCTCGTCGTGAATCAAATGGTAGTTTATACTGCACAGAATGGACAATATTATGGA
SEQ3103	GAAATAGCTCGTCGTGAATCAAATGGTAGTTTATACTGCACAGAATGGACAATATTATGGA
SEQ3104	GAAATAGCTCGTCGTGAATCAAATGGTAGTTTATACTGCACAGAATGGACAATATTATGGA
SEQ3105	GAAATAGCTCGTCGTGAATCAAATGGTAGTTTATACTGCACAGAATGGACAATATTATGGA
SEQ3106	GAAATAGCTCGTCGTGAATCAAATGGTAGTTTATACTGCACAGAATGGACAATATTATGGA
SEQ3107	GAAATAGCTCGTCGTGAATCAAATGGTAGTTTATACTGCACAGAATGGACAATATTATGGA
SEQ3108	GAAATAGCTCGTCGTGAATCAAATGGTAGTTTATACTGCACAGAATGGACAATATTATGGA
SEQ3109	GAAATAGCTCGTCGTGAATCAAATGGTAGTTTATACTGCACAGAATGGACAATATTATGGA
SEQ3110	GAAATAGCTCGTCGTGAATCAAATGGTAGTTTATACTGCACAGAATGGACAATATTATGGA
SEQ3111	GAAATAGCTCGTCGTGAATCAAATGGTAGTTTATACTGCACAGAATGGACAATATTATGGA
SEQ3101	AGATATCAACTGTCTCAATCTTACCTAAATGGCGACTTATCTCCTGAAAATCAAGAAAAA
SEQ3102	AGATATCAACTGTCTCAATCTTACCTAAATGGCGACTTATCTCCTGAAAATCAAGAAAAA
SEQ3103	AGATATCAACTGTCTCAATCTTACCTAAATGGCGACTTATCTCCTGAAAATCAAGAAAAA
SEQ3104	AGATATCAACTGTCTCAATCTTACCTAAATGGCGACTTATCTCCTGAAAATCAAGAAAAA
SEQ3105	AGATATCAACTGTCTCAATCTTACCTAAATGGCGACTTATCTCCTGAAAATCAAGAAAAA
SEQ3106	AGATATCAACTGTCTCAATCTTACCTAAATGGCGACTTATCTCCTGAAAATCAAGAAAAA
SEQ3107	AGATATCAACTGTCTCAATCTTACCTAAATGGCGACTTATCTCCTGAAAATCAAGAAAAA
SEQ3108	AGATATCAACTGTCTCAATCTTACCTAAATGGCGACTTATCTCCTGAAAATCAAGAAAAA
SEQ3109	AGATATCAACTGTCTCAATCTTACCTAAATGGCGACTTATCTCCTGAAAATCAAGAAAAA
SEQ3110	AGATATCAACTGTCTCAATCTTACCTAAATGGCGACTTATCTCCTGAAAATCAAGAAAAA
SEQ3111	AGATATCAACTGTCTCAATCTTACCTAAATGGCGACTTATCTCCTGAAAATCAAGAAAAA
SEQ3101	GTAGCGGACAATTATGTGGCTTCTCGTTACGGATCTTGGTCGGCAGCGCTATCATTTTGG
SEQ3102	GTAGCGGACAATTATGTGGTTTCTCGTTACGGATCTTGGTCGGCAGCGCTATCATTTTGG
SEQ3103	GTAGCGGACAATTATGTGGTTTCTCGTTACGGATCTTGGTCGGCAGCGCTATCATTTTGG
SEQ3104	GTAGCGGACAATTATGTGGTTTCTCGTTACGGATCTTGGTCGGCAGCGCTATCATTTTGG
SEQ3105	GTAGCGGACAATTATGTGGCTTCTCGTTACGGATCTTGGTCGGCAGCGCTATCATTTTGG
SEQ3106	GTAGCGGACAATTATGTGGTTTCTCGTTACGGATCTTGGTCGGCAGCGCTATCATTTTGG
SEQ3107	GTAGCGGACAATTATGTGGCTTCTCGTTACGGATCTTGGTCGGCAGCGCTATCATTTTGG
SEQ3108	GTAGCGGACAATTATGTGGCTTCTCGTTACGGATCTTGGTCGGCAGCGCTATCATTTTGG
SEQ3109	GTAGCGGACAATTATGTGGCTTCTCGTTACGGATCTTGGTCGGCAGCGCTATCATTTTGG
SEQ3110	GTAGCGGACAATTATGTGGCTTCTCGTTACGGATCTTGGTCGGCAGCGCTATCATTTTGG
SEQ3111	GTAGCGGACAATTATGTGGCTTCTCGTTACGGATCTTGGTCGGCAGCGCTATCATTTTGG

**Table 31: Comparative Sequences relating to SAG2148
(LysM domain protein)**

SEQ3101 AATAGTAACGGCTGGTAT
 SEQ3102 AATAGTAACGGCTGGTAT
 SEQ3103 AATAGTAACGGCTGGTAT
 SEQ3104 AATAGTAACGGCTGGTAT
 SEQ3105 AATAGTAACGGCTGGTAT
 SEQ3106 AATAGTAACGGCTGGTAT
 SEQ3107 AATAGTAACGGCTGGTAT
 SEQ3108 AATAGTAACGGCTGGTAT
 SEQ3109 AATAGTAACGGCTGGTAT
 SEQ3110 AATAGTAACGGCTGGTAT
 SEQ3111 AATAGTAACGGCTGGTAT

>SEQ ID NO 3150:15_1169NT frame: 1
 ASYTVKSGDTLSAIAKNHKTTVQELVSLNSISNADVISIGDVLKLDNSTASQAEAKSQPT
 IENSMNSSLSSSDSAAKEETARRESNGSYTAQNGQYYGRYQLSQSYLNGDLSPENQEK
 VADNYVASRYGWSAALSFWNSNGWY

>SEQ ID NO 3151:15_18RS21 frame: 1
 ASYTVKSGDTLSAIAKNHKTTVQELVSLNSISNADVISIGDVLKLDNSTASQAEAKSQPT
 IENSMNSSLSSSDSAAKEETARRESNGSYTAQNGQYYGRYQLSQSYLNGDLSPENQEK
 VADNYVVSRYGWSAALSFWNSNGWY

>SEQ ID NO 3152:15_2603 frame: 1
 ASYTVKSGDTLSAIAKNHKTTVQELVSLNSISNADVISIGDVLKLDNSTASQAEAKSQPT
 IENSMNSSLSSSDSAAKEETARRESNGSYTAQNGQYYGRYQLSQSYLNGDLSPENQEK
 VADNYVVSRYGWSAALSFWNSNGWY

>SEQ ID NO 3153:15_090 frame: 1
 ASYTVKSGDTLSAIAKNHKTTVQELVSLNSISNADVISIGDVLKLDNSKASQAEAKSQPT
 IENSMNSSLSSSDSAAKEETARRESNGSYTAQNGQYYGRYQLSQSYLNGDLSPENQEK
 VADNYVVSRYGWSAALSFWNSNGWY

>SEQ ID NO 3154:15_A909 frame: 1
 ASYTVKSGDTLSAIAKNHKTTVQELVSLNSISNADVISIGDVLKLDNSTASQAEAKSQPT
 IENSMNSSLSSSDSAAKEETARRESNGSYTAQNGQYYGRYQLSQSYLNGDLSPENQEK
 VADNYVASRYGWSAALSFWNSNGWY

>SEQ ID NO 3155:15_CJB110 frame: 1
 ASYTVKSGDTLSAIAKNHKTTVQELVSLNSISNADVISIGDVLKLDNSKASQAEAKSQPT
 IENSMNSSLSSSDSAAKEETARRESNGSYTAQNGQYYGRYQLSQSYLNGDLSPENQEK
 VADNYVVSRYGWSAALSFWNSNGWY

>SEQ ID NO 3156:15_COH1 frame: 1
 ASYTVKSGDTLSAIAKNHKTTVQ.LVSLNSISNADVISIGDVLKLDNSTASQAEAKSQPT
 IENSMNSSLSSSDSAAKEETARRESNGSYTAQNGQYYGRYQLSQSYLNGDLSPENQEK
 VADNYVASRYGWSAALSFWNSNGWY

>SEQ ID NO 3157:15_H36B frame: 1
 ASYTVKSGDTLSAIAKNHKTTVQELVSLNSISNADVISIGDVLKLDNSTASQAEAKSQPT
 IENSMNSSLSSSDSAAKEETARRESNGSYTAQNGQYYGRYQLSQSYLNGDLSPENQEK
 VADNYVASRYGWSAALSFWNSNGWY

>SEQ ID NO 3158:15_JM9130013 frame: 1
 ASYTVKSGDTLSAIAKNHKTTVQELVSLNSISNADVISIGDVLKLDNSTTSQAEAKSQPT
 IENSMNSSLSSSDSAAKEETARRESNGSYTAQNGQYYGRYQLSQSYLNGDLSPENQEK
 VADNYVASRYGWSAALSFWNSNGWY

>SEQ ID NO 3159:15_M732 frame: 1
 ASYTVKSGDTLSAIAKNHKTTVQ.LVSLNSISNADVISIGDVLKLDNSTASQAEAKSQPT
 IENSMNSSLSSSDSAAKEETARRESNGSYTAQNGQYYGRYQLSQSYLNGDLSPENQEK
 VADNYVASRYGWSAALSFWNSNGWY

>SEQ ID NO 3160:15_M781 frame: 1
 ASYTVKSGDTLSAIAKNHKTTVQ.LVSLNSISNADVISIGDVLKLDNSTASQAEAKSQPT
 IENSMNSSLSSSDSAAKEETARRESNGSYTAQNGQYYGRYQLSQSYLNGDLSPENQEK
 VADNYVASRYGWSAALSFWNSNGWY

**Table 31: Comparative Sequences relating to SAG2148
(LysM domain protein)**

SEQ3150	ASYTVKSGDTLSAIAKNHKTTVQELVSLNSISNADVISIGDVLKLDNSTASQAEAKSQPT
SEQ3151	ASYTVKSGDTLSAIAKNHKTTVQELVSLNSISNADVISIGDVLKLDNSTASQAEAKSQPT
SEQ3152	ASYTVKSGDTLSAIAKNHKTTVQELVSLNSISNADVISIGDVLKLDNSTASQAEAKSQPT
SEQ3153	ASYTVKSGDTLSAIAKNHKTTVQELVSLNSISNADVISIGDVLKLDNSKASQAEAKSQPT
SEQ3154	ASYTVKSGDTLSAIAKNHKTTVQELVSLNSISNADVISIGDVLKLDNSTASQAEAKSQPT
SEQ3155	ASYTVKSGDTLSAIAKNHKTTVQELVSLNSISNADVISIGDVLKLDNSKASQAEAKSQPT
SEQ3156	ASYTVKSGDTLSAIAKNHKTTVQ-LVSLNSISNADVISIGDVLKLDNSTASQAEAKSQPT
SEQ3157	ASYTVKSGDTLSAIAKNHKTTVQELVSLNSISNADVISIGDVLKLDNSTASQAEAKSQPT
SEQ3158	ASYTVKSGDTLSAIAKNHKTTVQELVSLNSISNADVISIGDVLKLDNSTTSQAEAKSQPT
SEQ3159	ASYTVKSGDTLSAIAKNHKTTVQ-LVSLNSISNADVISIGDVLKLDNSTASQAEAKSQPT
SEQ3160	ASYTVKSGDTLSAIAKNHKTTVQ-LVSLNSISNADVISIGDVLKLDNSTASQAEAKSQPT
SEQ3150	IENSMNSSSNLSSSDSAAKEEIIARRESNGSYTAQNGQYYGRYQLSQSYLNGDLSPENQEK
SEQ3151	IENSMNSSSNLSSSDSAAKEEIIARRESNGSYTAQNGQYYGRYQLSQSYLNGDLSPENQEK
SEQ3152	IENSMNSSSNLSSSDSAAKEEIIARRESNGSYTAQNGQYYGRYQLSQSYLNGDLSPENQEK
SEQ3153	IENSMNSSSNLSSSDSAAKEEIIARRESNGSYTAQNGQYYGRYQLSQSYLNGDLSPENQEK
SEQ3154	IENSMNSSSNLSSSDSAAKEEIIARRESNGSYTAQNGQYYGRYQLSQSYLNGDLSPENQEK
SEQ3155	IENSMNSSSNLSSSDSAAKEEIIARRESNGSYTAQNGQYYGRYQLSQSYLNGDLSPENQEK
SEQ3156	IENSMNSSSNLSSSDSAAKEEIIARRESNGSYTAQNGQYYGRYQLSQSYLNGDLSPENQEK
SEQ3157	IENSMNSSSNLSSSDSAAKEEIIARRESNGSYTAQNGQYYGRYQLSQSYLNGDLSPENQEK
SEQ3158	IENSMNSSSNLSSSDSAAKEEIIARRESNGSYTAQNGQYYGRYQLSQSYLNGDLSPENQEK
SEQ3159	IENSMNSSSNLSSSDSAAKEEIIARRESNGSYTAQNGQYYGRYQLSQSYLNGDLSPENQEK
SEQ3160	IENSMNSSSNLSSSDSAAKEEIIARRESNGSYTAQNGQYYGRYQLSQSYLNGDLSPENQEK
SEQ3150	VADNYVASRYGSWSAALSFWNSNGWY
SEQ3151	VADNYVVSRYGSWSAALSFWNSNGWY
SEQ3152	VADNYVVSRYGSWSAALSFWNSNGWY
SEQ3153	VADNYVVSRYGSWSAALSFWNSNGWY
SEQ3154	VADNYVASRYGSWSAALSFWNSNGWY
SEQ3155	VADNYVVSRYGSWSAALSFWNSNGWY
SEQ3156	VADNYVASRYGSWSAALSFWNSNGWY
SEQ3157	VADNYVASRYGSWSAALSFWNSNGWY
SEQ3158	VADNYVASRYGSWSAALSFWNSNGWY
SEQ3159	VADNYVASRYGSWSAALSFWNSNGWY
SEQ3160	VADNYVASRYGSWSAALSFWNSNGWY

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF00003	SAG0017	447	PcsB protein
ORF00004	SAG0018	322	ribose-phosphate pyrophosphokinase
ORF00005	SAG0019	391	aminotransferase, class I
ORF00006	SAG0020	253	recombination protein O
ORF00008	SAG0021	283	protease, putative
ORF00009	SAG0022	330	fatty acid/phospholipid synthesis protein PlsX
ORF00010	SAG0023	79	acyl carrier protein
ORF00011	SAG0024	234	phosphoribosylaminoimidazole-succinocarboxamide synthase
ORF00012	SAG0025	1241	phosphoribosylformylglycinamide synthase, putative
ORF00013	SAG0026	484	amidophosphoribosyltransferase
ORF00014	SAG0027	340	phosphoribosylformylglycinamide cyclo-ligase
ORF00015	SAG0028	182	phosphoribosylglycinamide formyltransferase
ORF00016	SAG0029	250	acetyltransferase, GNAT family
ORF00017	SAG0030	515	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase
ORF00018	SAG0031	283	peptidase, M23/M37 family
ORF00020	SAG0032	434	group B streptococcal surface immunogenic protein
ORF00021	SAG0033	232	N-acetylmannosamine-6-P epimerase, putative
ORF00022	SAG0034	438	sugar ABC transporter, sugar-binding protein
ORF00023	SAG0035	295	sugar ABC transporter, permease protein
ORF00024	SAG0036	276	sugar ABC transporter, permease protein
ORF00025	SAG0037	147	conserved hypothetical protein
ORF00026	SAG0038	220	conserved hypothetical protein
ORF00027	SAG0039	305	N-acetylneuraminate lyase, putative
ORF00028	SAG0040	293	ROK family protein
ORF00029	SAG0041	325	acetyl xylan esterase, putative
ORF00030	SAG0042	267	phosphosugar-binding transcriptional regulator, RpiR family, putative
ORF00031	SAG0043	421	phosphoribosylamine--glycine ligase
ORF00032	SAG0044	162	phosphoribosylaminoimidazole carboxylase, catalytic subunit
ORF00033	SAG0045	363	phosphoribosylaminoimidazole carboxylase, ATPase subunit
ORF00035	SAG0046	463	hypothetical protein
ORF00036	SAG0047	432	adenylosuccinate lyase
ORF00037	SAG0048	303	transcriptional regulator, Cro/Ci family
ORF00038	SAG0049	332	Holliday junction DNA helicase RuvB
ORF00039	SAG0050	145	phosphotyrosine protein phosphatase, low molecular weight
ORF00040	SAG0051	126	MORN motif family protein
ORF00041	SAG0052	592	membrane protein, putative
ORF00042	SAG0053	880	aldehyde-alcohol dehydrogenase
ORF00043	SAG0054	338	alcohol dehydrogenase, propanol-preferring
ORF00044	SAG0055	496	threonine synthase
ORF00045	SAG0056	412	MATE efflux family protein
ORF00046	SAG0057	102	ribosomal protein S10
ORF00047	SAG0058	208	ribosomal protein L3
ORF00048	SAG0059	207	ribosomal protein L4
ORF00049	SAG0060	98	ribosomal protein L23
ORF00050	SAG0061	277	ribosomal protein L2
ORF00052	SAG0062	92	ribosomal protein S19
ORF00054	SAG0063	114	ribosomal protein L22
ORF00055	SAG0064	217	ribosomal protein S3

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF00056	SAG0065	137	ribosomal protein L16
ORF00058	SAG0066	68	ribosomal protein L29
ORF00059	SAG0067	86	ribosomal protein S17
ORF00060	SAG0068	122	ribosomal protein L14
ORF00061	SAG0069	101	ribosomal protein L24
ORF00063	SAG0070	180	ribosomal protein L5
ORF00064	SAG0071	61	ribosomal protein S14, putative
ORF00065	SAG0072	132	ribosomal protein S8
ORF00066	SAG0073	178	ribosomal protein L6
ORF00068	SAG0074	118	ribosomal protein L18
ORF00069	SAG0075	164	ribosomal protein S5
ORF00070	SAG0076	59	ribosomal protein L30
ORF00071	SAG0077	146	ribosomal protein L15
ORF00072	SAG0078	434	preprotein translocase, SecY subunit
ORF00073	SAG0079	212	adenylate kinase
ORF00074	SAG0080	72	translation initiation factor IF-1
ORF00075	SAG0081	38	ribosomal protein L36
ORF00077	SAG0082	121	ribosomal protein S13
ORF00078	SAG0083	118	ribosomal protein S11
ORF00080	SAG0084	312	DNA-directed RNA polymerase, alpha subunit
ORF00081	SAG0085	128	ribosomal protein L17
ORF00087	SAG0086	97	hypothetical protein
ORF00088	SAG0087	59	hypothetical protein
ORF00089	SAG0088	56	hypothetical protein
ORF00090	SAG0089	183	conserved hypothetical protein
ORF00091	SAG0090	139	conserved hypothetical protein
ORF00093	SAG0091	144	transcriptional regulator ComX1, putative
ORF00094	SAG0092	230	phosphoglycerate mutase family protein
ORF00095	SAG0093	250	D-alanyl-D-alanine carboxypeptidase family protein
ORF00096	SAG0094	191	N-acetylmuramoyl-L-alanine amidase, family 4 protein
ORF00097	SAG0095	344	heat-inducible transcription repressor HrcA
ORF00098	SAG0096	190	heat shock protein GrpE
ORF00099	SAG0097	609	dnaK protein
ORF00100	SAG0098	379	dnaJ protein
ORF00101	SAG0099	415	transcriptional regulator, GntR family
ORF00102	SAG0100	258	tRNA pseudouridine synthase A
ORF00103	SAG0101	252	phosphomethylpyrimidine kinase, putative
ORF00104	SAG0102	154	conserved hypothetical protein
ORF00105	SAG0103	189	conserved hypothetical protein
ORF00106	SAG0104	280	conserved hypothetical protein
ORF00107	SAG0105	427	trigger factor
ORF00108	SAG0106	191	DNA-directed RNA polymerase, delta subunit, putative
ORF00109	SAG0107	534	CTP synthase
ORF00110	SAG0108	308	conserved hypothetical protein
ORF00111	SAG0109	148	deoxyuridine 5'-triphosphate nucleotidohydrolase
ORF00112	SAG0110	454	DNA repair protein RadA
ORF00113	SAG0111	165	carbonic anhydrase-related protein
ORF00115	SAG0112	439	pyridine nucleotide-disulphide oxidoreductase family protein
ORF00116	SAG0113	484	glutamyl-tRNA synthetase
ORF00117	SAG0114	322	ribose ABC transporter, periplasmic D-ribose-binding protein

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF00118	SAG0115	310	ribose ABC transporter, permease protein
ORF00119	SAG0116	492	ribose ABC transporter, ATP-binding protein
ORF00120	SAG0117	132	ribose ABC transporter protein RbsD
ORF00121	SAG0118	303	ribokinase
ORF00122	SAG0119	328	ribose operon repressor RbsR
ORF00123	SAG0120	32	hypothetical protein
ORF00124	SAG0121	362	permease, putative
ORF00125	SAG0122	228	ABC transporter, ATP-binding protein
ORF00126	SAG0123	223	DNA-binding response regulator
ORF00128	SAG0124	356	sensor histidine kinase
ORF00129	SAG0125	396	argininosuccinate synthase
ORF00130	SAG0126	462	argininosuccinate lyase
ORF00131	SAG0127	293	fructose-bisphosphate aldolase
ORF00132	SAG0128	305	L-2-hydroxyisocaproate dehydrogenase
ORF00133	SAG0129	62	ribosomal protein L28
ORF00134	SAG0130	121	conserved hypothetical protein
ORF00135	SAG0131	543	DAK2 domain protein
ORF00136	SAG0132	294	SPFH domain/Band 7 family protein
ORF00137	SAG0133	38	conserved hypothetical protein
ORF00138	SAG0134	96	hypothetical protein
ORF00141	SAG0135	246	amino acid ABC transporter, ATP-binding protein
ORF00142	SAG0136	516	amino acid ABC transporter, amino acid-binding protein/permease protein
ORF00143	SAG0137	627	conserved hypothetical protein
ORF00145	SAG0138	279	undecaprenol kinase, putative
ORF00146	SAG0139	251	negative regulator of competence MecA, putative
ORF00148	SAG0140	386	glycosyl transferase, group 4 family protein
ORF00149	SAG0141	256	ABC transporter, ATP-binding protein
ORF00150	SAG0142	420	conserved hypothetical protein
ORF00151	SAG0143	410	selenocysteine lyase
ORF00152	SAG0144	147	NifU family protein
ORF00153	SAG0145	472	conserved hypothetical protein
ORF00154	SAG0146	395	penicillin-binding protein 4, putative
ORF00155	SAG0147	411	D-alanyl-D-alanine carboxypeptidase
ORF00156	SAG0148	551	oligopeptide ABC transporter, substrate binding protein, putative
ORF00157	SAG0149	304	oligopeptide ABC transporter, permease protein
ORF00158	SAG0150	343	oligopeptide ABC transporter, permease protein
ORF00160	SAG0151	348	oligopeptide ABC transporter, ATP-binding protein
ORF00161	SAG0152	310	oligopeptide ABC transporter, ATP-binding protein
ORF00166	SAG0153	283	4-diphosphocytidyl-2C-methyl-D-erythritol kinase
ORF00167	SAG0154	147	adc operon repressor AdcR
ORF00168	SAG0155	236	zinc ABC transporter, ATP-binding protein
ORF00169	SAG0156	270	zinc ABC transporter, permease protein
ORF00172	SAG0158	419	tyrosyl-tRNA synthetase
ORF00173	SAG0159	765	penicillin-binding protein 1B, putative
ORF00174	SAG0160	1191	DNA-directed RNA polymerase, beta subunit
ORF00176	SAG0161	1216	DNA-directed RNA polymerase beta' subunit
ORF00178	SAG0162	121	conserved hypothetical protein
ORF00179	SAG0163	323	competence protein CglA
ORF00180	SAG0164	282	competence protein CglB
ORF00181	SAG0165	151	conserved hypothetical protein
ORF00182	SAG0166	123	conserved domain protein

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF00183	SAG0167	324	conserved hypothetical protein
ORF00184	SAG0168	397	acetate kinase
ORF00186	SAG0169	68	transcriptional regulator, Cro/C1 family
ORF00187	SAG0170	45	hypothetical protein
ORF00188	SAG0171	151	hypothetical protein
ORF00189	SAG0172	221	protease, putative
ORF00190	SAG0173	256	pyrroline-5-carboxylate reductase
ORF00191	SAG0174	355	glutamyl-aminopeptidase
ORF00192	SAG0175	79	hypothetical protein
ORF00193	SAG0176	94	conserved hypothetical protein
ORF00194	SAG0177	107	thioredoxin family protein
ORF00195	SAG0178	208	tRNA binding domain protein
ORF00196	SAG0179	238	conserved hypothetical protein
ORF00198	SAG0180	131	single-strand binding protein
ORF00199	SAG0181	214	hydrolase, haloacid dehalogenase-like family
ORF00200	SAG0182	581	sensor histidine kinase, putative
ORF00201	SAG0183	246	response regulator
ORF00203	SAG0184	151	conserved hypothetical protein
ORF00204	SAG0185	242	membrane protein, putative
ORF00205	SAG0186	36	hypothetical protein
ORF00206	SAG0187	542	oligopeptide ABC transporter, oligopeptide-binding protein
ORF00207	SAG0188	325	oligopeptide ABC transporter, permease protein
ORF00208	SAG0189	273	oligopeptide ABC transporter, permease protein
ORF00209	SAG0190	267	peptide ABC transporter, ATP-binding protein
ORF00210	SAG0191	208	peptide ABC transporter, ATP-binding protein
ORF00211	SAG0192	676	PTS system, IIBC components
ORF00212	SAG0193	541	alpha amylase family protein
ORF00214	SAG0194	639	transcriptional antiterminator, BglG family
ORF00216	SAG0195	377	IS1548, transposase
ORF00217	SAG0196	66	conserved domain protein
ORF00218	SAG0197	94	PTS system, IIB component, putative
ORF00219	SAG0198	451	PTS system, IIC component, putative
ORF00220	SAG0199	285	transketolase, N-terminal subunit
ORF00221	SAG0200	309	transketolase, C-terminal subunit
ORF00223	SAG0201	419	oxidoreductase, putative
ORF00224	SAG0202	89	ribosomal protein S15
ORF00225	SAG0203	709	polyribonucleotide nucleotidyltransferase
ORF00226	SAG0204	250	conserved hypothetical protein
ORF00227	SAG0205	194	serine O-acetyltransferase
ORF00228	SAG0206	60	hypothetical protein
ORF00229	SAG0207	447	cysteinyI-tRNA synthetase
ORF00230	SAG0208	128	conserved hypothetical protein
ORF00231	SAG0209	251	RNA methyltransferase, TrmH family, group 3
ORF00232	SAG0210	172	conserved hypothetical protein
ORF00233	SAG0211	286	DegV family protein
ORF00234	SAG0212	32	hypothetical protein
ORF00235	SAG0213	39	hypothetical protein
ORF00236	SAG0214	148	ribosomal protein L13
ORF00237	SAG0215	130	ribosomal protein S9
ORF00238	SAG0216	33	hypothetical protein
ORF00239	SAG0217	384	site-specific recombinase, phage integrase family
ORF00240	SAG0218	158	transcriptional regulator, Cro/C1 family
ORF00241	SAG0219	101	hypothetical protein

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF00242	SAG0220	92	conserved hypothetical protein
ORF00243	SAG0221	76	hypothetical protein
ORF00244	SAG0222	108	conserved domain protein
ORF00245	SAG0223	209	conserved hypothetical protein, fusion
ORF00246	SAG0224	332	replication initiation protein, putative
ORF00247	SAG0225	144	hypothetical protein
ORF00248	SAG0226	418	recombination protein
ORF00249	SAG0227	156	hypothetical protein
ORF00250	SAG0228	111	conserved hypothetical protein
ORF00251	SAG0229	95	conserved hypothetical protein
ORF00252	SAG0230	96	conserved hypothetical protein
ORF00253	SAG0231	135	hypothetical protein
ORF00254	SAG0232	186	hypothetical protein
ORF00255	SAG0233	226	hypothetical protein
ORF00256	SAG0234	128	hypothetical protein
ORF00257	SAG0235	93	hypothetical protein
ORF00258	SAG0236	32	hypothetical protein
ORF00259	SAG0237	34	hypothetical protein
ORF00260	SAG0238	41	hypothetical protein
ORF00261	SAG0239	286	transcriptional regulator MutR family
ORF00262	SAG0240	393	transporter, putative
ORF00263	SAG0241	213	amino acid ABC transporter, permease protein
ORF00264	SAG0242	308	amino acid ABC transporter, amino acid-binding protein
ORF00265	SAG0243	211	amino acid ABC transporter, permease protein
ORF00266	SAG0244	381	amino acid ABC transporter, ATP-binding protein
ORF00272	SAG0245	152	hypothetical protein
ORF00273	SAG0246	268	hypothetical protein
ORF00274	SAG0247	116	hypothetical protein
ORF00275	SAG0248	90	hypothetical protein
ORF00276	SAG0249	116	hypothetical protein
ORF00278	SAG0250	193	hypothetical protein
ORF00279	SAG0251	72	transcriptional regulator, Cro/C1 family
ORF00280	SAG0252	186	acetyltransferase, GNAT family
ORF00281	SAG0253	192	acetyltransferase, GNAT family
ORF00282	SAG0254	226	acetyltransferase, GNAT family
ORF00283	SAG0255	315	conserved hypothetical protein
ORF00284	SAG0256	163	RNA polymerase sigma factor, ECF subfamily
ORF00285	SAG0257	53	hypothetical protein
ORF00287	SAG0258	202	transcriptional regulator, TetR family
ORF00288	SAG0259	365	ABC transporter efflux protein, DrrB family, putative
ORF00289	SAG0260	238	ABC transporter, ATP-binding protein
ORF00290	SAG0261	129	IS1381, transposase OrfB
ORF00291	SAG0262	127	IS1381, transposase OrfA
ORF00292	SAG0263	171	hypothetical protein
ORF00293	SAG0264	103	conserved hypothetical protein
ORF00294	SAG0265	235	conserved hypothetical protein
ORF00295	SAG0266	382	N-acetylglucosamine-6-phosphate deacetylase
ORF00296	SAG0267	180	conserved hypothetical protein
ORF00297	SAG0268	304	glycyl-tRNA synthetase, alpha subunit
ORF00298	SAG0269	213	acyl carrier protein phosphodiesterase, putative
ORF00299	SAG0270	679	glycyl-tRNA synthetase, beta subunit
ORF00300	SAG0271	85	conserved hypothetical protein
ORF00301	SAG0272	87	membrane protein, putative

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF00302	SAG0273	502	glycerol kinase
ORF00303	SAG0274	609	alpha-glycerophosphate oxidase
ORF00304	SAG0275	232	glycerol uptake facilitator protein
ORF00305	SAG0276	445	NADH oxidase, putative
ORF00306	SAG0277	476	conserved hypothetical protein
ORF00307	SAG0278	661	transketolase
ORF00308	SAG0279	101	conserved hypothetical protein
ORF00309	SAG0280	244	ABC transporter, ATP-binding protein
ORF00310	SAG0281	534	membrane protein, putative
ORF00313	SAG0282	461	PTS system, IIBC components
ORF00314	SAG0283	267	glutamate 5-kinase
ORF00315	SAG0284	417	gamma-glutamyl phosphate reductase
ORF00316	SAG0285	298	conserved hypothetical protein TIGR00006
ORF00317	SAG0286	108	cell division protein FtsL, putative
ORF00318	SAG0287	752	penicillin-binding protein 2X
ORF00319	SAG0288	336	phospho-N-acetylmuramoyl-pentapeptide-transferase
ORF00320	SAG0289	447	ATP-dependent RNA helicase, DEAD/DEAH box family
ORF00321	SAG0290	270	ABC transporter, substrate-binding protein
ORF00322	SAG0291	267	amino acid ABC transporter, permease protein
ORF00323	SAG0292	247	amino acid ABC transporter, ATP-binding protein
ORF00324	SAG0293	74	conserved hypothetical protein
ORF00325	SAG0294	304	thioredoxin reductase
ORF00326	SAG0295	486	conserved hypothetical protein
ORF00327	SAG0296	273	NAD synthetase
ORF00328	SAG0297	444	aminopeptidase C
ORF00329	SAG0298	750	penicillin-binding protein 1A
ORF00330	SAG0299	199	recombination protein U
ORF00331	SAG0300	172	conserved hypothetical protein
ORF00332	SAG0301	40	hypothetical protein
ORF00333	SAG0302	110	conserved hypothetical protein
ORF00335	SAG0303	384	conserved hypothetical protein
ORF00336	SAG0304	487	conserved hypothetical protein
ORF00337	SAG0305	160	autoinducer-2 production protein LuxS
ORF00338	SAG0306	535	KH domain protein
ORF00340	SAG0307	33	hypothetical protein
ORF00341	SAG0308		ABC transporter, ATP-binding protein, FRAMESHIFT
ORF00343	SAG0309	246	ABC transporter, permease protein, putative
ORF00344	SAG0310	361	conserved hypothetical protein
ORF00345	SAG0311		DNA-binding response regulator POINT MUTATION
ORF00347	SAG0312	234	conserved hypothetical protein
ORF00348	SAG0313	209	guanylate kinase
ORF00349	SAG0314	104	DNA-directed RNA polymerase, omega subunit, putative
ORF00350	SAG0315	796	primosomal protein N'
ORF00351	SAG0316	311	methionyl-tRNA formyltransferase
ORF00352	SAG0317	440	Sun protein
ORF00353	SAG0318	245	serine/threonine phosphatase, putative
ORF00354	SAG0319	651	serine/threonine protein kinase
ORF00355	SAG0320	231	conserved hypothetical protein
ORF00356	SAG0321	339	sensor histidine kinase, putative
ORF00358	SAG0322	213	DNA-binding response regulator

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF00359	SAG0323	466	hydrolase, haloacid dehalogenase family/peptidyl-prolyl cis-trans isomerase, cyclophilin type
ORF00360	SAG0324	124	general stress protein, putative
ORF00361	SAG0325	258	pyruvate formate-lyase-activating enzyme
ORF00362	SAG0326	251	transcriptional regulator, DeoR family
ORF00363	SAG0327	327	transcriptional regulator, putative
ORF00364	SAG0328	107	PTS system, cellobiose-specific IIA component
ORF00366	SAG0329	106	PTS system, cellobiose-specific IIB component
ORF00367	SAG0330	433	PTS system, cellobiose-specific IIC component
ORF00368	SAG0331	818	formate acetyltransferase
ORF00369	SAG0332	222	transaldolase family protein
ORF00371	SAG0333	362	glycerol dehydrogenase
ORF00372	SAG0334	308	cysteine synthase A
ORF00373	SAG0335	214	conserved hypothetical protein TIGR00257
ORF00374	SAG0336	429	helicase, putative
ORF00375	SAG0337	221	competence protein F, putative
ORF00376	SAG0338	184	ribosomal subunit interface protein
ORF00382	SAG0339	450	aspartate kinase family protein
ORF00383	SAG0340	216	hydrolase, haloacid dehalogenase-like family
ORF00384	SAG0341	49	hypothetical protein
ORF00385	SAG0342	263	enoyl-CoA hydratase/isomerase family protein
ORF00386	SAG0343	144	transcriptional regulator, MarR family
ORF00387	SAG0344	323	3-oxoacyl-(acyl-carrier-protein) synthase III
ORF00388	SAG0345	74	acyl carrier protein
ORF00390	SAG0346	319	enoyl-(acyl-carrier-protein) reductase II
ORF00391	SAG0347	308	malonyl CoA-acyl carrier protein transacylase
ORF00392	SAG0348	244	3-oxoacyl-[acyl-carrier protein] reductase
ORF00393	SAG0349	410	3-oxoacyl-(acyl-carrier-protein) synthase II
ORF00394	SAG0350	166	acetyl-CoA carboxylase, biotin carboxyl carrier protein
ORF00395	SAG0351	140	(3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase
ORF00396	SAG0352	456	acetyl-CoA carboxylase, biotin carboxylase
ORF00397	SAG0353	291	acetyl-CoA carboxylase, carboxyl transferase, beta subunit
ORF00398	SAG0354	257	acetyl-CoA carboxylase, carboxyl transferase, alpha subunit
ORF00399	SAG0355	210	conserved hypothetical protein
ORF00400	SAG0356	425	seryl-tRNA synthetase
ORF00402	SAG0357	330	hypothetical protein
ORF00403	SAG0358	120	conserved hypothetical protein
ORF00404	SAG0359	303	PTS system, mannose-specific IID component
ORF00405	SAG0360	270	PTS system, mannose-specific IIC component
ORF00406	SAG0361	336	PTS system, mannose-specific IIB components
ORF00407	SAG0362	270	hydrolase, haloacid dehalogenase-like family
ORF00408	SAG0363	194	hypothetical protein
ORF00409	SAG0364	203	membrane protein, putative
ORF00410	SAG0365	473	xanthine/uracil permease family protein
ORF00411	SAG0366	169	conserved hypothetical protein TIGR00150, putative
ORF00412	SAG0367	186	acetyltransferase, GNAT family
ORF00413	SAG0368	435	transcriptional regulator, putative
ORF00414	SAG0369	98	conserved hypothetical protein
ORF00415	SAG0370	139	HIT family protein
ORF00416	SAG0371	167	hypothetical protein
ORF00417	SAG0372	85	hypothetical protein

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF00419	SAG0373	241	ABC transporter, ATP-binding protein
ORF00421	SAG0374	344	ABC transporter, permease protein
ORF00422	SAG0375	266	conserved hypothetical protein
ORF00423	SAG0376	211	conserved hypothetical protein TIGR00091
ORF00424	SAG0377	127	conserved hypothetical protein, POINT MUTATION
ORF00425	SAG0378	379	N utilization substance protein A
ORF00426	SAG0379	98	conserved hypothetical protein
ORF00427	SAG0380	100	ribosomal protein L7A family
ORF00428	SAG0381	927	translation initiation factor IF-2
ORF00429	SAG0382	122	ribosome-binding factor A
ORF00430	SAG0383	334	conserved hypothetical protein
ORF00431	SAG0384	138	transcriptional repressor CopY
ORF00432	SAG0385	744	copper-transporter ATPase CopA
ORF00433	SAG0386	68	copper-transporter protein CopZ
ORF00434	SAG0387	204	conserved hypothetical protein
ORF00435	SAG0388	270	hydrolase, haloacid dehalogenase-like family
ORF00436	SAG0389	880	DNA polymerase I
ORF00437	SAG0390	146	CoA binding domain protein
ORF00438	SAG0391	159	transcriptional regulator, Fur family
ORF00439	SAG0392	521	cell wall surface anchor family protein
ORF00440	SAG0393	228	DNA-binding response regulator
ORF00441	SAG0394	345	sensor histidine kinase
ORF00442	SAG0395	246	conserved hypothetical protein
ORF00443	SAG0396	380	queuine tRNA-ribosyltransferase
ORF00444	SAG0397	102	conserved hypothetical protein
ORF00445	SAG0398	179	bioY family protein
ORF00446	SAG0399	258	AtsA/ElaC family protein
ORF00447	SAG0400	168	cytidine/deoxycytidylate deaminase family protein
ORF00448	SAG0401	44	hypothetical protein
ORF00449	SAG0402	449	glucose-6-phosphate isomerase
ORF00450	SAG0403	175	5-formyltetrahydrofolate cyclo-ligase family protein
ORF00451	SAG0404	225	rhomboid family protein
ORF00452	SAG0405	347	lipoprotein
ORF00453	SAG0406	299	UTP-glucose-1-phosphate uridylyltransferase
ORF00454	SAG0407	338	glycerol-3-phosphate dehydrogenase (NAD(P)+)
ORF00455	SAG0408	109	ribonuclease P protein component
ORF00456	SAG0409	271	SpoIIJ family protein
ORF00458	SAG0410	273	R3H domain protein
ORF00463	SAG0411	177	conserved hypothetical protein
ORF00464	SAG0412	258	RecX protein
ORF00465	SAG0413	451	RNA methyltransferase, TrmA family
ORF00466	SAG0414	153	conserved hypothetical protein
ORF00467	SAG0415	142	acetyltransferase, GNAT family
ORF00468	SAG0416	1233	protease, putative
ORF00469	SAG0417	302	glycosyl transferase, group 2 family protein
ORF00470	SAG0418	336	ribonucleoside-diphosphate reductase 2, beta subunit
ORF00471	SAG0419	137	nrpI protein
ORF00472	SAG0420	721	ribonucleoside-diphosphate reductase 2, alpha subunit
ORF00473	SAG0421	1055	conserved hypothetical protein
ORF00474	SAG0422	129	conserved hypothetical protein
ORF00475	SAG0423	132	conserved domain protein

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF00476	SAG0424	94	hypothetical protein
ORF00478	SAG0425	105	carboxymuconolactone decarboxylase family protein
ORF00479	SAG0426	131	conserved hypothetical protein
ORF00480	SAG0427	129	transcriptional regulator, MerR family
ORF00482	SAG0428	345	alcohol dehydrogenase, zinc-containing
ORF00483	SAG0429	284	oxidoreductase, aldo/keto reductase family
ORF00484	SAG0430	287	cation efflux system protein
ORF00485	SAG0431	174	transcriptional regulator, TetR family
ORF00486	SAG0432	397	transcriptional regulator, AraC family
ORF00487	SAG0433	1389	surface protein Rib
ORF00488	SAG0434	61	transposase, IS256 family, truncation
ORF00489	SAG0435	97	DNA-damage-inducible protein J, putative
ORF00490	SAG0436	62	hypothetical protein
ORF00491	SAG0437	123	hypothetical protein
ORF00493	SAG0438	145	bacteriophage L54a, integrase, truncation
ORF00495	SAG0439		conserved hypothetical protein, FRAMESHIFT
ORF00496	SAG0440	84	conserved hypothetical protein
ORF00497	SAG0441	103	conserved domain protein
ORF00499	SAG0442	189	acetyltransferase, GNAT family
ORF00500	SAG0443	194	acetyltransferase, GNAT family
ORF00501	SAG0444	188	conserved hypothetical protein
ORF00502	SAG0445	883	valyl-tRNA synthetase
ORF00503	SAG0446	319	oxidoreductase, Gfo/ldh/MocA family
ORF00504	SAG0447	287	magnesium transporter, CorA family
ORF00506	SAG0448	391	transposase, IS256 family
ORF00507	SAG0449	354	conserved hypothetical protein
ORF00508	SAG0450	330	aspartate--ammonia ligase
ORF00510	SAG0451	149	bacteriocin transport accessory protein, putative
ORF00511	SAG0452	179	type II DNA modification methyltransferase, putative
ORF00512	SAG0453	96	hypothetical protein
ORF00513	SAG0454	161	phosphopantetheine adenylyltransferase
ORF00515	SAG0455	357	conserved hypothetical protein
ORF00518	SAG0456		conserved hypothetical protein, degenerate
ORF00519	SAG0457	192	conserved hypothetical protein
ORF00520	SAG0458	368	conserved hypothetical protein TIGR00048
ORF00521	SAG0459	171	VanZF domain protein
ORF00522	SAG0460	581	ABC transporter, ATP-binding/permease protein
ORF00523	SAG0461	579	ABC transporter, ATP-binding/permease protein
ORF00524	SAG0462	188	anthranilate synthase component II
ORF00525	SAG0463	179	bioY family protein
ORF00526	SAG0464	330	biotin synthetase
ORF00527	SAG0465	164	hypothetical protein
ORF00528	SAG0466	371	thiolase
ORF00531	SAG0467	409	AMP-binding enzyme domain protein
ORF00532	SAG0468	210	endonuclease III
ORF00533	SAG0469	131	type IV prepilin peptidase-related protein
ORF00534	SAG0470	69	conserved hypothetical protein
ORF00535	SAG0471	322	glucokinase
ORF00536	SAG0472	126	rhodanese domain protein
ORF00537	SAG0473	613	elongation factor Tu family protein
ORF00538	SAG0474	81	conserved hypothetical protein
ORF00540	SAG0475	451	UDP-N-acetylmuramoylalanine--D-glutamate ligase

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF00541	SAG0476	358	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase
ORF00542	SAG0477	378	cell division protein DivIB, putative
ORF00544	SAG0478	429	cell division protein FtsA
ORF00545	SAG0479	426	cell division protein FtsZ
ORF00546	SAG0480	224	ylmE protein, putative
ORF00547	SAG0481	201	ylmF protein
ORF00548	SAG0482	84	YGGT family protein
ORF00549	SAG0483	262	ylmH protein
ORF00550	SAG0484	256	cell division protein DivIVA, putative
ORF00552	SAG0485	930	isoleucyl-tRNA synthetase
ORF00553	SAG0486	100	conserved hypothetical protein
ORF00554	SAG0487	151	MutT/nudix family protein
ORF00555	SAG0488	753	ATP-dependent Clp protease, ATP-binding subunit
ORF00556	SAG0489	34	hypothetical protein
ORF00557	SAG0490	76	conserved hypothetical protein
ORF00558	SAG0491	230	amino acid ABC transporter, permease protein
ORF00559	SAG0492	244	amino acid ABC transporter, ATP-binding protein
ORF00560	SAG0493	564	phosphoglucomutase/phosphomannomutase family protein
ORF00562	SAG0494	284	methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase
ORF00563	SAG0495	278	conserved hypothetical protein
ORF00564	SAG0496	446	exodeoxyribonuclease VII, large subunit
ORF00565	SAG0497	71	exodeoxyribonuclease VII, small subunit
ORF00566	SAG0498	290	geranyltranstransferase, putative
ORF00567	SAG0499	275	hemolysin A
ORF00568	SAG0500	157	arginine repressor ArgR, putative
ORF00570	SAG0501	552	DNA repair protein RecN
ORF00571	SAG0502	278	DegV family protein
ORF00572	SAG0503	279	Lipase/Acylhydrolase, putative
ORF00573	SAG0504	200	conserved hypothetical protein
ORF00574	SAG0505	91	DNA-binding protein HU
ORF00575	SAG0506	65	hypothetical protein
ORF00576	SAG0507	310	dihydroorotate dehydrogenase A
ORF00577	SAG0508	411	beta-lactam resistance factor
ORF00578	SAG0509	403	beta-lactam resistance factor
ORF00579	SAG0510	406	murM protein, putative
ORF00580	SAG0511	270	hydrolase, haloacid dehalogenase-like family
ORF00581	SAG0512	438	HD domain protein
ORF00582	SAG0513	128	conserved hypothetical protein
ORF00583	SAG0514	894	cation-transporting ATPase, E1-E2 family
ORF00584	SAG0515	286	conserved hypothetical protein
ORF00585	SAG0516	643	fructose-1,6-bisphosphatase, putative
ORF00586	SAG0517	374	iron-sulfur cluster-binding protein, putative
ORF00587	SAG0518		peptide chain release factor 2, FRAMESHIFT
ORF00588	SAG0519	230	cell division ABC transporter, ATP-binding protein FtsE
ORF00589	SAG0520	309	cell division ABC transporter, permease protein FtsX
ORF00590	SAG0521	236	carboxymethylenebutenolidase-related protein
ORF00591	SAG0522	232	metallo-beta-lactamase superfamily protein

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF00592	SAG0523	254	oxidoreductase, short chain dehydrogenase/reductase family
ORF00593	SAG0524	835	DNA polymerase III, epsilon subunit/ATP-dependent helicase DinG
ORF00595	SAG0525	397	aspartate aminotransferase
ORF00596	SAG0526	448	asparaginyl-tRNA synthetase
ORF00597	SAG0527	185	conserved hypothetical protein
ORF00598	SAG0528	327	inosine-uridine preferring nucleoside hydrolase
ORF00599	SAG0529	38	hypothetical protein
ORF00600	SAG0530	137	OsmC/Ohr family protein
ORF00601	SAG0531	296	conserved hypothetical protein
ORF00602	SAG0532	324	conserved hypothetical protein
ORF00603	SAG0533	303	Uncharacterized BCR, COG1481
ORF00604	SAG0534	465	dipeptidase
ORF00605	SAG0535	506	zinc ABC transporter, zinc-binding adhesion liprotein
ORF00606	SAG0536	86	ribosomal protein L31
ORF00607	SAG0537	311	DHH family protein
ORF00608	SAG0538	340	adenosine deaminase, putative
ORF00609	SAG0539	147	flavodoxin
ORF00610	SAG0540	91	chorismate mutase, putative
ORF00611	SAG0541	398	voltage-gated chloride channel family protein
ORF00612	SAG0542	127	IS1381, transposase OrfA
ORF00613	SAG0543	129	IS1381, transposase OrfB
ORF00614	SAG0544	115	ribosomal protein L19
ORF00615	SAG0545	359	site-specific recombinase, phage integrase family
ORF00617	SAG0546	67	conserved domain protein
ORF00618	SAG0547	185	hypothetical protein
ORF00619	SAG0548	265	repressor protein, putative
ORF00620	SAG0549	47	hypothetical protein
ORF00621	SAG0550	74	conserved hypothetical protein
ORF00622	SAG0551	52	conserved hypothetical protein
ORF00623	SAG0552	62	hypothetical protein
ORF00624	SAG0553	268	hypothetical protein
ORF00626	SAG0554	63	transcriptional regulator, Cro/C1 family
ORF00627	SAG0555	249	antirepressor, putative
ORF00628	SAG0556	47	hypothetical protein
ORF00630	SAG0557	76	hypothetical protein
ORF00632	SAG0558	74	hypothetical protein
ORF00633	SAG0559	286	conserved hypothetical protein
ORF00634	SAG0560	77	conserved hypothetical protein
ORF00635	SAG0561	46	hypothetical protein
ORF00636	SAG0562	84	hypothetical protein
ORF00637	SAG0563	53	hypothetical protein
ORF00638	SAG0564	160	conserved hypothetical protein
ORF00639	SAG0565	224	conserved domain protein
ORF00640	SAG0566	138	single-strand binding protein
ORF00641	SAG0567	439	reverse transcriptase/maturase family protein
ORF00642	SAG0568	67	conserved hypothetical protein
ORF00643	SAG0569	158	conserved hypothetical protein
ORF00644	SAG0570	115	hypothetical protein
ORF00645	SAG0571	43	hypothetical protein
ORF00646	SAG0572	138	conserved hypothetical protein
ORF00647	SAG0573	54	hypothetical protein

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxx Ref No.	aa	Annotation
ORF00648	SAG0574	89	conserved hypothetical protein
ORF00649	SAG0575	110	hypothetical protein
ORF00650	SAG0576	43	hypothetical protein
ORF00652	SAG0577	177	conserved hypothetical protein
ORF00653	SAG0578	88	conserved hypothetical protein
ORF00654	SAG0581	118	conserved hypothetical protein
ORF00655	SAG0582	422	conserved hypothetical protein
ORF00656	SAG0583	406	conserved hypothetical protein
ORF00657	SAG0584	62	conserved hypothetical protein, truncation
ORF00658	SAG0585	471	conserved hypothetical protein
ORF00659	SAG0586	154	conserved hypothetical protein
ORF00660	SAG0587	300	structural protein, putative
ORF00661	SAG0588	71	conserved hypothetical protein
ORF00662	SAG0589	143	conserved hypothetical protein
ORF00663	SAG0590	112	conserved hypothetical protein
ORF00664	SAG0591	78	conserved hypothetical protein
ORF00665	SAG0592	111	conserved hypothetical protein
ORF00666	SAG0593	185	structural protein
ORF00667	SAG0594	81	conserved hypothetical protein
ORF00668	SAG0595	123	conserved hypothetical protein
ORF00669	SAG0596	670	PbIA, internal deletion
ORF00670	SAG0597	506	minor structural protein, putative
ORF00671	SAG0598	1374	minor structural protein, putative
ORF00672	SAG0599	668	minor structural protein, putative
ORF00673	SAG0600	109	hypothetical protein
ORF00674	SAG0601	70	hypothetical protein
ORF00675	SAG0602	100	conserved hypothetical protein
ORF00676	SAG0603	111	holin, putative
ORF00677	SAG0604	239	lysin, putative
ORF00678	SAG0605	323	conserved hypothetical protein
ORF00679	SAG0606	66	conserved hypothetical protein
ORF00681	SAG0607	56	conserved hypothetical protein
ORF00682	SAG0608	59	hypothetical protein
ORF00683	SAG0609	193	site-specific recombinase, phage integrase family
ORF00685	SAG0610	134	conserved hypothetical protein
ORF00687	SAG0611		transposase, degenerate FRAMESHIFT
ORF00689	SAG0612	53	conserved hypothetical protein, FRAMESHIFT
ORF00690	SAG0613	425	transmembrane protein Vexp1
ORF00691	SAG0614	218	ABC transporter, ATP-binding protein Vexp2
ORF00692	SAG0615	458	transmembrane protein Vexp3
ORF00693	SAG0616	217	DNA-binding response regulator VncR
ORF00694	SAG0617	439	sensor histidine kinase VncS
ORF00695	SAG0618	195	transposase OrfB, IS3 family, truncation
ORF00697	SAG0619	66	conserved hypothetical protein
ORF00698	SAG0620	62	hypothetical protein
ORF00699	SAG0621	401	rod shape-determining protein RodA, putative□
ORF00700	SAG0622	186	hydrolase, haloacid dehalogenase-like family
ORF00701	SAG0623	650	DNA gyrase, B subunit
ORF00702	SAG0624	574	septation ring formation regulator EzrA, putative
ORF00703	SAG0625	213	phosphoserine phosphatase SerB
ORF00704	SAG0626	161	MutT/nudix family protein
ORF00705	SAG0627	151	conserved hypothetical protein
ORF00706	SAG0628	435	enolase
ORF00707	SAG0629	354	conserved domain protein

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF00708	SAG0630	427	3-phosphoshikimate 1-carboxyvinyltransferase
ORF00709	SAG0631	170	shikimate kinase
ORF00710	SAG0632	457	psr protein
ORF00711	SAG0633	451	RNA methyltransferase, TrmA family
ORF00712	SAG0634	70	hypothetical protein
ORF00713	SAG0635	245	acid phosphatase precursor, class B
ORF00714	SAG0636	172	conserved hypothetical protein
ORF00717	SAG0637		transcriptional regulator, TetR family, putative, FRAMESHIFT
ORF00718	SAG0638	109	cell wall surface anchor family protein
ORF00720	SAG0639	273	transposase OrfB, IS3 family
ORF00721	SAG0640	91	transposase OrfA, IS3 family
ORF00722	SAG0641		Tn5252, Orf 10 protein, degenerate POINT MUTATION
ORF00723	SAG0642	59	hypothetical protein
ORF00725	SAG0643		chaperonin, 33 kDa DEGENERATE
ORF00726	SAG0644	402	transcriptional regulator, AraC family
ORF00727	SAG0645	554	cell wall surface anchor family protein, putative
ORF00728	SAG0646	307	cell wall surface anchor family protein
ORF00729	SAG0647	305	sortase family protein
ORF00731	SAG0648	260	sortase family protein
ORF00732	SAG0649	890	cell wall surface anchor family protein, putative
ORF00734	SAG0650	189	sortase family protein, FRAMESHIFT
ORF00735	SAG0651	201	hypothetical protein
ORF00737	SAG0653	76	conserved hypothetical protein, DEGENERATE
ORF00738	SAG0654	34	hypothetical protein
ORF00740	SAG0656	36	hypothetical protein
ORF00741	SAG0657	89	hypothetical protein
ORF00742	SAG0658	383	lipoprotein, putative
ORF00743	SAG0659	330	ABC transporter, ATP-binding protein
ORF00744	SAG0660	272	membrane protein
ORF00745	SAG0661	261	conserved hypothetical protein
ORF00747	SAG0663	282	cylD protein
ORF00748	SAG0664	240	cylG protein
ORF00749	SAG0665	101	acyl carrier protein AcpC
ORF00750	SAG0666	158	cylZ protein FRAMESHIFT
ORF00751	SAG0667	309	cylA protein
ORF00752	SAG0668	292	cylB protein
ORF00753	SAG0669	667	cylE protein
ORF00754	SAG0670	317	cylF protein
ORF00755	SAG0671	731	cylI protein
ORF00756	SAG0672	403	cylJ protein
ORF00757	SAG0673	191	cylK protein
ORF00758	SAG0674	113	hypothetical protein
ORF00759	SAG0675	171	surface protein antigen-related protein
ORF00760	SAG0676	885	serine protease, subtilase family, putative
ORF00761	SAG0677	1062	hypothetical protein
ORF00762	SAG0678		endopeptidase O DEGENERATE
ORF00766	SAG0679	286	hydrolase, alpha/beta fold family, putative
ORF00767	SAG0680	339	hypothetical protein
ORF00768	SAG0681	353	conserved domain protein
ORF00769	SAG0682	409	permease, putative
ORF00770	SAG0683		transmembrane protein Vexp3, putative FRAMESHIFT
ORF00774	SAG0684	223	ABC transporter, ATP-binding protein

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF00775	SAG0685	472	conserved hypothetical protein
ORF00776	SAG0686	261	DNA-entry nuclease, putative
ORF00777	SAG0687	212	DedA family protein, putative
ORF00778	SAG0688	218	ABC transporter, ATP-binding protein
ORF00779	SAG0689	257	membrane protein, putative
ORF00780	SAG0690	272	conserved hypothetical protein
ORF00781	SAG0691	294	transcriptional regulator, LysR family
ORF00783	SAG0692	193	regulatory protein, putative
ORF00785	SAG0693	377	IS1548, transposase
ORF00786	SAG0694	173	regulatory protein, putative, truncation
ORF00787	SAG0695	330	D-lactate dehydrogenase
ORF00788	SAG0696	516	sodium:galactoside symporter family protein, putative
ORF00789	SAG0697	341	2-keto-3-deoxygluconate kinase
ORF00790	SAG0698	599	beta-glucuronidase
ORF00791	SAG0699	223	transcriptional regulator, GntR family
ORF00792	SAG0700	205	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase
ORF00793	SAG0701	466	Glucuronate isomerase
ORF00794	SAG0702	348	mannonate dehydratase
ORF00795	SAG0703	279	D-mannonate oxidoreductase
ORF00796	SAG0704	270	hydrolase, haloacid dehalogenase-like family
ORF00797	SAG0705	596	glycosyl hydrolase, family 3
ORF00798	SAG0706	361	proline dipeptidase
ORF00799	SAG0707	334	transcriptional regulator, RegM family
ORF00800	SAG0708	488	alpha amylase family protein
ORF00801	SAG0709	332	glycosyl transferase, group 1 family protein
ORF00802	SAG0710	444	glycosyl transferase, group 1 family protein
ORF00803	SAG0711	647	threonyl-tRNA synthetase
ORF00804	SAG0712	234	DNA-binding response regulator
ORF00805	SAG0713	339	conserved hypothetical protein
ORF00806	SAG0714	188	conserved hypothetical protein
ORF00807	SAG0715	216	amino acid ABC transporter, permease protein
ORF00808	SAG0716	231	amino acid ABC transporter, permease protein
ORF00809	SAG0717	266	amino acid ABC transporter, amino acid-binding protein
ORF00810	SAG0718	251	amino acid ABC transporter, ATP-binding protein
ORF00811	SAG0719	236	DNA-binding response regulator
ORF00812	SAG0720	449	sensory box histidine kinase
ORF00813	SAG0721	269	metallo-beta-lactamase family protein
ORF00814	SAG0722	122	conserved hypothetical protein
ORF00815	SAG0723	236	ribonuclease III
ORF00816	SAG0724	1179	SMC family protein
ORF00817	SAG0725	265	hydrolase, haloacid dehalogenase-like family
ORF00818	SAG0726	274	hydrolase, haloacid dehalogenase-like family
ORF00819	SAG0727	536	signal recognition particle-docking protein FtsY
ORF00820	SAG0728	270	ABC transporter, substrate-binding protein
ORF00821	SAG0729	300	ABC transporter, permease protein, putative
ORF00822	SAG0730	42	ABC transporter, ATP-binding protein
ORF00823	SAG0731	347	bacterial luciferase family protein
ORF00824	SAG0732	720	transcriptional accessory protein Tex, putative
ORF00825	SAG0733	142	conserved hypothetical protein
ORF00826	SAG0734	87	phage shock protein C, putative
ORF00827	SAG0735	44	hypothetical protein
ORF00828	SAG0736	311	HPr(Ser) kinase/phosphatase

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF00830	SAG0737	257	prolipoprotein diacylglycerol transferase
ORF00832	SAG0738	132	conserved hypothetical protein
ORF00833	SAG0739	143	conserved hypothetical protein
ORF00834	SAG0740	91	conserved hypothetical protein
ORF00835	SAG0741	303	peptidase, U32 family, putative
ORF00836	SAG0742	428	peptidase, U32 family
ORF00837	SAG0743	70	conserved hypothetical protein
ORF00838	SAG0744	265	membrane protein, putative
ORF00839	SAG0745	446	Mn ²⁺ /Fe ²⁺ transporter, NRAMP family
ORF00840	SAG0746	369	riboflavin biosynthesis protein RibD
ORF00841	SAG0747	208	riboflavin synthase, alpha subunit
ORF00842	SAG0748	397	riboflavin biosynthesis protein RibA
ORF00843	SAG0749	156	riboflavin synthase, beta subunit
ORF00844	SAG0750	496	lysyl-tRNA synthetase
ORF00845	SAG0751	300	hydrolase, haloacid dehalogenase-like family
ORF00846	SAG0752	213	phosphoglycerate mutase family protein
ORF00847	SAG0753	157	ebsC family protein, putative
ORF00848	SAG0754	205	conserved domain protein
ORF00850	SAG0755	282	peptidase, U32 family
ORF00852	SAG0756	174	conserved hypothetical protein
ORF00853	SAG0757	129	lipoprotein, putative
ORF00855	SAG0758	599	oligoendopeptidase F, putative
ORF00856	SAG0759	931	phosphoenolpyruvate carboxylase
ORF00857	SAG0760	377	IS1548, transposase
ORF00859	SAG0761	422	cell division protein, FtsW/RodA/SpoVE family
ORF00861	SAG0762	398	translation elongation factor Tu
ORF00863	SAG0763	252	triosephosphate isomerase
ORF00865	SAG0764	230	phosphoglycerate mutase
ORF00866	SAG0765	681	penicillin-binding protein 2b
ORF00867	SAG0766	198	recombination protein RecR
ORF00868	SAG0767	348	D-alanine--D-alanine ligase
ORF00869	SAG0768	455	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanyl ligase
ORF00870	SAG0769	406	oxalate:formate antiporter
ORF00871	SAG0770	228	conserved hypothetical protein
ORF00872	SAG0771	512	cell wall surface anchor family protein
ORF00873	SAG0772	514	peptide chain release factor 3
ORF00874	SAG0773	126	conserved hypothetical protein
ORF00876	SAG0774	244	ABC transporter, ATP-binding protein
ORF00878	SAG0775	220	ABC transporter, permease protein
ORF00879	SAG0776	276	lipoprotein, putative
ORF00880	SAG0777	528	ATP-dependent RNA helicase, DEAD/DEAH box family
ORF00882	SAG0778	88	conserved hypothetical protein
ORF00883	SAG0779	254	conserved hypothetical protein
ORF00884	SAG0780	246	acyltransferase family protein
ORF00885	SAG0781	217	competence protein CeiA
ORF00887	SAG0782	745	DNA internalization-related competence protein ComEC/Rec2
ORF00888	SAG0783	269	hydrolase, haloacid dehalogenase-like family
ORF00889	SAG0784	314	sugar-binding transcriptional regulator, LacI family
ORF00890	SAG0785	330	conserved hypothetical protein
ORF00891	SAG0786	242	conserved domain protein
ORF00892	SAG0787	345	DNA polymerase III, delta subunit, putative□

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF00893	SAG0788	202	superoxide dismutase, Fe-Mn
ORF00894	SAG0789	283	transcriptional antiterminator LicT
ORF00895	SAG0790	622	PTS system, beta-glucosides-specific IIBC components
ORF00896	SAG0791	475	6-phospho-beta-glucosidase
ORF00898	SAG0792	364	conserved hypothetical protein
ORF00899	SAG0793	380	conserved hypothetical protein TIGR00045
ORF00900	SAG0794	418	permease, GntP family
ORF00902	SAG0795	354	conserved hypothetical protein
ORF00903	SAG0796	147	transcriptional regulator, MarR family
ORF00904	SAG0797	342	S-adenosylmethionine:tRNA ribosyltransferase-isomerase
ORF00905	SAG0798	226	membrane protein, putative
ORF00906	SAG0799	233	glucosamine-6-phosphate isomerase
ORF00907	SAG0800	318	Glutathione S-transferases domain protein
ORF00908	SAG0801	239	ribosomal small subunit pseudouridine synthase
ORF00909	SAG0802	38	hypothetical protein
ORF00910	SAG0803	383	major facilitator family protein
ORF00911	SAG0804	315	competence protein CoiA
ORF00912	SAG0805	601	oligoendopeptidase B
ORF00913	SAG0806	208	hydrolase, haloacid dehalogenase-like family
ORF00914	SAG0807	235	O-methyltransferase family protein
ORF00916	SAG0808	309	protease maturation protein, putative
ORF00918	SAG0809	161	conserved hypothetical protein
ORF00919	SAG0810	872	alanyl-tRNA synthetase
ORF00921	SAG0811	238	membrane protein, putative
ORF00922	SAG0812	272	glycosyl transferase, family 8
ORF00923	SAG0813	81	hypothetical protein
ORF00924	SAG0814	95	conserved domain protein
ORF00925	SAG0815	71	transcriptional regulator, Cro/Ci family
ORF00926	SAG0816	253	conserved hypothetical protein
ORF00927	SAG0817	187	conserved hypothetical protein
ORF00928	SAG0818	319	ribonucleoside-diphosphate reductase 2, beta subunit
ORF00929	SAG0819	719	ribonucleoside-diphosphate reductase 2, alpha subunit
ORF00930	SAG0820	74	ribonucleoside-diphosphate reductase 2, NrdH-redoxin
ORF00931	SAG0821	87	phosphocarrier protein HPr
ORF00932	SAG0822	577	phosphoenolpyruvate-protein phosphotransferase
ORF00933	SAG0823	475	glyceraldehyde-3-phosphate dehydrogenase, NADP-dependent
ORF00934	SAG0824	417	polysaccharide deacetylase family protein
ORF00935	SAG0825	360	ATP-dependent RNA helicase, DEAD/DEAH box family
ORF00936	SAG0826	209	uridine kinase
ORF00937	SAG0827	165	conserved hypothetical protein
ORF00938	SAG0828	554	DNA polymerase III, gamma and tau subunits
ORF00939	SAG0829	64	conserved hypothetical protein
ORF00940	SAG0830	311	biotin--acetyl-CoA-carboxylase ligase
ORF00941	SAG0831	398	S-adenosylmethionine synthetase
ORF00942	SAG0832	753	hypothetical protein
ORF00943	SAG0833	181	hypothetical protein
ORF00944	SAG0834	42	hypothetical protein
ORF00945	SAG0835	188	conserved hypothetical protein

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF00946	SAG0836	184	conserved hypothetical protein
ORF00948	SAG0837	428	ABC transporter, ATP-binding protein
ORF00950	SAG0838	233	hypothetical protein
ORF00951	SAG0839	226	transcriptional regulator, TenA family
ORF00952	SAG0840	265	phosphomethylpyrimidine kinase
ORF00953	SAG0841	256	hydroxyethylthiazole kinase
ORF00954	SAG0842	223	thiamine-phosphate pyrophosphorylase
ORF00955	SAG0843	419	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
ORF00956	SAG0844	184	acetyltransferase, GNAT family
ORF00957	SAG0845	427	CBS domain protein
ORF00958	SAG0846	286	methionine aminopeptidase, type I
ORF00959	SAG0847	306	ribonuclease BN, putative
ORF00961	SAG0848	151	GtrA family protein
ORF00962	SAG0849	169	conserved hypothetical protein
ORF00963	SAG0850	652	DNA ligase, NAD-dependent
ORF00964	SAG0851	339	BmrU protein, putative
ORF00966	SAG0852	766	pullulanase, putative
ORF00967	SAG0853	622	1,4-alpha-glucan branching enzyme
ORF00968	SAG0854	379	glucose-1-phosphate adenylyltransferase
ORF00969	SAG0855		glycogen biosynthesis protein GlgD FRAMESHIFT
ORF00971	SAG0856	476	glycogen synthase
ORF00972	SAG0857	66	ATP synthase F0, C subunit
ORF00973	SAG0858	238	ATP synthase F0, A subunit
ORF00974	SAG0859	165	ATP synthase F0, B subunit
ORF00975	SAG0860	178	ATP synthase F1, delta subunit
ORF00976	SAG0861	501	ATP synthase F1, alpha subunit
ORF00977	SAG0862	293	ATP synthase F1, gamma subunit
ORF00978	SAG0863	468	ATP synthase F1, beta subunit
ORF00979	SAG0864	137	ATP synthase F1, epsilon subunit
ORF00980	SAG0865	76	conserved hypothetical protein
ORF00981	SAG0866	423	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
ORF00982	SAG0867	63	conserved hypothetical protein
ORF00983	SAG0868	285	DNA-entry nuclease
ORF00984	SAG0869	346	phenylalanyl-tRNA synthetase, alpha subunit
ORF00985	SAG0870	173	acetyltransferase, GNAT family
ORF00986	SAG0871	801	phenylalanyl-tRNA synthetase, beta subunit
ORF00987	SAG0872	300	conserved hypothetical protein
ORF00988	SAG0873	1077	exonuclease RxB
ORF00989	SAG0874	1207	exonuclease RxA
ORF00990	SAG0875	305	magnesium transporter, CorA family, putative
ORF00991	SAG0876	458	tRNA modification GTPase TrmE
ORF00992	SAG0877	636	ABC transporter, ATP-binding protein
ORF00993	SAG0878	322	acetoin dehydrogenase, thymine PPi dependent, E1 component, alpha subunit
ORF00994	SAG0879	332	acetoin dehydrogenase, thymine PPi dependent, E1 component, beta subunit
ORF00995	SAG0880	462	acetoin dehydrogenase, thymine PPi dependent, E2 component, dihydrolipoamide acetyltransferase
ORF00996	SAG0881	585	acetoin dehydrogenase, thymine PPi dependent, E3 component, dihydrolipoamide dehydrogenase
ORF00997	SAG0882	329	lipoate-protein ligase A
ORF00998	SAG0883	261	cobyrinic acid synthase, putative

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF00999	SAG0884	447	mur ligase family protein
ORF01000	SAG0885	283	conserved hypothetical protein TIGR00159
ORF01001	SAG0886	319	Gram-positive signal peptide, YSIRK family domain protein
ORF01002	SAG0887	450	phosphoglucomutase/phosphomannomutase family protein
ORF01003	SAG0888	123	conserved hypothetical protein
ORF01004	SAG0889	126	conserved hypothetical protein
ORF01005	SAG0890	376	oxygen-independent coproporphyrinogen III oxidase, putative
ORF01006	SAG0891	245	conserved hypothetical protein
ORF01007	SAG0892	256	hydrolase, haloacid dehalogenase-like family
ORF01008	SAG0893	218	conserved hypothetical protein
ORF01009	SAG0894	1370	conserved hypothetical protein
ORF01010	SAG0895	289	lipoyl-binding domain protein
ORF01011	SAG0896	108	oxidoreductase, putative
ORF01012	SAG0897	221	conserved hypothetical protein
ORF01013	SAG0898	83	hypothetical protein
ORF01014	SAG0899	57	hypothetical protein
ORF01015	SAG0900	56	hypothetical protein
ORF01016	SAG0901	127	hypothetical protein
ORF01018	SAG0902	45	hypothetical protein
ORF01019	SAG0903	44	hypothetical protein
ORF01021	SAG0904	56	hypothetical protein
ORF01022	SAG0905	138	nucleoside diphosphate kinase
ORF01023	SAG0906	610	GTP-binding protein LepA
ORF01024	SAG0907	877	streptococcal histidine triad family protein
ORF01025	SAG0908	203	HD domain protein
ORF01026	SAG0909	154	acetyltransferase, GNAT family
ORF01027	SAG0910	144	PilB-related protein
ORF01030	SAG0911	930	cation-transporting ATPase, E1-E2 family
ORF01031	SAG0912	367	nucleoside diphosphate kinase domain protein
ORF01032	SAG0913	212	chloramphenicol acetyltransferase
ORF01033	SAG0914	203	conserved hypothetical protein
ORF01034	SAG0915	405	Tn916, transposase
ORF01035	SAG0916	67	Tn916, excisionase
ORF01037	SAG0918	76	Tn916, hypothetical protein
ORF01038	SAG0919	157	Tn916, hypothetical protein
ORF01039	SAG0921	117	Tn916, transcriptional regulator, putative
ORF01040	SAG0923	639	Tn916, tetracycline resistance protein
ORF01041	SAG0925	310	Tn916, hypothetical protein
ORF01042	SAG0926	333	Tn916, NLP/P60 family protein
ORF01044	SAG0927	725	Tn916, hypothetical protein FRAMESHIFT
ORF01047	SAG0928		Tn916, hypothetical protein FRAMESHIFT
ORF01048	SAG0929	168	Tn916, hypothetical protein
ORF01049	SAG0930	165	Tn916, hypothetical protein
ORF01050	SAG0931	73	Tn916, hypothetical protein
ORF01051	SAG0932	401	Tn916, transcriptional regulator, putative
ORF01052	SAG0933	461	Tn916, FtsK/SpoIIIE family protein
ORF01053	SAG0934	128	Tn916, hypothetical protein
ORF01054	SAG0935	104	Tn916, hypothetical protein
ORF01056	SAG0937		ABC transporter, ATP-binding protein, FRAMESHIFT
ORF01057	SAG0938	122	transcriptional regulator, GntR family
ORF01058	SAG0939	1034	DNA polymerase III, alpha subunit

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF01059	SAG0940	340	6-phosphofructokinase
ORF01060	SAG0941	500	pyruvate kinase
ORF01061	SAG0942	185	signal peptidase I, putative
ORF01062	SAG0943	47	hypothetical protein
ORF01063	SAG0944	604	glucosamine-fructose-6-phosphate aminotransferase (isomerizing)
ORF01064	SAG0945	377	IS1548, transposase
ORF01066	SAG0946	109	phnA protein
ORF01068	SAG0947	213	amino acid ABC transporter, permease protein
ORF01069	SAG0948	209	amino acid ABC transporter, ATP-binding protein
ORF01070	SAG0949	276	amino acid ABC transporter, amino acid-binding protein
ORF01072	SAG0950	82	ribosomal protein S20
ORF01073	SAG0951	306	pantothenate kinase
ORF01074	SAG0952	196	conserved hypothetical protein
ORF01075	SAG0953	129	cytidine deaminase
ORF01076	SAG0954	349	lipoprotein
ORF01077	SAG0955	511	sugar ABC transporter, ATP-binding protein
ORF01078	SAG0956	353	sugar ABC transporter, permease protein, putative
ORF01079	SAG0957	318	sugar ABC transporter, permease protein, putative
ORF01080	SAG0958	456	NADH oxidase
ORF01081	SAG0959	329	L-lactate dehydrogenase
ORF01082	SAG0960	819	DNA gyrase, A subunit
ORF01083	SAG0961	247	sortase SrtA
ORF01084	SAG0962	137	glyoxylase family protein
ORF01085	SAG0963	320	conserved hypothetical protein
ORF01086	SAG0964	375	Na ⁺ /H ⁺ exchanger family protein
ORF01087	SAG0965	127	IS1381, transposase OrfA
ORF01088	SAG0966	129	IS1381, transposase OrfB
ORF01089	SAG0967	520	GMP synthase
ORF01090	SAG0968	232	transcriptional regulator, GntR family
ORF01091	SAG0969	444	gid protein
ORF01092	SAG0970	247	acetyltransferase, GNAT family
ORF01093	SAG0971	282	lipoprotein, putative
ORF01095	SAG0972		conserved hypothetical protein, FRAMESHIFT
ORF01096	SAG0973	320	nisin-resistance protein, putative
ORF01097	SAG0974	250	ABC transporter, ATP-binding protein
ORF01098	SAG0975	651	ABC transporter, permease protein, putative
ORF01099	SAG0976	222	DNA-binding response regulator
ORF01100	SAG0977	312	sensor histidine kinase
ORF01101	SAG0978	356	site-specific recombinase, phage integrase family
ORF01102	SAG0979	553	ABC transporter, substrate binding protein, putative
ORF01103	SAG0980	257	conserved hypothetical protein
ORF01104	SAG0981	228	SatD
ORF01106	SAG0982	521	signal recognition particle protein
ORF01108	SAG0983	110	conserved hypothetical protein
ORF01109	SAG0984	437	sensor histidine kinase CiaH
ORF01110	SAG0985	226	DNA-binding response regulator CiaR
ORF01111	SAG0986	849	aminopeptidase N
ORF01112	SAG0987	217	phosphate transport system regulatory protein PhoU

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF01113	SAG0988	252	phosphate ABC transporter, ATP-binding protein PstB, putative
ORF01114	SAG0989	267	phosphate ABC transporter, ATP-binding protein PstB, putative
ORF01115	SAG0990	295	phosphate ABC transporter, permease protein PstA, putative
ORF01116	SAG0991	305	phosphate ABC transporter, permease protein
ORF01117	SAG0992	286	phosphate ABC transporter, phosphate-binding protein
ORF01118	SAG0993	436	NOL1/NOP2/sun family protein
ORF01119	SAG0994	254	inositol monophosphatase family protein
ORF01120	SAG0995	93	conserved hypothetical protein
ORF01121	SAG0996	137	conserved hypothetical protein
ORF01122	SAG0997	310	macrolide-efflux protein mreA/riboflavin biosynthesis protein RibF
ORF01123	SAG0998	294	tRNA pseudouridine synthase B
ORF01124	SAG0999	143	acetyltransferase, GNAT family
ORF01125	SAG1000	423	conserved hypothetical protein
ORF01126	SAG1001	196	conserved hypothetical protein
ORF01127	SAG1002	292	protease, putative
ORF01128	SAG1003	876	permease, putative
ORF01129	SAG1004	233	ABC transporter, ATP-binding protein
ORF01131	SAG1005	706	DNA topoisomerase I
ORF01132	SAG1006	280	DprA/SMF protein, putative DNA processing factor
ORF01133	SAG1007	342	iron-compound ABC transporter, iron-compound-binding protein
ORF01134	SAG1008	253	iron compound ABC transporter, ATP-binding protein
ORF01135	SAG1009	324	iron compound ABC transporter, permease protein
ORF01136	SAG1010	320	iron compound ABC transporter, permease protein
ORF01137	SAG1011	182	acetyltransferase, CysE/LacA/LpxA/NodL family
ORF01138	SAG1012	253	ribonuclease HII
ORF01139	SAG1013	283	GTP-binding protein
ORF01140	SAG1014	190	conserved hypothetical protein
ORF01142	SAG1015	494	carbon starvation protein CstA, putative
ORF01143	SAG1016	244	response regulator
ORF01144	SAG1017	579	sensor histidine kinase, putative
ORF01145	SAG1018	40	hypothetical protein
ORF01146	SAG1019	39	conserved hypothetical protein, FRAMESHIFT
ORF01148	SAG1020	227	hypothetical protein
ORF01149	SAG1021	107	hypothetical protein
ORF01150	SAG1022	177	hypothetical protein
ORF01151	SAG1023	48	hypothetical protein
ORF01152	SAG1024	183	hypothetical protein
ORF01153	SAG1025	149	hypothetical protein
ORF01156	SAG1026		immunogenic secreted protein, DEGENERATE
ORF01157	SAG1027	84	conserved hypothetical protein
ORF01158	SAG1028	196	hypothetical protein
ORF01159	SAG1029	101	hypothetical protein
ORF01160	SAG1030	304	conserved hypothetical protein
ORF01161	SAG1031	120	extracellular protein, putative POINT MUTATION
ORF01162	SAG1032	85	conserved hypothetical protein
ORF01164	SAG1033	1309	FtsK/SpoIIIE family protein
ORF01166	SAG1034	55	hypothetical protein

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF01167	SAG1035	424	conserved hypothetical protein
ORF01168	SAG1036	80	conserved hypothetical protein
ORF01169	SAG1037	157	hypothetical protein
ORF01172	SAG1038	1003	phage infection protein, putative
ORF01173	SAG1039	96	conserved hypothetical protein
ORF01174	SAG1040	260	conserved domain protein
ORF01175	SAG1041	107	hypothetical protein
ORF01176	SAG1042	1060	carbamoyl-phosphate synthase, large subunit
ORF01177	SAG1043	358	carbamoyl-phosphate synthase, small subunit
ORF01178	SAG1044	307	aspartate carbamoyltransferase
ORF01179	SAG1045	430	dihydroorotase, multifunctional complex type
ORF01180	SAG1046	209	orotate phosphoribosyltransferase
ORF01181	SAG1047	233	orotidine 5'-phosphate decarboxylase
ORF01182	SAG1048	410	membrane protein, putative
ORF01183	SAG1049	513	ABC transporter, ATP-binding protein
ORF01184	SAG1050	112	ribonucleotide reductase, truncation
ORF01185	SAG1051	358	aspartate-semialdehyde dehydrogenase
ORF01186	SAG1052	47	cell wall surface anchor family protein, putative
ORF01187	SAG1053	30	hypothetical protein
ORF01188	SAG1054	531	cardiolipin synthetase
ORF01189	SAG1055	556	formate-tetrahydrofolate ligase
ORF01190	SAG1056	339	lipoate-protein ligase A
ORF01191	SAG1057	292	conserved hypothetical protein
ORF01192	SAG1058	272	conserved hypothetical protein
ORF01193	SAG1059	110	glycine cleavage system H protein, putative
ORF01194	SAG1060	328	bacterial luciferase family protein
ORF01195	SAG1061	399	oxidoreductase, FMN-binding
ORF01197	SAG1062	282	lipoate-protein ligase A family protein
ORF01198	SAG1063	228	flavoprotein-related protein
ORF01199	SAG1064	180	flavoprotein family protein
ORF01200	SAG1065	190	membrane protein, putative
ORF01201	SAG1066	572	phosphoglucomutase
ORF01202	SAG1067	178	IS861, transposase OrfA
ORF01203	SAG1068	277	IS861, transposase OrfB
ORF01204	SAG1069	65	hypothetical protein
ORF01205	SAG1070	577	ABC transporter, ATP-binding/permease protein
ORF01206	SAG1071	573	ABC transporter, ATP-binding/permease protein
ORF01207	SAG1072	200	conserved hypothetical protein
ORF01208	SAG1073	325	conserved hypothetical protein
ORF01209	SAG1074	418	Serine hydroxymethyltransferase
ORF01210	SAG1075	183	Sua5/YciO/YrdC/YwiC family protein
ORF01211	SAG1076	276	modification methylase, HemK family
ORF01212	SAG1077	359	peptide chain release factor 1
ORF01213	SAG1078	189	thymidine kinases
ORF01214	SAG1079	60	4-oxalocrotonate tautomerase
ORF01215	SAG1080	47	hypothetical protein
ORF01216	SAG1081	312	ApbE family protein
ORF01217	SAG1082	200	conserved hypothetical protein
ORF01218	SAG1083	411	conserved hypothetical protein
ORF01219	SAG1084	262	formate/nitrite transporter family protein
ORF01220	SAG1085	424	xanthine permease
ORF01221	SAG1086	193	xanthine phosphoribosyltransferase
ORF01222	SAG1087	327	guanosine monophosphate reductase
ORF01223	SAG1088	446	drug resistance transporter, EmrB/QacA family, putative

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF01224	SAG1089	230	conserved hypothetical protein
ORF01225	SAG1090	666	potassium uptake protein, putative
ORF01226	SAG1091	216	oxidoreductase, short chain dehydrogenase/reductase family, FRAMESHIFT
ORF01227	SAG1092	330	phosphate acetyltransferase
ORF01228	SAG1093	294	ribosomal large subunit pseudouridine synthase, RluD subfamily
ORF01229	SAG1094	278	conserved hypothetical protein
ORF01230	SAG1095	223	GTP pyrophosphokinase family protein
ORF01231	SAG1096	190	conserved hypothetical protein
ORF01232	SAG1097	324	ribose-phosphate pyrophosphokinase
ORF01233	SAG1098	371	cysteine desulphurase
ORF01234	SAG1099	115	conserved hypothetical protein
ORF01235	SAG1100	210	DNA-binding protein
ORF01236	SAG1101	226	DNA repair protein RadC
ORF01237	SAG1102	377	membrane protein, putative
ORF01238	SAG1103	478	6-phospho-beta-glucosidase
ORF01239	SAG1104	204	platelet activating factor, putative
ORF01240	SAG1105	273	hydrolase, haloacid dehalogenase-like family
ORF01241	SAG1106	309	transcriptional regulator, AraC family, putative
ORF01242	SAG1107	510	voltage-gated chloride channel family protein
ORF01243	SAG1108	357	spermidine/putrescine ABC transporter, spermidine/putrescine-binding protein
ORF01244	SAG1109	258	spermidine/putrescine ABC transporter, permease protein
ORF01245	SAG1110	264	spermidine/putrescine ABC transporter, permease protein
ORF01246	SAG1111	384	spermidine/putrescine ABC transporter, ATP-binding protein
ORF01247	SAG1112	300	UDP-N-acetylenolpyruvoylglucosamine reductase
ORF01248	SAG1113	162	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase
ORF01249	SAG1114	120	dihydroneopterin aldolase
ORF01250	SAG1115	267	dihydropteroate synthase
ORF01251	SAG1116	187	GTP cyclohydrolase I
ORF01252	SAG1117	420	folylpolyglutamate synthase
ORF01253	SAG1118	295	rarD protein
ORF01254	SAG1119	288	homoserine kinase
ORF01255	SAG1120	427	homoserine dehydrogenase
ORF01256	SAG1121	295	polysaccharide deacetylase family protein
ORF01257	SAG1122	515	transporter, BCCT family protein
ORF01258	SAG1123	34	hypothetical protein
ORF01259	SAG1124	458	aldehyde dehydrogenase family protein
ORF01260	SAG1125	335	membrane protein
ORF01261	SAG1126	228	conserved hypothetical protein
ORF01262	SAG1127	113	conserved hypothetical protein, FRAMESHIFT
ORF01263		187	hypothetical protein
ORF01264	SAG1128	65	transcriptional regulator, Cro/C1 family
ORF01265	SAG1129	36	hypothetical protein
ORF01266	SAG1130	49	hypothetical protein
ORF01268	SAG1131	164	thiol peroxidase
ORF01269	SAG1132	219	conserved hypothetical protein
ORF01272	SAG1133	254	conserved hypothetical protein

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF01273	SAG1134	213	transcriptional regulator, GntR family/potassium uptake protein, TrkA family
ORF01274	SAG1135	183	gls24 protein, putative
ORF01275	SAG1136		conserved hypothetical protein FRAMESHIFT
ORF01276	SAG1137	180	gls24 protein, putative
ORF01277	SAG1138	64	conserved hypothetical protein
ORF01279	SAG1139	193	conserved hypothetical protein
ORF01280	SAG1140	82	conserved hypothetical protein
ORF01281	SAG1141	112	conserved hypothetical protein
ORF01282	SAG1142	759	ATP-dependent DNA helicase PcrA
ORF01283	SAG1143	100	conserved hypothetical protein, FRAMESHIFT
ORF01284	SAG1144	441	uracil permease
ORF01285	SAG1145	448	sodium:alanine symporter family protein
ORF01286	SAG1146	411	cation efflux family protein
ORF01287	SAG1147	130	conserved hypothetical protein
ORF01288	SAG1148	231	membrane protein, putative
ORF01289	SAG1149	207	conserved hypothetical protein
ORF01290	SAG1150	400	ribosomal protein S1
ORF01291	SAG1151	76	conserved hypothetical protein
ORF01292	SAG1152	340	branched-chain amino acid aminotransferase
ORF01294	SAG1153	819	DNA topoisomerase IV, A subunit
ORF01295	SAG1154	653	DNA topoisomerase IV, B subunit
ORF01296	SAG1155	207	conserved hypothetical protein TIGR00023
ORF01297	SAG1156	217	uracil-DNA glycosylase
ORF01298	SAG1157	161	conserved hypothetical protein
ORF01299	SAG1158	413	CMP-N-acetylneuraminic acid synthetase NeuA
ORF01300	SAG1159	209	neuD protein
ORF01301	SAG1160	384	UDP-N-acetylglucosamine-2-epimerase NeuC
ORF01302	SAG1161	341	N-acetyl neuramic acid synthetase NeuB
ORF01303	SAG1162	466	cpsL protein
ORF01304	SAG1163	318	cpsVK protein
ORF01305	SAG1164	321	cpsVJ protein
ORF01306	SAG1165	327	cpsVO protein
ORF01307	SAG1166	295	cpsVN protein
ORF01308	SAG1167	241	cpsVM protein
ORF01309	SAG1168	364	cpsVH protein
ORF01310	SAG1169	163	CpsVG
ORF01311	SAG1170	149	CpsF
ORF01312	SAG1171	462	CpsE
ORF01313	SAG1172	229	CpsD protein
ORF01314	SAG1173	230	cpsC protein
ORF01315	SAG1174	243	capsular polysaccharide biosynthesis protein CpsB
ORF01316	SAG1175	485	capsular polysaccharide biosynthesis protein CpsA
ORF01317	SAG1176	290	capsular polysaccharide synthesis operon transcriptional regulator CpsY
ORF01318	SAG1177	255	cpslaS protein
ORF01319	SAG1178	236	purine nucleoside phosphorylase
ORF01320	SAG1179	418	voltage-gated chloride channel family protein, putative
ORF01321	SAG1180	269	purine nucleoside phosphorylase
ORF01322	SAG1181	135	arsenate reductase
ORF01323	SAG1182	403	phosphopentomutase
ORF01324	SAG1183	223	ribose 5-phosphate isomerase

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF01326	SAG1184	236	conserved hypothetical protein
ORF01327	SAG1185	262	tributylin esterase
ORF01328	SAG1186	553	metallo-beta-lactamase superfamily protein
ORF01329	SAG1187	253	ABC transporter, ATP-binding protein
ORF01330	SAG1188	287	ABC transporter, permease protein
ORF01331	SAG1189	334	conserved hypothetical protein
ORF01332	SAG1190	551	adherence and virulence protein A
ORF01333	SAG1191	239	alpha-acetolactate decarboxylase
ORF01334	SAG1192	560	acetolactate synthase, catabolic
ORF01335	SAG1193	408	TPR domain protein
ORF01336	SAG1194	396	membrane protein
ORF01337	SAG1195	153	MutT/nudix family protein
ORF01338	SAG1196	160	mutator MutT protein
ORF01339	SAG1197	1072	hyaluronidase
ORF01340	SAG1198	348	dTDP-glucose 4,6-dehydratase
ORF01341	SAG1199	197	dTDP-4-dehydrorhamnose 3,5-epimerase
ORF01342	SAG1200	289	glucose-1-phosphate thymidyltransferase
ORF01343	SAG1201	367	iminodiacetate oxidase, putative
ORF01344	SAG1202	262	conserved hypothetical protein TIGR00486
ORF01345	SAG1203	227	conserved hypothetical protein
ORF01346	SAG1204	226	DNA replication protein Dnad, putative
ORF01347	SAG1205	172	adenine phosphoribosyltransferase
ORF01348	SAG1206	854	conserved domain protein
ORF01349	SAG1207	32	hypothetical protein
ORF01350	SAG1208	732	single-stranded-DNA-specific exonuclease RecJ
ORF01351	SAG1209	253	oxidoreductase, short chain dehydrogenase/reductase family
ORF01352	SAG1210	309	metallo-beta-lactamase superfamily protein
ORF01353	SAG1211	215	conserved hypothetical protein
ORF01354	SAG1212	412	GTP-binding protein HflX
ORF01355	SAG1213	296	tRNA delta(2)-isopentenylpyrophosphate transferase
ORF01356	SAG1214	58	hypothetical protein
ORF01357	SAG1215	305	exfoliative toxin A, putative
ORF01358	SAG1216	1252	pullulanase, putative
ORF01361	SAG1217		conserved hypothetical protein, FRAMESHIFT
ORF01362	SAG1218	194	conserved hypothetical protein
ORF01363	SAG1219	468	peptidase, M20/M25/M40 family
ORF01364	SAG1220	200	nitroreductase family protein
ORF01365	SAG1221		glycerophosphoryl diester phosphodiesterase, putative, POINT MUTATION
ORF01367	SAG1222	593	excinuclease ABC, C subunit
ORF01368	SAG1223	255	conserved hypothetical protein
ORF01369	SAG1224	446	MATE efflux family protein
ORF01370	SAG1225	136	conserved hypothetical protein
ORF01371	SAG1226	165	conserved hypothetical protein
ORF01372	SAG1227	198	conserved hypothetical protein
ORF01373	SAG1228	96	ISSdy1, transposase OrfA
ORF01374	SAG1229	259	ISSdy1, transposase OrfB
ORF01375	SAG1230	96	conserved hypothetical protein
ORF01377	SAG1231		transposase OrfB, IS3 family, degenerate FRAMESHIFT
ORF01379	SAG1232	77	transposase OrfB, IS3 family, truncation
ORF01380	SAG1233	822	streptococcal histidine triad family protein
ORF01381	SAG1234	306	laminin-binding surface protein

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF01382	SAG1235	425	GBS1, group II intron, maturase
ORF01383	SAG1236		c5a peptidase precursor FRAMESHIFT
ORF01384	SAG1237	444	hypothetical protein
ORF01385	SAG1238	202	hypothetical protein
ORF01386	SAG1239	76	conserved hypothetical protein
ORF01387	SAG1240	125	conserved hypothetical protein, truncation
ORF01388	SAG1241	78	transposase OrfA, IS3 family
ORF01389	SAG1242	67	transposase OrfB, IS3 family, truncation
ORF01390	SAG1243	96	ISSdy1, transposase OrfA FRAMESHIFT
ORF01391	SAG1244	259	ISSdy1, transposase OrfB
ORF01392	SAG1245	38	hypothetical protein
ORF01393	SAG1246	389	hypothetical protein
ORF01394	SAG1247	399	integrase, phage family
ORF01395	SAG1248	75	conserved hypothetical protein
ORF01396	SAG1249	74	transcriptional regulator, Cro/C1 family
ORF01397	SAG1250	621	Tn5252, relaxase
ORF01398	SAG1251	121	Tn5252, Orf 9 protein
ORF01399	SAG1252	120	Tn5252, Orf 10 protein
ORF01401	SAG1253	435	transposase, ISL3 family
ORF01403	SAG1254	546	mercuric reductase
ORF01404	SAG1255	130	mercuric resistance operon regulatory protein MerR
ORF01406	SAG1256	142	IS861, transposase OrfB, truncation
ORF01407	SAG1257	709	cation-transporting ATPase, E1-E2 family
ORF01408	SAG1258	122	cadmium efflux system accessory protein
ORF01409	SAG1259	99	conserved hypothetical protein
ORF01410	SAG1260	262	hypothetical protein
ORF01411	SAG1261	198	conserved hypothetical protein
ORF01412	SAG1262	695	cation-transporting ATPase, E1-E2 family
ORF01414	SAG1263		conserved domain protein, FRAMESHIFT
ORF01415	SAG1264	148	transcriptional repressor CopY, putative
ORF01416	SAG1265	206	cadmium resistance transporter, putative
ORF01417	SAG1266	152	hypothetical protein
ORF01418	SAG1267	108	hypothetical protein
ORF01419	SAG1268	230	repressor protein, putative
ORF01420	SAG1269	44	hypothetical protein
ORF01421	SAG1270	471	ImpB/MucB/SamB family protein
ORF01423	SAG1271	116	conserved hypothetical protein
ORF01424	SAG1272	102	conserved hypothetical protein
ORF01425	SAG1273	118	conserved hypothetical protein
ORF01426	SAG1274	129	conserved hypothetical protein
ORF01427	SAG1275	75	hypothetical protein
ORF01428	SAG1276	358	conserved hypothetical protein
ORF01430	SAG1277	163	hypothetical protein
ORF01431	SAG1278	96	hypothetical protein
ORF01432	SAG1279	99	conserved domain protein
ORF01433	SAG1280	2274	Helicases conserved C-terminal domain protein
ORF01434	SAG1281	183	hypothetical protein
ORF01435	SAG1282	63	lipoprotein, putative
ORF01436	SAG1283	1631	cell wall surface anchor family protein
ORF01437	SAG1284	196	abortive infection protein AbiGI
ORF01438	SAG1285	281	abortive infection protein AbiGII
ORF01439	SAG1286	933	conserved hypothetical protein
ORF01440	SAG1287	776	conserved hypothetical protein
ORF01441	SAG1288	117	conserved hypothetical protein, DEGENERATE

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF01442	SAG1289	284	conserved hypothetical protein
ORF01443	SAG1290	80	hypothetical protein
ORF01444	SAG1291	605	Tn5252, Orf 21 protein, internal deletion
ORF01445	SAG1292	162	hypothetical protein
ORF01446	SAG1293	194	protease, putative
ORF01447	SAG1294	77	conserved hypothetical protein
ORF01449	SAG1295	127	conserved hypothetical protein
ORF01450	SAG1296	142	conserved hypothetical protein
ORF01451	SAG1297	451	type II DNA modification methyltransferase Spn5252IP
ORF01452	SAG1298	31	hypothetical protein
ORF01453	SAG1299	272	conserved hypothetical protein
ORF01454	SAG1300	57	conserved hypothetical protein
ORF01455	SAG1301	121	ribosomal protein L7/L12
ORF01456	SAG1302	166	ribosomal protein L10
ORF01458	SAG1303	702	ATP-dependent Clp protease, ATP-binding subunit
ORF01459	SAG1304	32	hypothetical protein
ORF01460	SAG1305	314	homocysteine S-methyltransferase MmuM, putative
ORF01461	SAG1306	458	amino acid permease
ORF01463	SAG1307	216	hypothetical protein
ORF01464	SAG1308	167	hypothetical protein
ORF01465	SAG1309	30	hypothetical protein
ORF01466	SAG1310	182	transcriptional regulator, TetR family
ORF01467	SAG1311	198	GTP-binding protein
ORF01468	SAG1312	408	ATP-dependent Clp protease, ATP-binding subunit ClpX
ORF01469	SAG1313	56	conserved hypothetical protein
ORF01470	SAG1314	164	dihydrofolate reductase
ORF01471	SAG1315	279	thymidylate synthase
ORF01472	SAG1316	390	HMG-CoA synthase
ORF01473	SAG1317	427	3-hydroxy-3-methylglutaryl-CoA reductase
ORF01474	SAG1318	149	conserved hypothetical protein
ORF01475	SAG1319	187	hemolysin III, putative
ORF01476	SAG1320	304	conserved hypothetical protein TIGR00147
ORF01477	SAG1321	284	glutathione S-transferase family protein
ORF01478	SAG1322	72	conserved domain protein
ORF01479	SAG1323	331	isopentenyl-diphosphate delta-isomerase
ORF01480	SAG1324	330	phosphomevalonate kinase
ORF01481	SAG1325	314	diphosphomevalonate decarboxylase
ORF01482	SAG1326	292	mevalonate kinase, putative
ORF01483	SAG1327	409	sensor histidine kinase
ORF01484	SAG1328	228	DNA-binding response regulator
ORF01485	SAG1329	208	GTP pyrophosphokinase family protein
ORF01486	SAG1330	68	hypothetical protein
ORF01488	SAG1331	979	R5 protein
ORF01489	SAG1332	146	transcriptional regulator, MarR family, putative
ORF01490	SAG1333	690	5'-nucleotidase family protein
ORF01491	SAG1334	136	polypeptide deformylase, putative
ORF01492	SAG1335	449	NADP-specific glutamate dehydrogenase
ORF01494	SAG1336	169	conserved hypothetical protein
ORF01495	SAG1337	589	ABC transporter, ATP-binding/permease protein
ORF01496	SAG1338	579	ABC transporter, ATP-binding/permease protein
ORF01497	SAG1339	157	acetyltransferase, GNAT family

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF01498	SAG1340	622	ABC transporter, ATP-binding protein
ORF01499	SAG1341	402	polyA polymerase family protein
ORF01500	SAG1342	282	DegV family protein
ORF01501	SAG1343	126	conserved hypothetical protein
ORF01502	SAG1344	177	hypothetical protein
ORF01503	SAG1345	164	conserved hypothetical protein
ORF01504	SAG1346	641	PTS system, fructose specific IIBC components
ORF01505	SAG1347	303	1-phosphofructokinase
ORF01506	SAG1348	247	lactose phosphotransferase system repressor
ORF01507	SAG1349	411	beta-lactam resistance factor
ORF01508	SAG1350	544	surface antigen-related protein
ORF01509	SAG1351	307	2-dehydropantoate 2-reductase, putative
ORF01510	SAG1352	356	regulatory protein, putative
ORF01511	SAG1353	330	pyridine nucleotide-disulphide oxidoreductase family protein
ORF01512	SAG1354	251	tRNA (guanine-N1)-methyltransferase
ORF01513	SAG1355	172	16S rRNA processing protein RimM
ORF01515	SAG1356	503	transcriptional regulator, RofA family
ORF01516	SAG1357	80	KH domain protein
ORF01517	SAG1358	90	ribosomal protein S16
ORF01518	SAG1359	415	permease, putative
ORF01519	SAG1360	236	ABC transporter, ATP-binding protein
ORF01520	SAG1361	414	conserved hypothetical protein
ORF01522	SAG1362	532	carbamoyl-phosphate synthase, large subunit, putative
ORF01523	SAG1363	356	carbamoyl-phosphate synthase, small subunit
ORF01524	SAG1364	173	pyrimidine operon regulatory protein
ORF01525	SAG1365	296	ribosomal large subunit pseudouridine synthase, RluD subfamily
ORF01526	SAG1366	154	lipoprotein signal peptidase
ORF01527	SAG1367	301	transcriptional regulator, LysR family
ORF01528	SAG1368	94	ribosomal protein L27
ORF01529	SAG1369	112	conserved hypothetical protein
ORF01530	SAG1370	104	ribosomal protein L21
ORF01531	SAG1371	392	conserved hypothetical protein
ORF01532	SAG1372	404	thiamine biosynthesis protein ThiI
ORF01533	SAG1373	381	cysteine desulphurase
ORF01535	SAG1374	150	conserved hypothetical protein
ORF01536	SAG1375	449	glutathione reductase
ORF01537	SAG1376	111	conserved hypothetical protein
ORF01538	SAG1377	388	chorismate synthase
ORF01539	SAG1378	355	3-dehydroquinate synthase
ORF01540	SAG1379	225	3-dehydroquinate dehydratase
ORF01541	SAG1380	385	conserved hypothetical protein
ORF01542	SAG1381	714	sulfatase
ORF01543	SAG1382	119	ribosomal protein L20
ORF01544	SAG1383	66	ribosomal protein L35
ORF01545	SAG1384	176	translation initiation factor IF-3
ORF01546	SAG1385	227	cytidylate kinase
ORF01547	SAG1386	174	conserved hypothetical protein
ORF01548	SAG1387	65	ferredoxin, 4Fe-4S
ORF01549	SAG1388	163	conserved hypothetical protein
ORF01550	SAG1389	406	peptidase t
ORF01551	SAG1390	544	polysaccharide biosynthesis protein, putative

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF01552	SAG1391	484	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase
ORF01553	SAG1392	264	iron compound ABC transporter, ATP-binding protein
ORF01554	SAG1393	310	iron compound ABC transporter, substrate-binding protein
ORF01555	SAG1394	341	iron compound ABC transporter, permease protein
ORF01556	SAG1395	333	iron compound ABC transporter, permease protein
ORF01557	SAG1396	217	conserved hypothetical protein
ORF01558	SAG1397	311	inorganic pyrophosphatase, manganese-dependent
ORF01559	SAG1398	262	pyruvate formate-lyase-activating enzyme
ORF01560	SAG1399	444	CBS domain protein
ORF01561	SAG1400	188	conserved hypothetical protein
ORF01563	SAG1401	311	conserved hypothetical protein TIGR01212
ORF01564	SAG1402	213	PAP2 family protein
ORF01565	SAG1403	194	membrane protein, putative
ORF01566	SAG1404	308	cell wall surface anchor family protein
ORF01567	SAG1405	294	sortase family protein
ORF01568	SAG1406	293	sortase family protein
ORF01569	SAG1407	705	cell wall surface anchor family protein
ORF01570	SAG1408	901	cell wall surface anchor family protein
ORF01571	SAG1409	326	transcriptional regulator, RofA family FRAMESHIFT
ORF01572	SAG1410	379	glycosyl transferase, group 1 family protein
ORF01573	SAG1411	282	exopolysaccharide biosynthesis protein, putative
ORF01574	SAG1412	474	exopolysaccharide biosynthesis protein, putative
ORF01575	SAG1413	454	hypothetical protein
ORF01576	SAG1414	308	glycosyl transferase, group 2 family protein
ORF01577	SAG1415	311	glycosyl transferase, group 2 family protein
ORF01578	SAG1416	352	dTDP-glucose 4,6-dehydratase, putative
ORF01579	SAG1417	240	4-diphosphocytidyl-2C-methyl-D-erythritol synthase, putative
ORF01580	SAG1418	259	licD protein, putative
ORF01581	SAG1419	577	hypothetical protein
ORF01582	SAG1420	117	conserved hypothetical protein
ORF01583	SAG1421	243	glycosyl transferase, group 2 family protein
ORF01584	SAG1422	313	glycosyl transferase, group 2 family protein
ORF01585	SAG1423	384	conserved hypothetical protein
ORF01586	SAG1424	284	dTDP-4-dehydrorhamnose reductase
ORF01587	SAG1425	113	conserved hypothetical protein
ORF01589	SAG1426	369	RNA polymerase sigma-70 factor
ORF01590	SAG1427	602	DNA primase
ORF01591	SAG1428	125	large conductance mechanosensitive channel protein
ORF01592	SAG1429	58	ribosomal protein S21
ORF01593	SAG1430	167	conserved hypothetical protein
ORF01594	SAG1431	268	amino acid ABC transporter, amino acid-binding protein
ORF01596	SAG1432	347	ammonium transporter family protein
ORF01597	SAG1433	375	conserved hypothetical protein
ORF01598	SAG1434	328	rhodanese family protein
ORF01599	SAG1435	101	conserved hypothetical protein
ORF01600	SAG1436	457	glycerol-3-phosphate transporter, putative

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF01601	SAG1437	55	hypothetical protein
ORF01602	SAG1438	754	glycogen phosphorylase
ORF01603	SAG1439	498	4-alpha-glucanotransferase
ORF01604	SAG1440	342	maltose operon repressor MalR, putative
ORF01605	SAG1441	415	maltose/maltodextrin ABC transporter, maltose/maltodextrin-binding protein
ORF01606	SAG1442	456	maltose ABC transporter, permease protein
ORF01607	SAG1443	278	maltose ABC transporter, permease protein
ORF01608	SAG1444	490	proton/peptide symporter family protein
ORF01610	SAG1445		MutT/nudix family protein, FRAMESHIFT
ORF01611	SAG1446	62	hypothetical protein
ORF01612	SAG1447	441	conserved hypothetical protein
ORF01613	SAG1448	502	glycosyl transferase, group 1 family protein
ORF01614	SAG1449	795	preprotein translocase SecA subunit, putative
ORF01615	SAG1450	330	conserved domain protein
ORF01617	SAG1451	494	conserved hypothetical protein
ORF01618	SAG1452	514	conserved hypothetical protein
ORF01619	SAG1453	409	preprotein translocase SecY family protein
ORF01621	SAG1454	398	conserved hypothetical protein
ORF01622	SAG1455	295	glycosyl transferase, group 2 family protein
ORF01623	SAG1456	312	glycosyl transferase, family 8, degenerate
ORF01624	SAG1457	129	IS1381, transposase OrfB
ORF01625	SAG1458	127	IS1381, transposase OrfA
ORF01626	SAG1459	413	glycosyl transferase family 8
ORF01627	SAG1460	401	glycosyl transferase, family 8
ORF01628	SAG1461	335	conserved hypothetical protein
ORF01630	SAG1462	970	cell wall surface anchor family protein
ORF01632	SAG1463		transcriptional regulator, RofA family POINT MUTATION
ORF01634	SAG1464	663	excinuclease ABC, B subunit
ORF01635	SAG1465	306	protease, putative
ORF01636	SAG1466	727	glutamine ABC transporter, glutamine-binding protein/permease protein, putative
ORF01637	SAG1467	246	glutamine ABC transporter, ATP-binding protein, GlnQ putative
ORF01638	SAG1468	116	conserved hypothetical protein
ORF01639	SAG1469	52	conserved hypothetical protein
ORF01640	SAG1470	437	GTP-binding protein, GTP1/Obg family
ORF01641	SAG1471	42	conserved hypothetical protein
ORF01643	SAG1472	413	aminopeptidase PepS
ORF01645	SAG1473	192	cell wall surface anchor family protein
ORF01646	SAG1474	680	amidase family protein
ORF01647	SAG1475	240	ribosomal small subunit pseudouridine synthase A
ORF01648	SAG1476	280	oxidoreductase, aldo/keto reductase family
ORF01650	SAG1477	224	nitroreductase family protein
ORF01651	SAG1478	130	lactoylglutathione lyase
ORF01652	SAG1479	308	glycosyl transferase, group 2 family protein
ORF01653	SAG1480	462	amino acid permease
ORF01654	SAG1481	155	SsrA-binding protein
ORF01655	SAG1482	801	exoribonuclease, VacB/Rnb family
ORF01657	SAG1483	78	preprotein translocase, SecG subunit
ORF01658	SAG1485	389	multi-drug resistance protein
ORF01660	SAG1486	548	hypothetical protein
ORF01661	SAG1487	233	ABC transporter, ATP binding protein

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF01662	SAG1488	195	dephospho-CoA kinase
ORF01663	SAG1489	273	formamidopyrimidine-DNA glycosylase
ORF01665	SAG1490	282	transcriptional regulator, MutR family
ORF01666	SAG1491	530	hypothetical protein
ORF01667	SAG1492	58	hypothetical protein
ORF01668	SAG1493		hypothetical protein
ORF01670	SAG1494	32	hypothetical protein
ORF01672	SAG1495	81	protease, putative, POINT MUTATION
ORF01673	SAG1496	110	hypothetical protein
ORF01674	SAG1497	37	hypothetical protein
ORF01675	SAG1498	133	hypothetical protein
ORF01677	SAG1499	299	GTP-binding protein Era
ORF01678	SAG1500	132	diacylglycerol kinase
ORF01679	SAG1501	161	conserved hypothetical protein TIGR00043
ORF01680	SAG1502	268	tetracenomycin polyketide synthesis O-methyltransferase TcmP, putative
ORF01681	SAG1503	39	hypothetical protein
ORF01682	SAG1504	38	hypothetical protein
ORF01683	SAG1505	158	MutT/nudix family protein
ORF01684	SAG1506	267	hypothetical protein
ORF01685	SAG1507	345	PhoH family protein
ORF01686	SAG1508	590	67 kDa Myosin-crossreactive streptococcal antigen
ORF01687	SAG1509	71	conserved hypothetical protein
ORF01688	SAG1510	169	peptide methionine sulfoxide reductase
ORF01689	SAG1511	284	conserved hypothetical protein
ORF01690	SAG1512	185	ribosome recycling factor
ORF01691	SAG1513	242	uridylate kinase
ORF01692	SAG1514	226	peptide ABC transporter, ATP-binding protein
ORF01693	SAG1515	262	peptide ABC transporter, ATP-binding protein
ORF01694	SAG1516	255	peptide ABC transporter, permease protein
ORF01695	SAG1517	314	peptide ABC transporter, permease protein
ORF01696	SAG1518	525	peptide ABC transporter, peptide-binding protein
ORF01697	SAG1519	229	ribosomal protein L1
ORF01698	SAG1520	141	ribosomal protein L11
ORF01699	SAG1521	388	transposase, IS30 family, putative
ORF01700	SAG1522	460	transporter, major facilitator family
ORF01702	SAG1523	404	peptidase, M20/M25/M40 family
ORF01703	SAG1524	294	transcriptional regulator, LysR family
ORF01704	SAG1525	117	conserved hypothetical protein
ORF01705	SAG1526	178	IS861, transposase OrfA
ORF01706	SAG1527	277	IS861, transposase OrfB
ORF01707	SAG1528	571	chorismate binding enzyme
ORF01708	SAG1529	785	FtsK/SpoIIIE family protein
ORF01709	SAG1530	267	peptidyl-prolyl cis-trans isomerase, cyclophilin-type
ORF01710	SAG1531	277	manganese ABC transporter, permease protein
ORF01711	SAG1532	238	manganese ABC transporter, ATP-binding protein
ORF01712	SAG1533	308	manganese ABC transporter, manganese-binding adhesion lipoprotein
ORF01713	SAG1534	215	iron-dependent transcriptional regulator
ORF01714	SAG1535	229	5-methylthioadenosine nucleosidase/S-adenosylhomocysteine nucleosidase
ORF01715	SAG1536	89	conserved hypothetical protein
ORF01716	SAG1537	184	MutT/nudix family protein

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF01718	SAG1538	459	UDP-N-acetylglucosamine pyrophosphorylase
ORF01719	SAG1539	31	hypothetical protein
ORF01720	SAG1540	137	conserved hypothetical protein
ORF01721	SAG1541	125	glyoxalase family protein
ORF01722	SAG1542	318	oxidoreductase, Gfo/ldh/MocA family
ORF01724	SAG1543		conserved hypothetical protein, FRAMESHIFT
ORF01725	SAG1544	232	gluconate 5-dehydrogenase, putative
ORF01726	SAG1545	78	conserved hypothetical protein
ORF01727	SAG1546	82	conserved hypothetical protein
ORF01729	SAG1547	166	acetyltransferase, GNAT family
ORF01730	SAG1548	422	glycosyl transferase, group 2 family protein
ORF01731	SAG1549	127	IS1381, transposase OrfA
ORF01732	SAG1550	129	IS1381, transposase OrfB
ORF01733	SAG1551	67	hypothetical protein
ORF01734	SAG1552	719	conserved hypothetical protein
ORF01735	SAG1553	477	hypothetical protein
ORF01736	SAG1554	225	hypothetical protein
ORF01737	SAG1555	231	hypothetical protein
ORF01738	SAG1556	445	branched-chain amino acid transport system II carrier protein
ORF01739	SAG1557	665	methionyl-tRNA synthetase
ORF01740	SAG1558	291	tellurite resistance protein TehB
ORF01741	SAG1559	231	membrane protein, putative
ORF01742	SAG1560	40	hypothetical protein
ORF01743	SAG1561	405	PTS system component, putative
ORF01744	SAG1562	280	conserved hypothetical protein
ORF01745	SAG1563	275	exodeoxyribonuclease
ORF01746	SAG1564	118	conserved hypothetical protein
ORF01747	SAG1565	158	methylated-DNA--protein-cysteine S-methyltransferase
ORF01748	SAG1566	393	D-isomer specific 2-hydroxyacid dehydrogenase family protein
ORF01749	SAG1567	182	acetyltransferase, GNAT family
ORF01750	SAG1568		phosphoserine aminotransferase FRAMESHIFT
ORF01752	SAG1569	211	copper homeostasis protein CutC, putative
ORF01753	SAG1570	34	conserved hypothetical protein
ORF01754	SAG1571	53	hypothetical protein
ORF01755	SAG1572	287	tetrapyrrole methylase family protein
ORF01756	SAG1573	108	conserved hypothetical protein
ORF01758	SAG1574	287	DNA polymerase III, delta prime subunit, putative
ORF01759	SAG1575	211	thymidylate kinase
ORF01761	SAG1576	267	transposase, IS30 family, putative, truncation
ORF01763	SAG1577	219	AcuB family protein
ORF01764	SAG1578	236	branched-chain amino acid ABC transporter, ATP-binding protein
ORF01765	SAG1579	254	branched-chain amino acid ABC transporter, ATP-binding protein
ORF01766	SAG1580	317	branched-chain amino acid ABC transporter, permease protein
ORF01767	SAG1581	289	branched-chain amino acid ABC transporter, permease protein
ORF01769	SAG1582	388	branched-chain amino acid ABC transporter, amino acid-binding protein
ORF01770	SAG1583	81	conserved hypothetical protein
ORF01772	SAG1584	377	IS1548, transposase

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF01773	SAG1585	196	ATP-dependent Clp protease, proteolytic subunit ClpP
ORF01774	SAG1586	209	uracil phosphoribosyltransferase
ORF01775	SAG1587	389	aminotransferase, class I
ORF01777	SAG1588	182	RNA methyltransferase, TrmH family, group 2
ORF01778	SAG1589	450	amino acid permease, putative
ORF01779	SAG1590	449	potassium uptake protein, Trk family
ORF01780	SAG1591	475	cation uptake protein, Trk family
ORF01781	SAG1592	83	conserved hypothetical protein TIGR00278
ORF01782	SAG1593	240	ribosomal large subunit pseudouridine synthase B
ORF01783	SAG1594	194	conserved hypothetical protein TIGR00281
ORF01784	SAG1595	235	Uncharacterized ACR, COG1354
ORF01785	SAG1596	246	integrase/recombinase, phage integrase family
ORF01786	SAG1597	157	CBS domain protein
ORF01787	SAG1598	173	conserved hypothetical protein
ORF01788	SAG1599	324	HAM1 protein
ORF01789	SAG1600	264	glutamate racemase
ORF01790	SAG1601	79	conserved hypothetical protein
ORF01791	SAG1602	180	membrane protein, putative
ORF01792	SAG1603	173	transcriptional regulator, biotin repressor family
ORF01793	SAG1604	229	membrane protein, putative
ORF01794	SAG1605	167	conserved hypothetical protein
ORF01795	SAG1606	247	RNA methyltransferase, TrmH family
ORF01796	SAG1607	92	acylphosphatase
ORF01797	SAG1608	310	membrane protein, putative
ORF01799	SAG1609	221	amino acid ABC transporter, permease protein
ORF01800	SAG1610	285	amino acid ABC transporter, substrate-binding protein
ORF01801	SAG1611	486	amidase family protein
ORF01802	SAG1612	160	transcription elongation factor GreA
ORF01803	SAG1613	600	Uncharacterized BCR, YceG family COG1559, putative
ORF01804	SAG1614	167	acetyltransferase, GNAT family
ORF01805	SAG1615	443	UDP-N-acetylmuramate--alanine ligase
ORF01806	SAG1616	205	conserved hypothetical protein
ORF01807	SAG1617	32	hypothetical protein
ORF01808	SAG1618	1032	Snf2 family protein
ORF01810	SAG1619	377	IS1548, transposase
ORF01811	SAG1620	436	phosphoglycerate dehydrogenase-related protein
ORF01812	SAG1621	300	primosomal protein DnaI
ORF01813	SAG1622	391	conserved hypothetical protein
ORF01814	SAG1623	159	conserved hypothetical protein TIGR00244
ORF01815	SAG1624	501	sensor histidine kinase CsrS
ORF01816	SAG1625	229	DNA-binding response regulator CsrR
ORF01817	SAG1626	177	conserved hypothetical protein
ORF01818	SAG1627	296	heat shock protein HtpX
ORF01820	SAG1628	184	lemA protein
ORF01821	SAG1629	237	glucose-inhibited division protein B
ORF01822	SAG1630	459	sodium transport family protein
ORF01823	SAG1631	223	potassium uptake protein, Trk family, putative
ORF01824	SAG1632	276	cobalt transport family protein
ORF01825	SAG1633	558	ABC transporter, ATP-binding protein
ORF01826	SAG1634	212	conserved hypothetical protein
ORF01827	SAG1635	402	sodium:dicarboxylate symporter family protein

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF01828	SAG1636	455	branched-chain amino acid transport system II carrier protein
ORF01829	SAG1637	351	alcohol dehydrogenase, zinc-containing
ORF01830	SAG1638	230	ABC transporter, permease protein
ORF01831	SAG1639	356	ABC transporter, ATP-binding protein
ORF01832	SAG1640	458	peptidase, M20/M25/M40 family
ORF01833	SAG1641	274	lipoprotein, putative
ORF01834	SAG1642	277	ABC transporter, substrate-binding protein
ORF01835	SAG1643	229	glutamine amidotransferase, class I
ORF01836	SAG1644	37	hypothetical protein
ORF01837	SAG1645	238	conserved hypothetical protein TIGR01033
ORF01838	SAG1646	32	hypothetical protein
ORF01839	SAG1647	328	dihydroxyacetone kinase family protein
ORF01840	SAG1648	178	transcriptional regulator, TetR family, putative
ORF01842	SAG1649	37	hypothetical protein
ORF01843	SAG1650	329	dihydroxyacetone kinase family protein
ORF01844	SAG1651	192	dihydroxyacetone kinase family protein
ORF01845	SAG1652	124	conserved hypothetical protein
ORF01846	SAG1653	237	glycerol uptake facilitator protein
ORF01847	SAG1654	134	conserved hypothetical protein
ORF01848	SAG1655	237	transcriptional regulator, MerR family
ORF01849	SAG1656	369	conserved hypothetical protein
ORF01850	SAG1657	83	hypothetical protein
ORF01851	SAG1658	244	conserved hypothetical protein
ORF01852	SAG1659	118	iojap-related protein
ORF01853	SAG1660	173	isochorismatase family protein
ORF01854	SAG1661	195	conserved hypothetical protein TIGR00488
ORF01855	SAG1662	210	conserved hypothetical protein TIGR00482
ORF01856	SAG1663	105	conserved hypothetical protein TIGR00253
ORF01857	SAG1664	372	GTP-binding protein
ORF01858	SAG1665	177	hydrolase, haloacid dehalogenase-like family
ORF01859	SAG1666	295	membrane protein
ORF01860	SAG1667	480	glutamyl-tRNA(Gln) amidotransferase, B subunit
ORF01861	SAG1668	488	glutamyl-tRNA(Gln) amidotransferase, A subunit
ORF01862	SAG1669	100	glutamyl-tRNA(Gln) amidotransferase, C subunit
ORF01863	SAG1670	881	pyruvate phosphate dikinase
ORF01864	SAG1671	276	conserved hypothetical protein
ORF01865	SAG1672	170	CBS domain protein
ORF01866	SAG1673	377	3-hydroxyacyl-CoA dehydrogenase family protein
ORF01867	SAG1674	182	isochorismatase family protein
ORF01869	SAG1675	261	transcriptional regulator CodY, putative
ORF01870	SAG1676	403	aminotransferase, class I
ORF01871	SAG1677	137	universal stress protein family FRAMESHIFT
ORF01872	SAG1678	460	hydrolase, haloacid dehalogenase-like family
ORF01873	SAG1679	320	asparaginase family protein
ORF01874	SAG1680	292	shikimate 5-dehydrogenase
ORF01875	SAG1681	304	oxidoreductase, aldo/keto reductase family
ORF01876	SAG1682	671	ATP-dependent DNA helicase RecG
ORF01877	SAG1683	512	immunogenic secreted protein, putative
ORF01878	SAG1684	366	alanine racemase
ORF01879	SAG1685	119	holo-(acyl-carrier-protein) synthase
ORF01880	SAG1686	335	phospho-2-dehydro-3-deoxyheptonate aldolase
ORF01881	SAG1687	842	preprotein translocase, SecA subunit
ORF01882	SAG1688	315	mannose-6-phosphate isomerase, class I
ORF01883	SAG1689	293	fructokinase

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF01885	SAG1690	639	PTS system IIABC components
ORF01886	SAG1691	479	sucrose-6-phosphate hydrolase
ORF01887	SAG1692	320	sucrose operon repressor ScrR
ORF01888	SAG1693	144	N utilization substance protein B
ORF01889	SAG1694	129	conserved hypothetical protein
ORF01890	SAG1695	186	translation elongation factor P
ORF01892	SAG1696	38	hypothetical protein
ORF01893	SAG1697	48	hypothetical protein
ORF01894	SAG1698	99	conserved hypothetical protein
ORF01895	SAG1699	30	hypothetical protein
ORF01896	SAG1700	76	hypothetical protein
ORF01897	SAG1701	56	hypothetical protein
ORF01898	SAG1702	41	hypothetical protein
ORF01899	SAG1703	54	hypothetical protein
ORF01900	SAG1704	150	cytidine/deoxycytidylate deaminase family protein
ORF01902	SAG1705		peptidase, M24 family POINT MUTATION
ORF01903	SAG1706	238	conserved hypothetical protein
ORF01904	SAG1707	499	drug resistance transporter, EmrB/QacA family
ORF01905	SAG1708	38	hypothetical protein
ORF01906	SAG1709	942	excinuclease ABC, A subunit
ORF01907	SAG1710	223	conserved hypothetical protein
ORF01908	SAG1711	314	magnesium transporter, CorA family
ORF01909	SAG1712	79	ribosomal protein S18
ORF01910	SAG1713	163	single-strand binding protein
ORF01911	SAG1714	95	ribosomal protein S6
ORF01912	SAG1715	374	A/G-specific adenine glycosylase
ORF01913	SAG1716	197	transcriptional regulator, Cro/Ci family
ORF01914	SAG1717	104	thioredoxin
ORF01915	SAG1718	166	PAP2 family protein
ORF01916	SAG1719	779	MutS2 family protein
ORF01917	SAG1720	180	conserved hypothetical protein
ORF01918	SAG1721	103	conserved hypothetical protein
ORF01919	SAG1722	297	ribonuclease HIII
ORF01920	SAG1723	197	signal peptidase I
ORF01921	SAG1724	806	helicase, putative
ORF01922	SAG1725	160	conserved hypothetical protein
ORF01923	SAG1726	364	DNA-damage inducible protein P
ORF01924	SAG1727	770	formate acetyltransferase
ORF01925	SAG1728	124	FMN-binding protein
ORF01926	SAG1729	309	conserved hypothetical protein
ORF01927	SAG1730	251	proteinase, putative, degenerate, FRAMESHIFT
ORF01928	SAG1731	298	membrane protein, putative
ORF01929	SAG1732	282	glycerol uptake facilitator protein, putative
ORF01930	SAG1733	150	universal stress protein family
ORF01931	SAG1734	400	transporter, putative
ORF01932	SAG1735	219	transcriptional regulator, Crp/Fnr family
ORF01933	SAG1736	761	X-pro dipeptidyl-peptidase
ORF01934	SAG1737	119	hypothetical protein
ORF01936	SAG1738	326	polyprenyl synthetase family protein
ORF01937	SAG1739	582	ABC transporter, ATP-binding protein CydC
ORF01938	SAG1740	572	ABC transporter, ATP-binding protein CydD
ORF01939	SAG1741	339	cytochrome d ubiquinol oxidase, subunit II
ORF01940	SAG1742	475	cytochrome d oxidase, subunit I
ORF01941	SAG1743	402	pyridine nucleotide-disulphide oxidoreductase family protein

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF01942	SAG1744	299	prenyltransferase, UbiA family
ORF01943	SAG1745	148	hypothetical protein
ORF01944	SAG1746	35	hypothetical protein
ORF01945	SAG1747	99	conserved hypothetical protein TIGR00103
ORF01946	SAG1748	396	cyclopropane-fatty-acyl-phospholipid synthase
ORF01947	SAG1749	241	transcriptional regulator, merR family
ORF01948	SAG1750	195	exonuclease
ORF01949	SAG1751	178	conserved hypothetical protein
ORF01950	SAG1752	375	conserved hypothetical protein TIGR00275
ORF01951	SAG1753	260	conserved hypothetical protein
ORF01952	SAG1754	89	ribosomal protein S14
ORF01953	SAG1755	38	hypothetical protein
ORF01954	SAG1756	341	conserved hypothetical protein
ORF01957	SAG1757	336	O-sialoglycoprotein endopeptidase family protein
ORF01958	SAG1758	135	ribosomal-protein-alanine acetyltransferase, putative
ORF01960	SAG1759	230	glycoprotease family protein, putative
ORF01961	SAG1760	76	conserved hypothetical protein
ORF01962	SAG1761	559	metallo-beta-lactamase superfamily protein
ORF01963	SAG1762	169	conserved hypothetical protein
ORF01964	SAG1763	448	glutamine synthetase, type I
ORF01965	SAG1764	123	transcriptional regulator GlnR
ORF01967	SAG1765	179	conserved hypothetical protein
ORF01969	SAG1766	398	phosphoglycerate kinase
ORF01970	SAG1767	289	acid phosphatase
ORF01971	SAG1768	336	glyceraldehyde 3-phosphate dehydrogenase
ORF01972	SAG1769	692	translation elongation factor G
ORF01973	SAG1770	156	ribosomal protein S7
ORF01974	SAG1771	137	ribosomal protein S12
ORF01975	SAG1772	270	pur operon repressor
ORF01976	SAG1773	313	HD domain protein
ORF01977	SAG1774	424	conserved hypothetical protein
ORF01978	SAG1775	210	conserved hypothetical protein
ORF01979	SAG1776	220	ribulose-phosphate 3-epimerase
ORF01980	SAG1777	290	conserved hypothetical protein TIGR00157
ORF01981	SAG1778	283	rRNA (guanine-N1-)-methyltransferase, putative
ORF01983	SAG1779	290	dimethyladenosine transferase
ORF01984	SAG1780	163	hypothetical protein
ORF01985	SAG1781	186	primase-related protein
ORF01987	SAG1782	260	deoxyribonuclease, TatD family
ORF01988	SAG1783	90	hypothetical protein
ORF01989	SAG1784	130	hypothetical protein
ORF01990	SAG1785	430	hypothetical protein
ORF01991	SAG1786	130	hypothetical protein
ORF01992	SAG1787	420	dltD protein
ORF01993	SAG1788	79	D-alanyl carrier protein
ORF01994	SAG1789	421	dltB protein
ORF01996	SAG1790	511	D-alanine-activating enzyme
ORF01997	SAG1791	395	sensor histidine kinase
ORF01998	SAG1792	224	DNA-binding response regulator
ORF01999	SAG1793	44	ribosomal protein L34
ORF02000	SAG1794	451	membrane protein, putative
ORF02001	SAG1795	388	transposase, IS30 family, putative
ORF02002	SAG1796	575	amino acid ABC transporter, permease protein
ORF02004	SAG1797	407	amino acid ABC transporter, ATP-binding protein

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF02005	SAG1798	39	hypothetical protein
ORF02006	SAG1799	792	xylulose-5-phosphate/fructose-6-phosphate phosphoketolase
ORF02007	SAG1800	363	conserved hypothetical protein
ORF02008	SAG1801	559	transcriptional antiterminator, BglG family
ORF02009	SAG1802	253	conserved hypothetical protein
ORF02010	SAG1803	505	carbohydrate kinase, FGGY family
ORF02011	SAG1804	329	hypothetical protein
ORF02012	SAG1805	483	PTS system component, putative
ORF02015	SAG1806	318	glyoxylate reductase, NADH-dependent
ORF02016	SAG1807	339	hypothetical protein
ORF02017	SAG1808	327	sugar binding transcriptional regulator, LacI family
ORF02018	SAG1809	215	transaldolase family protein
ORF02019	SAG1810	238	carbohydrate isomerase, AraD/FucA family
ORF02020	SAG1811	287	hexulose-6-phosphate isomerase, putative
ORF02021	SAG1812	221	hexulose-6-phosphate synthase, putative
ORF02022	SAG1813	161	PTS system, IIA component
ORF02023	SAG1814	92	PTS system, IIB component
ORF02024	SAG1815	479	transport protein SgaT, putative
ORF02025	SAG1816	205	hypothetical protein
ORF02026	SAG1817	157	hypothetical protein
ORF02027	SAG1818	430	adenylosuccinate synthetase
ORF02028	SAG1819	340	perfringolysin O regulator protein
ORF02029	SAG1820	224	conserved hypothetical protein
ORF02030	SAG1821	750	glutamate--cysteine ligase-related protein
ORF02031	SAG1822	272	conserved hypothetical protein
ORF02032	SAG1823	418	conserved hypothetical protein
ORF02033	SAG1824	291	chaperonin, 33 kDa
ORF02034	SAG1825	325	NifR3/Smm1 family protein
ORF02035	SAG1826	213	deoxynucleoside kinase family protein
ORF02036	SAG1827	163	phosphinothricin N-acetyltransferase
ORF02037	SAG1828	815	ATP-dependent Clp protease, ATP-binding subunit
ORF02038	SAG1829	154	transcriptional regulator CtsR
ORF02039	SAG1830	153	conserved hypothetical protein
ORF02040	SAG1831	346	translation elongation factor Ts
ORF02041	SAG1832	256	ribosomal protein S2
ORF02042	SAG1833	186	alkyl hydroperoxide reductase, subunit C
ORF02043	SAG1834	510	alkyl hydroperoxide reductase, subunit F
ORF02044	SAG1835	134	conserved hypothetical protein
ORF02045	SAG1836	61	conserved hypothetical protein
ORF02046	SAG1837	468	lysine, putative
ORF02047	SAG1838	109	holin, putative
ORF02048	SAG1839	136	conserved hypothetical protein
ORF02049	SAG1840	112	hypothetical protein
ORF02050	SAG1841	76	conserved domain protein
ORF02051	SAG1842	1224	PblB, putative
ORF02053	SAG1843	240	conserved hypothetical protein
ORF02056	SAG1844	911	conserved hypothetical protein
ORF02057	SAG1845	42	hypothetical protein
ORF02058	SAG1846	158	hypothetical protein
ORF02059	SAG1847	227	conserved hypothetical protein
ORF02060	SAG1848	114	conserved hypothetical protein
ORF02061	SAG1849	115	hypothetical protein

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF02062	SAG1850	101	hypothetical protein
ORF02063	SAG1851	111	conserved domain protein
ORF02064	SAG1852	420	conserved domain protein
ORF02066	SAG1853	180	protease, putative
ORF02067	SAG1854	380	conserved hypothetical protein
ORF02068	SAG1855	570	terminase large subunit, putative
ORF02069	SAG1856	161	hypothetical protein
ORF02070	SAG1858	95	hypothetical protein
ORF02071	SAG1859	180	site-specific recombinase, phage integrase family
ORF02072	SAG1860	154	conserved hypothetical protein
ORF02073	SAG1861	119	transcriptional regulator, Cro/Ci family
ORF02075	SAG1862	86	hypothetical protein
ORF02076	SAG1863	138	single-strand binding protein
ORF02077	SAG1864	68	hypothetical protein
ORF02078	SAG1865	74	conserved hypothetical protein
ORF02079	SAG1866	109	conserved hypothetical protein
ORF02080	SAG1867	163	conserved hypothetical protein
ORF02081	SAG1868	134	hypothetical protein
ORF02082	SAG1869	437	type II DNA modification methyltransferase, putative
ORF02083	SAG1870	273	DNA replication protein DnaC, putative
ORF02084	SAG1871	248	conserved hypothetical protein
ORF02085	SAG1872	200	hypothetical protein
ORF02086	SAG1873	443	replicative DNA helicase
ORF02087	SAG1874	87	hypothetical protein
ORF02088	SAG1875	94	conserved hypothetical protein
ORF02089	SAG1876	176	HNH endonuclease family protein
ORF02090	SAG1877	236	antirepressor protein, putative
ORF02091	SAG1878	102	conserved domain protein
ORF02092	SAG1879	156	hypothetical protein
ORF02093	SAG1880	54	hypothetical protein
ORF02094	SAG1881	51	hypothetical protein
ORF02095	SAG1882	120	repressor protein, putative
ORF02097	SAG1884	134	hypothetical protein
ORF02098	SAG1885	356	site-specific recombinase, phage integrase family
ORF02100	SAG1886	32	hypothetical protein
ORF02101	SAG1887	689	Na ⁺ /H ⁺ exchanger family protein
ORF02102	SAG1888	78	hypothetical protein
ORF02103	SAG1889	317	microcin immunity protein MccF, putative
ORF02104	SAG1890	631	endopeptidase O
ORF02105	SAG1891	327	oxidoreductase, Gfo/Idh/MocA family
ORF02107	SAG1892	358	membrane protein, putative
ORF02108	SAG1893	59	hypothetical protein
ORF02109	SAG1894	214	Cyclic nucleotide-binding domain protein
ORF02110	SAG1895	204	polypeptide deformylase
ORF02111	SAG1896	333	sugar binding transcriptional regulator RegR
ORF02112	SAG1897	634	conserved hypothetical protein
ORF02113	SAG1898	271	PTS system, IID component
ORF02114	SAG1899	288	PTS system, IIC component
ORF02115	SAG1900	164	PTS system, IIB component
ORF02116	SAG1901	398	glucuronidase
ORF02118	SAG1902	144	PTS system, IIA component
ORF02119	SAG1903	34	hypothetical protein

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF02120	SAG1904	270	oxidoreductase, short-chain dehydrogenase/reductase family
ORF02121	SAG1905	212	conserved hypothetical protein
ORF02122	SAG1906	335	carbohydrate kinase, PfkB family
ORF02123	SAG1907	212	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase
ORF02124	SAG1908	499	hypothetical protein
ORF02125	SAG1909	204	nitroreductase family protein
ORF02126	SAG1910	141	transcriptional regulator, MarR family
ORF02127	SAG1911	1468	DNA polymerase III, alpha subunit, Gram-positive type
ORF02128	SAG1912	194	N-acetylmuramoyl-L-alanine amidase, family 4 protein
ORF02129	SAG1913	617	prolyl-tRNA synthetase
ORF02130	SAG1914	419	membrane-associated zinc metalloprotease, putative
ORF02131	SAG1915	264	phosphatidate cytidyltransferase
ORF02132	SAG1916	250	undecaprenyl diphosphate synthase
ORF02133	SAG1917	113	preprotein translocase, YajC subunit
ORF02134	SAG1918	114	conserved hypothetical protein
ORF02135	SAG1919	387	malate oxidoreductase
ORF02136	SAG1920	445	citrate carrier protein, CCS family
ORF02137	SAG1921	508	sensor histidine kinase family protein
ORF02138	SAG1922	229	response regulator
ORF02139	SAG1923	331	UDP-glucose 4-epimerase
ORF02140	SAG1924	535	glucan 1,6-alpha-glucosidase
ORF02141	SAG1925	377	sugar ABC transporter, ATP-binding protein
ORF02142	SAG1926	283	helix-turn-helix domain protein, fis-type
ORF02143	SAG1927	298	lacX protein
ORF02144	SAG1928	325	tagatose 1,6-diphosphate aldolase
ORF02145	SAG1929	310	tagatose-6-phosphate kinase
ORF02146	SAG1930	171	galactose-6-phosphate isomerase, LacB subunit
ORF02147	SAG1931	141	galactose-6-phosphate isomerase, LacA subunit
ORF02148	SAG1932	816	neuraminidase
ORF02149	SAG1933	482	PTS system, IIC component, putative
ORF02150	SAG1934	101	PTS system, IIB component, putative
ORF02152	SAG1935	157	PTS system, IIA component, putative
ORF02153	SAG1936	258	lactose phosphotransferase system repressor
ORF02156	SAG1937		streptococcal histidine triad family protein, degenerate, FRAMESHIFT
ORF02157	SAG1938	307	adhesion lipoprotein, putative
ORF02158	SAG1939	147	conserved hypothetical protein TIGR00256
ORF02159	SAG1940	738	GTP pyrophosphokinase
ORF02160	SAG1941	800	2',3'-cyclic-nucleotide 2'-phosphodiesterase
ORF02161	SAG1942	151	nrdI protein, putative
ORF02162	SAG1943	345	conserved hypothetical protein
ORF02163	SAG1944	165	conserved hypothetical protein
ORF02164	SAG1945	345	iron ABC transporter, iron-binding protein
ORF02165	SAG1946	257	DNA-binding response regulator
ORF02166	SAG1947	549	conserved hypothetical protein
ORF02167	SAG1948	275	PTS system, IID component
ORF02168	SAG1949	269	PTS system, IIC component
ORF02169	SAG1950	163	PTS system, IIB component
ORF02170	SAG1951	141	PTS system, IIA component, putative
ORF02171	SAG1952	353	membrane protein, putative
ORF02172	SAG1953	60	hypothetical protein

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF02173	SAG1954	384	hypothetical protein
ORF02174	SAG1955	282	ABC transporter, ATP-binding protein
ORF02175	SAG1956	96	conserved domain protein
ORF02176	SAG1957	250	response regulator
ORF02177	SAG1958	276	conserved hypothetical protein
ORF02178	SAG1959	727	PTS system, IIBC components
ORF02179	SAG1960	551	sensor histidine kinase
ORF02180	SAG1961	225	phosphate regulon response regulator PhoB
ORF02181	SAG1962	218	phosphate transport system regulatory protein PhoU, putative
ORF02182	SAG1963	253	phosphate ABC transporter, ATP-binding protein
ORF02183	SAG1964	292	phosphate ABC transporter, permease protein
ORF02184	SAG1965	281	phosphate ABC transporter, permease protein
ORF02186	SAG1966	293	hemolysin precursor, putative
ORF02187	SAG1967	195	hypothetical protein
ORF02188	SAG1968	246	conserved hypothetical protein TIGR00046
ORF02189	SAG1969	317	ribosomal protein L11 methyltransferase
ORF02190	SAG1970	102	conserved hypothetical protein
ORF02191	SAG1971	41	hypothetical protein
ORF02192	SAG1972	238	transcriptional regulator, MerR family
ORF02194	SAG1973	156	acetyltransferase, GNAT family
ORF02195	SAG1974	152	MutT/nudix family protein
ORF02196	SAG1975	47	hypothetical protein
ORF02197	SAG1976	156	conserved hypothetical protein
ORF02198	SAG1977	163	acetyltransferase, GNAT family
ORF02199	SAG1978	422	ATPase, AAA family
ORF02201	SAG1979	253	hypothetical protein
ORF02202	SAG1980	300	ABC transporter, ATP-binding protein
ORF02203	SAG1981	68	hypothetical protein
ORF02205	SAG1982	359	transcriptional regulator, Cro/Ci family
ORF02206	SAG1983	105	conserved hypothetical protein
ORF02207	SAG1984	188	conserved hypothetical protein TIGR00730
ORF02208	SAG1985	51	hypothetical protein
ORF02209	SAG1986	375	integrase, phage family, putative
ORF02210	SAG1987	61	conserved hypothetical protein
ORF02211	SAG1988	342	conserved hypothetical protein
ORF02212	SAG1989	139	hypothetical protein
ORF02213	SAG1990	127	hypothetical protein
ORF02214	SAG1991	204	transcriptional regulator, Cro/Ci family
ORF02215	SAG1992	518	conserved hypothetical protein
ORF02216	SAG1993	373	site-specific recombinase, phage integrase family
ORF02217	SAG1994	108	conserved hypothetical protein
ORF02219	SAG1995	210	hypothetical protein
ORF02221	SAG1996	263	cell wall anchor protein-related protein
ORF02223	SAG1997	182	hypothetical protein
ORF02224	SAG1998	457	hypothetical protein
ORF02225	SAG1999	47	hypothetical protein
ORF02226	SAG2000	666	membrane protein, putative
ORF02227	SAG2001	756	conjugal transfer protein, interruption-C
ORF02228	SAG2002	129	IS1381, transposase OrfB
ORF02229	SAG2003	127	IS1381, transposase OrfA
ORF02230	SAG2005	138	conserved hypothetical protein
ORF02231	SAG2006	88	conserved hypothetical protein
ORF02232	SAG2007	317	conserved hypothetical protein

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF02233	SAG2008	84	conserved hypothetical protein
ORF02234	SAG2009	88	conserved hypothetical protein
ORF02235	SAG2010	157	hypothetical protein
ORF02236	SAG2011	160	conserved hypothetical protein
ORF02237	SAG2012	90	hypothetical protein
ORF02238	SAG2013	189	hypothetical protein
ORF02239	SAG2014	449	hypothetical protein
ORF02240	SAG2015	99	transcriptional regulator, Cro/Ci family
ORF02241	SAG2016	125	hypothetical protein
ORF02242	SAG2017	429	transcriptional regulator, Cro/Ci family
ORF02243	SAG2018	553	FtsK/SpoIIIE family protein
ORF02244	SAG2019	153	hypothetical protein
ORF02245	SAG2020	98	hypothetical protein
ORF02246	SAG2021	826	cell wall surface anchor family protein
ORF02247	SAG2022	417	transposase, ISL3 family
ORF02249	SAG2023	546	mercuric reductase
ORF02250	SAG2024	130	mercuric resistance operon regulatory protein MerR
ORF02251	SAG2025	522	Mn2+/Fe2+ transporter, NRAMP family
ORF02252	SAG2026	240	membrane protein, putative
ORF02253	SAG2027	205	ABC transporter, ATP-binding protein
ORF02254	SAG2028	36	conserved hypothetical protein
ORF02255	SAG2029	284	streptomycin resistance protein
ORF02257	SAG2030	130	hypothetical protein
ORF02258	SAG2031	202	hypothetical protein
ORF02259	SAG2032	111	conserved hypothetical protein
ORF02260	SAG2033	162	acetyltransferase, GNAT family
ORF02261	SAG2034	247	membrane protein, putative
ORF02262	SAG2035	300	ABC transporter, ATP-binding protein
ORF02263	SAG2036	68	hypothetical protein
ORF02264	SAG2037	358	transcriptional regulator, Cro/Ci family
ORF02265	SAG2038	204	PAP2 family protein
ORF02266	SAG2039	98	conserved hypothetical protein
ORF02267	SAG2040	186	conserved hypothetical protein TIGR00730
ORF02268	SAG2041	287	protease, putative
ORF02269	SAG2042	100	rhodanese family protein
ORF02270	SAG2043	255	cAMP factor
ORF02271	SAG2044	62	hypothetical protein
ORF02272	SAG2045	179	DNA topology modulation protein FlhR, putative
ORF02273	SAG2046	361	glycerol dehydrogenase, putative
ORF02274	SAG2047	235	conserved hypothetical protein
ORF02275	SAG2048	614	5-methyltetrahydrofolate--homocysteine methyltransferase, putative
ORF02276	SAG2049	745	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase
ORF02277	SAG2050	107	conserved hypothetical protein
ORF02278	SAG2051	230	branched-chain amino acid transport protein AzlC, putative
ORF02279	SAG2052	41	hypothetical protein
ORF02280	SAG2053	1570	serine protease, subtilase family, putative
ORF02281	SAG2054	228	DNA-binding response regulator
ORF02282	SAG2055	462	sensor histidine kinase
ORF02283	SAG2056	202	chromosome assembly-related protein
ORF02285	SAG2057	833	leucyl-tRNA synthetase
ORF02286	SAG2058	415	major facilitator family protein

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF02287	SAG2059	281	conserved hypothetical protein
ORF02288	SAG2060	398	glycosyl transferase, family 8
ORF02289	SAG2061	401	glycosyl transferase, family 8
ORF02290	SAG2062	179	transcription antitermination protein NusG
ORF02291	SAG2063	630	pathogenicity protein, putative
ORF02292	SAG2064	57	preprotein translocase, SecE subunit, putative
ORF02293	SAG2066	773	penicillin-binding protein 2A
ORF02294	SAG2067	294	ribosomal large subunit pseudouridine synthase, RluD subfamily
ORF02295	SAG2068	546	Lyme disease proteins of unknown function, putative
ORF02296	SAG2069	403	phosphopentomutase
ORF02297	SAG2070	223	deoxyribose-phosphate aldolase
ORF02298	SAG2071	400	Na ⁺ dependent nucleoside transporter
ORF02300	SAG2072	259	uridine phosphorylase
ORF02301	SAG2073	245	transcriptional regulator, GntR family
ORF02302	SAG2074	540	60 kda chaperonin
ORF02303	SAG2075	94	chaperonin, 10 kDa
ORF02305	SAG2076	267	ABC transporter, ATP-binding protein
ORF02306	SAG2077	298	ABC transporter, permease protein
ORF02307	SAG2078	320	lipoprotein, putative
ORF02308	SAG2079	265	hydrolase, haloacid dehalogenase-like family
ORF02309	SAG2080	286	glyoxalase family protein
ORF02310	SAG2081	243	conserved hypothetical protein
ORF02311	SAG2082	205	anaerobic ribonucleoside-triphosphate reductase activating protein
ORF02312	SAG2083	163	acetyltransferase, GNAT family
ORF02313	SAG2084	310	virulence factor MviM, putative
ORF02314	SAG2085	47	conserved hypothetical protein
ORF02315	SAG2086	723	anaerobic ribonucleoside-triphosphate reductase
ORF02316	SAG2087	495	conserved hypothetical protein
ORF02317	SAG2088	40	hypothetical protein
ORF02318	SAG2089	105	conserved hypothetical protein
ORF02319	SAG2090	136	conserved hypothetical protein TIGR00250
ORF02320	SAG2091	88	conserved hypothetical protein
ORF02321	SAG2092	132	conserved hypothetical protein
ORF02322	SAG2093	379	recA protein
ORF02323	SAG2094		competence/damage-inducible protein CinA FRAMESHIFT
ORF02325	SAG2095	183	DNA-3-methyladenine glycosylase I
ORF02327	SAG2096	196	Holliday junction DNA helicase RuvA
ORF02328	SAG2097	418	transporter, putative
ORF02329	SAG2098	659	DNA mismatch repair protein HexB
ORF02330	SAG2099	33	hypothetical protein
ORF02331	SAG2100	67	cold shock protein, CSD family
ORF02332	SAG2101	858	DNA mismatch repair protein HexA
ORF02333	SAG2102	145	arginine repressor ArgR, putative
ORF02334	SAG2103	563	arginyl-tRNA synthetase
ORF02335	SAG2104	102	conserved hypothetical protein
ORF02337	SAG2105	290	conserved hypothetical protein
ORF02338	SAG2106	314	conserved hypothetical protein
ORF02339	SAG2107	583	aspartyl-tRNA synthetase
ORF02340	SAG2108	426	histidyl-tRNA synthetase
ORF02341	SAG2109	60	ribosomal protein L32

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF02342	SAG2110	49	ribosomal protein L33
ORF02343	SAG2111	173	conserved hypothetical protein
ORF02344	SAG2112	494	site-specific recombinase, phage integrase family
ORF02345	SAG2113	82	conserved hypothetical protein
ORF02346	SAG2114	342	conserved hypothetical protein
ORF02347	SAG2115	143	hypothetical protein
ORF02349	SAG2116	151	conserved hypothetical protein
ORF02350	SAG2117	71	hypothetical protein
ORF02351	SAG2118	306	transcriptional regulator, Cro/C1 family
ORF02352	SAG2119	373	conserved domain protein
ORF02355	SAG2120	56	hypothetical protein
ORF02356	SAG2121	176	hypothetical protein
ORF02357	SAG2122	223	DNA-binding response regulator
ORF02358	SAG2123	454	sensor histidine kinase
ORF02359	SAG2124	517	membrane protein, putative
ORF02360	SAG2125	308	carbamate kinase
ORF02361	SAG2126	332	ornithine carbamoyltransferase
ORF02362	SAG2127	431	sensor histidine kinase
ORF02363	SAG2128	277	response regulator
ORF02364	SAG2129	240	amino acid ABC transporter, ATP-binding protein
ORF02365	SAG2130	504	amino acid ABC transporter, permease and amino acid binding protein
ORF02367	SAG2131	847	membrane protein, putative
ORF02368	SAG2132	247	conserved hypothetical protein
ORF02369	SAG2133	118	conserved hypothetical protein
ORF02370	SAG2134	772	membrane protein, putative
ORF02371	SAG2135	179	transcriptional regulator, TetR family, putative
ORF02372	SAG2136	98	conserved hypothetical protein
ORF02373	SAG2137	203	ribosomal protein S4
ORF02374	SAG2138	95	conserved hypothetical protein
ORF02375	SAG2139	451	replicative DNA helicase
ORF02376	SAG2140	150	ribosomal protein L9
ORF02377	SAG2141	660	DHH family protein
ORF02378	SAG2142	613	glucose inhibited division protein A
ORF02379	SAG2143	203	conserved hypothetical protein TIGR00427
ORF02380	SAG2144	373	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
ORF02381	SAG2145	222	L-serine dehydratase, iron-sulfur-dependent, beta subunit
ORF02382	SAG2146	290	L-serine dehydratase, iron-sulfur-dependent, alpha subunit
ORF02383	SAG2147	234	conserved hypothetical protein
ORF02384	SAG2148	179	LysM domain protein
ORF02385	SAG2149	264	cobalt transport family protein
ORF02386	SAG2150	280	ABC transporter, ATP-binding protein
ORF02387	SAG2151	279	ABC transporter, ATP-binding protein, FRAMESHIFT
ORF02388	SAG2152	180	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
ORF02389	SAG2153	427	peptidase, M16 family
ORF02390	SAG2154	414	conserved hypothetical protein
ORF02391	SAG2155	117	conserved hypothetical protein
ORF02392	SAG2156	369	recF protein
ORF02393	SAG2157	278	transporter, putative
ORF02395	SAG2158	220	transcriptional regulator, Cro/C1 family

Table 32: Conversion of ORF Ref Nos. with SAG Ref Nos.

ORF Ref No.	SAGxxxx Ref No.	aa	Annotation
ORF02396	SAG2159	493	inosine-5'-monophosphate dehydrogenase
ORF02397	SAG2160	161	transcriptional regulator, ArgR family
ORF02398	SAG2161	226	transcriptional regulator, Crp/Fnr family
ORF02399	SAG2162	234	conserved hypothetical protein
ORF02400	SAG2163	410	arginine deiminase
ORF02401	SAG2164	136	acetyltransferase, GNAT family
ORF02402	SAG2165	337	ornithine carbamoyltransferase
ORF02403	SAG2166	475	arginine/ornithine antiporter
ORF02404	SAG2167	318	carbamate kinase
ORF02405	SAG2168	341	tryptophanyl-tRNA synthetase
ORF02406	SAG2169	230	conserved hypothetical protein
ORF02407	SAG2170	290	conserved hypothetical protein
ORF02408	SAG2171	539	ABC transporter, ATP-binding protein
ORF02409	SAG2172	859	ABC transporter, permease protein, putative
ORF02410	SAG2173	159	conserved hypothetical protein TIGR00246
ORF02411	SAG2174	409	serine protease
ORF02412	SAG2175	257	partitioning protein, ParB family
ORF02413	SAG0001	453	chromosomal replication initiator protein DnaA
ORF02415	SAG0002	378	DNA polymerase III, beta subunit
ORF02416	SAG0003	293	diacylglycerol kinase catalytic domain protein, putative
ORF02417	SAG0004	65	conserved hypothetical protein
ORF02418	SAG0005	67	hypothetical protein
ORF02419	SAG0006	371	conserved hypothetical GTP-binding protein
ORF02420	SAG0007	191	peptidyl-tRNA hydrolase
ORF02421	SAG0008	1165	transcription-repair coupling factor
ORF02422	SAG0009	31	hypothetical protein
ORF02423	SAG0010	90	S4 domain protein
ORF02424	SAG0011	123	cell division protein DivIC, putative
ORF02425	SAG0012	44	conserved hypothetical protein
ORF02426	SAG0013	428	conserved hypothetical protein
ORF02427	SAG0014	424	MesJ/Ycf62 family protein
ORF02428	SAG0015	180	hypoxanthine-guanine phosphoribosyltransferase
ORF02429	SAG0016	658	cell division protein FtsH
ORF03000	SAG0157		Dnase-related protein, DEGENERATE
ORF03001	SAG0579	142	conserved hypothetical protein
ORF03002	SAG0580	111	conserved hypothetical protein, truncation
ORF03003	SAG0652		Tn5252, Orf 28 protein, degenerate
ORF03004	SAG0655	57	conserved hypothetical protein
ORF03005	SAG0662	101	cylX protein
ORF03006	SAG0917	83	Tn916, hypothetical protein
ORF03007	SAG0920	23	Tn916, hypothetical protein
ORF03008	SAG0922	61	Tn916, hypothetical protein
ORF03009	SAG0924	28	Tn916, tetM leader peptide
ORF03010	SAG0936	39	Tn916, hypothetical protein
ORF03011	SAG1484	48	ribosomal protein L33
ORF03012	SAG1857	119	HNH endonuclease family protein
ORF03013	SAG1883	128	conserved hypothetical protein
ORF03014	SAG2065	50	ribosomal protein L33
ORF03015	SAG2004	67	conjugal transfer protein, interruption-N

Table 33: List of GAS ORFs which are shared with GBS and Spn

gi 13621326 gb AAK33146.1	gi 13621393 gb AAK33207.1
gi 13621327 gb AAK33147.1	gi 13621394 gb AAK33208.1
gi 13621328 gb AAK33148.1	gi 13621397 gb AAK33210.1
gi 13621329 gb AAK33149.1	gi 13621398 gb AAK33211.1
gi 13621330 gb AAK33150.1	gi 13621399 gb AAK33212.1
gi 13621331 gb AAK33151.1	gi 13621401 gb AAK33214.1
gi 13621332 gb AAK33152.1	gi 13621403 gb AAK33215.1
gi 13621333 gb AAK33153.1	gi 13621404 gb AAK33216.1
gi 13621334 gb AAK33154.1	gi 13621405 gb AAK33217.1
gi 13621335 gb AAK33155.1	gi 13621407 gb AAK33218.1
gi 13621337 gb AAK33156.1	gi 13621408 gb AAK33219.1
gi 13621340 gb AAK33158.1	gi 13621409 gb AAK33220.1
gi 13621341 gb AAK33159.1	gi 13621413 gb AAK33224.1
gi 13621343 gb AAK33160.1	gi 13621415 gb AAK33226.1
gi 13621344 gb AAK33161.1	gi 13621416 gb AAK33227.1
gi 13621346 gb AAK33163.1	gi 13621418 gb AAK33229.1
gi 13621347 gb AAK33164.1	gi 13621419 gb AAK33230.1
gi 13621348 gb AAK33165.1	gi 13621424 gb AAK33234.1
gi 13621349 gb AAK33166.1	gi 13621425 gb AAK33235.1
gi 13621350 gb AAK33167.1	gi 13621426 gb AAK33236.1
gi 13621353 gb AAK33169.1	gi 13621434 gb AAK33243.1
gi 13621354 gb AAK33170.1	gi 13621450 gb AAK33258.1
gi 13621355 gb AAK33171.1	gi 13621455 gb AAK33262.1
gi 13621357 gb AAK33173.1	gi 13621456 gb AAK33263.1
gi 13621358 gb AAK33174.1	gi 13621457 gb AAK33264.1
gi 13621359 gb AAK33175.1	gi 13621467 gb AAK33273.1
gi 13621361 gb AAK33176.1	gi 13621468 gb AAK33274.1
gi 13621362 gb AAK33177.1	gi 13621469 gb AAK33275.1
gi 13621363 gb AAK33178.1	gi 13621470 gb AAK33276.1
gi 13621364 gb AAK33179.1	gi 13621471 gb AAK33277.1
gi 13621365 gb AAK33180.1	gi 13621472 gb AAK33278.1
gi 13621366 gb AAK33181.1	gi 13621473 gb AAK33279.1
gi 13621367 gb AAK33182.1	gi 13621476 gb AAK33281.1
gi 13621368 gb AAK33183.1	gi 13621477 gb AAK33282.1
gi 13621369 gb AAK33184.1	gi 13621478 gb AAK33283.1
gi 13621370 gb AAK33185.1	gi 13621480 gb AAK33285.1
gi 13621372 gb AAK33186.1	gi 13621481 gb AAK33286.1
gi 13621373 gb AAK33187.1	gi 13621491 gb AAK33295.1
gi 13621374 gb AAK33188.1	gi 13621494 gb AAK33298.1
gi 13621375 gb AAK33189.1	gi 13621496 gb AAK33299.1
gi 13621376 gb AAK33190.1	gi 13621501 gb AAK33304.1
gi 13621377 gb AAK33191.1	gi 13621502 gb AAK33305.1
gi 13621378 gb AAK33192.1	gi 13621505 gb AAK33307.1
gi 13621379 gb AAK33193.1	gi 13621506 gb AAK33308.1
gi 13621380 gb AAK33194.1	gi 13621507 gb AAK33309.1
gi 13621382 gb AAK33196.1	gi 13621510 gb AAK33312.1
gi 13621383 gb AAK33197.1	gi 13621511 gb AAK33313.1
gi 13621384 gb AAK33198.1	gi 13621513 gb AAK33315.1
gi 13621385 gb AAK33199.1	gi 13621516 gb AAK33317.1
gi 13621386 gb AAK33200.1	gi 13621518 gb AAK33319.1
gi 13621387 gb AAK33201.1	gi 13621521 gb AAK33322.1
gi 13621388 gb AAK33202.1	gi 13621522 gb AAK33323.1
gi 13621389 gb AAK33203.1	gi 13621523 gb AAK33324.1
gi 13621390 gb AAK33204.1	gi 13621524 gb AAK33325.1
gi 13621391 gb AAK33205.1	gi 13621525 gb AAK33326.1
gi 13621392 gb AAK33206.1	gi 13621527 gb AAK33327.1

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gi 13621528 gb AAK33328.1	gi 13621595 gb AAK33389.1
gi 13621529 gb AAK33329.1	gi 13621596 gb AAK33390.1
gi 13621530 gb AAK33330.1	gi 13621597 gb AAK33391.1
gi 13621531 gb AAK33331.1	gi 13621598 gb AAK33392.1
gi 13621532 gb AAK33332.1	gi 13621599 gb AAK33393.1
gi 13621533 gb AAK33333.1	gi 13621600 gb AAK33394.1
gi 13621534 gb AAK33334.1	gi 13621602 gb AAK33395.1
gi 13621535 gb AAK33335.1	gi 13621603 gb AAK33396.1
gi 13621536 gb AAK33336.1	gi 13621604 gb AAK33397.1
gi 13621537 gb AAK33337.1	gi 13621605 gb AAK33398.1
gi 13621539 gb AAK33338.1	gi 13621606 gb AAK33399.1
gi 13621540 gb AAK33339.1	gi 13621607 gb AAK33400.1
gi 13621541 gb AAK33340.1	gi 13621608 gb AAK33401.1
gi 13621542 gb AAK33341.1	gi 13621609 gb AAK33402.1
gi 13621543 gb AAK33342.1	gi 13621611 gb AAK33404.1
gi 13621544 gb AAK33343.1	gi 13621614 gb AAK33406.1
gi 13621546 gb AAK33345.1	gi 13621615 gb AAK33407.1
gi 13621547 gb AAK33346.1	gi 13621616 gb AAK33408.1
gi 13621548 gb AAK33347.1	gi 13621617 gb AAK33409.1
gi 13621550 gb AAK33348.1	gi 13621618 gb AAK33410.1
gi 13621551 gb AAK33349.1	gi 13621619 gb AAK33411.1
gi 13621552 gb AAK33350.1	gi 13621620 gb AAK33412.1
gi 13621553 gb AAK33351.1	gi 13621621 gb AAK33413.1
gi 13621554 gb AAK33352.1	gi 13621622 gb AAK33414.1
gi 13621555 gb AAK33353.1	gi 13621623 gb AAK33415.1
gi 13621557 gb AAK33355.1	gi 13621624 gb AAK33416.1
gi 13621559 gb AAK33356.1	gi 13621625 gb AAK33417.1
gi 13621560 gb AAK33357.1	gi 13621627 gb AAK33419.1
gi 13621561 gb AAK33358.1	gi 13621629 gb AAK33420.1
gi 13621562 gb AAK33359.1	gi 13621630 gb AAK33421.1
gi 13621563 gb AAK33360.1	gi 13621631 gb AAK33422.1
gi 13621564 gb AAK33361.1	gi 13621633 gb AAK33424.1
gi 13621565 gb AAK33362.1	gi 13621634 gb AAK33425.1
gi 13621566 gb AAK33363.1	gi 13621636 gb AAK33427.1
gi 13621567 gb AAK33364.1	gi 13621637 gb AAK33428.1
gi 13621569 gb AAK33365.1	gi 13621638 gb AAK33429.1
gi 13621571 gb AAK33367.1	gi 13621640 gb AAK33430.1
gi 13621572 gb AAK33368.1	gi 13621642 gb AAK33432.1
gi 13621573 gb AAK33369.1	gi 13621644 gb AAK33434.1
gi 13621574 gb AAK33370.1	gi 13621645 gb AAK33435.1
gi 13621575 gb AAK33371.1	gi 13621647 gb AAK33437.1
gi 13621576 gb AAK33372.1	gi 13621648 gb AAK33438.1
gi 13621577 gb AAK33373.1	gi 13621650 gb AAK33440.1
gi 13621579 gb AAK33374.1	gi 13621651 gb AAK33441.1
gi 13621581 gb AAK33376.1	gi 13621652 gb AAK33442.1
gi 13621582 gb AAK33377.1	gi 13621657 gb AAK33446.1
gi 13621583 gb AAK33378.1	gi 13621658 gb AAK33447.1
gi 13621584 gb AAK33379.1	gi 13621660 gb AAK33449.1
gi 13621585 gb AAK33380.1	gi 13621670 gb AAK33458.1
gi 13621586 gb AAK33381.1	gi 13621671 gb AAK33459.1
gi 13621588 gb AAK33383.1	gi 13621672 gb AAK33460.1
gi 13621589 gb AAK33384.1	gi 13621675 gb AAK33462.1
gi 13621590 gb AAK33385.1	gi 13621676 gb AAK33463.1
gi 13621592 gb AAK33386.1	gi 13621678 gb AAK33465.1
gi 13621593 gb AAK33387.1	gi 13621680 gb AAK33467.1
gi 13621594 gb AAK33388.1	gi 13621681 gb AAK33468.1

Table 33: List of GAS ORFs which are shared with GBS and Spn

gi 13621682 gb AAK33469.1	gi 13621796 gb AAK33573.1
gi 13621683 gb AAK33470.1	gi 13621797 gb AAK33574.1
gi 13621684 gb AAK33471.1	gi 13621799 gb AAK33576.1
gi 13621685 gb AAK33472.1	gi 13621800 gb AAK33577.1
gi 13621688 gb AAK33474.1	gi 13621802 gb AAK33579.1
gi 13621689 gb AAK33475.1	gi 13621806 gb AAK33583.1
gi 13621690 gb AAK33476.1	gi 13621808 gb AAK33584.1
gi 13621691 gb AAK33477.1	gi 13621809 gb AAK33585.1
gi 13621692 gb AAK33478.1	gi 13621810 gb AAK33586.1
gi 13621693 gb AAK33479.1	gi 13621811 gb AAK33587.1
gi 13621694 gb AAK33480.1	gi 13621812 gb AAK33588.1
gi 13621695 gb AAK33481.1	gi 13621813 gb AAK33589.1
gi 13621697 gb AAK33483.1	gi 13621814 gb AAK33590.1
gi 13621698 gb AAK33484.1	gi 13621817 gb AAK33592.1
gi 13621700 gb AAK33485.1	gi 13621818 gb AAK33593.1
gi 13621701 gb AAK33486.1	gi 13621819 gb AAK33594.1
gi 13621702 gb AAK33487.1	gi 13621820 gb AAK33595.1
gi 13621714 gb AAK33498.1	gi 13621821 gb AAK33596.1
gi 13621715 gb AAK33499.1	gi 13621822 gb AAK33597.1
gi 13621717 gb AAK33501.1	gi 13621823 gb AAK33598.1
gi 13621718 gb AAK33502.1	gi 13621824 gb AAK33599.1
gi 13621719 gb AAK33503.1	gi 13621825 gb AAK33600.1
gi 13621720 gb AAK33504.1	gi 13621826 gb AAK33601.1
gi 13621726 gb AAK33509.1	gi 13621828 gb AAK33602.1
gi 13621727 gb AAK33510.1	gi 13621829 gb AAK33603.1
gi 13621729 gb AAK33512.1	gi 13621830 gb AAK33604.1
gi 13621730 gb AAK33513.1	gi 13621831 gb AAK33605.1
gi 13621731 gb AAK33514.1	gi 13621834 gb AAK33608.1
gi 13621732 gb AAK33515.1	gi 13621835 gb AAK33609.1
gi 13621733 gb AAK33516.1	gi 13621836 gb AAK33610.1
gi 13621734 gb AAK33517.1	gi 13621837 gb AAK33611.1
gi 13621735 gb AAK33518.1	gi 13621839 gb AAK33612.1
gi 13621736 gb AAK33519.1	gi 13621840 gb AAK33613.1
gi 13621741 gb AAK33523.1	gi 13621841 gb AAK33614.1
gi 13621742 gb AAK33524.1	gi 13621842 gb AAK33615.1
gi 13621743 gb AAK33525.1	gi 13621843 gb AAK33616.1
gi 13621744 gb AAK33526.1	gi 13621844 gb AAK33617.1
gi 13621745 gb AAK33527.1	gi 13621898 gb AAK33667.1
gi 13621747 gb AAK33528.1	gi 13621901 gb AAK33670.1
gi 13621756 gb AAK33537.1	gi 13621902 gb AAK33671.1
gi 13621773 gb AAK33552.1	gi 13621904 gb AAK33672.1
gi 13621774 gb AAK33553.1	gi 13621907 gb AAK33675.1
gi 13621775 gb AAK33554.1	gi 13621908 gb AAK33676.1
gi 13621777 gb AAK33556.1	gi 13621909 gb AAK33677.1
gi 13621778 gb AAK33557.1	gi 13621910 gb AAK33678.1
gi 13621779 gb AAK33558.1	gi 13621912 gb AAK33680.1
gi 13621781 gb AAK33559.1	gi 13621924 gb AAK33690.1
gi 13621782 gb AAK33560.1	gi 13621929 gb AAK33694.1
gi 13621785 gb AAK33563.1	gi 13621930 gb AAK33695.1
gi 13621786 gb AAK33564.1	gi 13621931 gb AAK33696.1
gi 13621787 gb AAK33565.1	gi 13621933 gb AAK33698.1
gi 13621788 gb AAK33566.1	gi 13621934 gb AAK33699.1
gi 13621789 gb AAK33567.1	gi 13621935 gb AAK33700.1
gi 13621790 gb AAK33568.1	gi 13621936 gb AAK33701.1
gi 13621793 gb AAK33571.1	gi 13621937 gb AAK33702.1
gi 13621794 gb AAK33572.1	gi 13621938 gb AAK33703.1

Table 33: List of GAS ORFs which are shared with GBS and Spn

gi 13621939 gb AAK33704.1	gi 13622034 gb AAK33790.1
gi 13621942 gb AAK33706.1	gi 13622035 gb AAK33791.1
gi 13621944 gb AAK33708.1	gi 13622039 gb AAK33794.1
gi 13621945 gb AAK33709.1	gi 13622041 gb AAK33796.1
gi 13621946 gb AAK33710.1	gi 13622042 gb AAK33797.1
gi 13621950 gb AAK33714.1	gi 13622043 gb AAK33798.1
gi 13621953 gb AAK33716.1	gi 13622044 gb AAK33799.1
gi 13621954 gb AAK33717.1	gi 13622045 gb AAK33800.1
gi 13621955 gb AAK33718.1	gi 13622046 gb AAK33801.1
gi 13621956 gb AAK33719.1	gi 13622048 gb AAK33802.1
gi 13621957 gb AAK33720.1	gi 13622049 gb AAK33803.1
gi 13621958 gb AAK33721.1	gi 13622050 gb AAK33804.1
gi 13621959 gb AAK33722.1	gi 13622051 gb AAK33805.1
gi 13621961 gb AAK33723.1	gi 13622052 gb AAK33806.1
gi 13621975 gb AAK33736.1	gi 13622054 gb AAK33808.1
gi 13621977 gb AAK33738.1	gi 13622055 gb AAK33809.1
gi 13621978 gb AAK33739.1	gi 13622056 gb AAK33810.1
gi 13621979 gb AAK33740.1	gi 13622058 gb AAK33812.1
gi 13621980 gb AAK33741.1	gi 13622060 gb AAK33813.1
gi 13621981 gb AAK33742.1	gi 13622062 gb AAK33815.1
gi 13621982 gb AAK33743.1	gi 13622064 gb AAK33817.1
gi 13621985 gb AAK33745.1	gi 13622065 gb AAK33818.1
gi 13621986 gb AAK33746.1	gi 13622068 gb AAK33821.1
gi 13621987 gb AAK33747.1	gi 13622069 gb AAK33822.1
gi 13621989 gb AAK33749.1	gi 13622070 gb AAK33823.1
gi 13621990 gb AAK33750.1	gi 13622071 gb AAK33824.1
gi 13621992 gb AAK33752.1	gi 13622073 gb AAK33825.1
gi 13621993 gb AAK33753.1	gi 13622074 gb AAK33826.1
gi 13621994 gb AAK33754.1	gi 13622075 gb AAK33827.1
gi 13621996 gb AAK33755.1	gi 13622077 gb AAK33829.1
gi 13621997 gb AAK33756.1	gi 13622079 gb AAK33831.1
gi 13621998 gb AAK33757.1	gi 13622083 gb AAK33834.1
gi 13621999 gb AAK33758.1	gi 13622085 gb AAK33836.1
gi 13622000 gb AAK33759.1	gi 13622086 gb AAK33837.1
gi 13622001 gb AAK33760.1	gi 13622087 gb AAK33838.1
gi 13622002 gb AAK33761.1	gi 13622088 gb AAK33839.1
gi 13622003 gb AAK33762.1	gi 13622089 gb AAK33840.1
gi 13622004 gb AAK33763.1	gi 13622090 gb AAK33841.1
gi 13622005 gb AAK33764.1	gi 13622091 gb AAK33842.1
gi 13622006 gb AAK33765.1	gi 13622092 gb AAK33843.1
gi 13622008 gb AAK33766.1	gi 13622093 gb AAK33844.1
gi 13622009 gb AAK33767.1	gi 13622095 gb AAK33845.1
gi 13622010 gb AAK33768.1	gi 13622096 gb AAK33846.1
gi 13622012 gb AAK33770.1	gi 13622097 gb AAK33847.1
gi 13622013 gb AAK33771.1	gi 13622162 gb AAK33908.1
gi 13622017 gb AAK33774.1	gi 13622163 gb AAK33909.1
gi 13622018 gb AAK33775.1	gi 13622164 gb AAK33910.1
gi 13622019 gb AAK33776.1	gi 13622165 gb AAK33911.1
gi 13622020 gb AAK33777.1	gi 13622166 gb AAK33912.1
gi 13622021 gb AAK33778.1	gi 13622169 gb AAK33914.1
gi 13622024 gb AAK33781.1	gi 13622170 gb AAK33915.1
gi 13622025 gb AAK33782.1	gi 13622171 gb AAK33916.1
gi 13622026 gb AAK33783.1	gi 13622172 gb AAK33917.1
gi 13622031 gb AAK33787.1	gi 13622174 gb AAK33919.1
gi 13622032 gb AAK33788.1	gi 13622175 gb AAK33920.1
gi 13622033 gb AAK33789.1	gi 13622176 gb AAK33921.1

Table 33: List of GAS ORFs which are shared with GBS and Spn

gi 13622177 gb AAK33922.1	gi 13622269 gb AAK34006.1
gi 13622179 gb AAK33923.1	gi 13622271 gb AAK34007.1
gi 13622180 gb AAK33924.1	gi 13622272 gb AAK34008.1
gi 13622181 gb AAK33925.1	gi 13622273 gb AAK34009.1
gi 13622182 gb AAK33926.1	gi 13622274 gb AAK34010.1
gi 13622183 gb AAK33927.1	gi 13622275 gb AAK34011.1
gi 13622184 gb AAK33928.1	gi 13622276 gb AAK34012.1
gi 13622185 gb AAK33929.1	gi 13622277 gb AAK34013.1
gi 13622186 gb AAK33930.1	gi 13622278 gb AAK34014.1
gi 13622189 gb AAK33932.1	gi 13622279 gb AAK34015.1
gi 13622190 gb AAK33933.1	gi 13622281 gb AAK34017.1
gi 13622191 gb AAK33934.1	gi 13622282 gb AAK34018.1
gi 13622192 gb AAK33935.1	gi 13622283 gb AAK34019.1
gi 13622198 gb AAK33940.1	gi 13622284 gb AAK34020.1
gi 13622200 gb AAK33942.1	gi 13622285 gb AAK34021.1
gi 13622201 gb AAK33943.1	gi 13622287 gb AAK34022.1
gi 13622204 gb AAK33946.1	gi 13622288 gb AAK34023.1
gi 13622205 gb AAK33947.1	gi 13622289 gb AAK34024.1
gi 13622207 gb AAK33949.1	gi 13622290 gb AAK34025.1
gi 13622208 gb AAK33950.1	gi 13622294 gb AAK34029.1
gi 13622211 gb AAK33952.1	gi 13622295 gb AAK34030.1
gi 13622213 gb AAK33954.1	gi 13622296 gb AAK34031.1
gi 13622214 gb AAK33955.1	gi 13622297 gb AAK34032.1
gi 13622215 gb AAK33956.1	gi 13622298 gb AAK34033.1
gi 13622216 gb AAK33957.1	gi 13622299 gb AAK34034.1
gi 13622217 gb AAK33958.1	gi 13622301 gb AAK34035.1
gi 13622218 gb AAK33959.1	gi 13622306 gb AAK34040.1
gi 13622219 gb AAK33960.1	gi 13622326 gb AAK34058.1
gi 13622222 gb AAK33962.1	gi 13622328 gb AAK34060.1
gi 13622223 gb AAK33963.1	gi 13622329 gb AAK34061.1
gi 13622224 gb AAK33964.1	gi 13622330 gb AAK34062.1
gi 13622233 gb AAK33972.1	gi 13622332 gb AAK34064.1
gi 13622235 gb AAK33974.1	gi 13622333 gb AAK34065.1
gi 13622236 gb AAK33975.1	gi 13622335 gb AAK34066.1
gi 13622237 gb AAK33976.1	gi 13622338 gb AAK34069.1
gi 13622239 gb AAK33978.1	gi 13622339 gb AAK34070.1
gi 13622240 gb AAK33979.1	gi 13622340 gb AAK34071.1
gi 13622241 gb AAK33980.1	gi 13622341 gb AAK34072.1
gi 13622242 gb AAK33981.1	gi 13622343 gb AAK34073.1
gi 13622243 gb AAK33982.1	gi 13622350 gb AAK34080.1
gi 13622244 gb AAK33983.1	gi 13622351 gb AAK34081.1
gi 13622250 gb AAK33988.1	gi 13622352 gb AAK34082.1
gi 13622252 gb AAK33990.1	gi 13622353 gb AAK34083.1
gi 13622253 gb AAK33991.1	gi 13622355 gb AAK34084.1
gi 13622255 gb AAK33993.1	gi 13622356 gb AAK34085.1
gi 13622256 gb AAK33994.1	gi 13622357 gb AAK34086.1
gi 13622257 gb AAK33995.1	gi 13622358 gb AAK34087.1
gi 13622259 gb AAK33996.1	gi 13622359 gb AAK34088.1
gi 13622260 gb AAK33997.1	gi 13622360 gb AAK34089.1
gi 13622261 gb AAK33998.1	gi 13622361 gb AAK34090.1
gi 13622262 gb AAK33999.1	gi 13622362 gb AAK34091.1
gi 13622263 gb AAK34000.1	gi 13622363 gb AAK34092.1
gi 13622264 gb AAK34001.1	gi 13622364 gb AAK34093.1
gi 13622265 gb AAK34002.1	gi 13622366 gb AAK34094.1
gi 13622266 gb AAK34003.1	gi 13622367 gb AAK34095.1
gi 13622268 gb AAK34005.1	gi 13622368 gb AAK34096.1

Table 33: List of GAS ORFs which are shared with GBS and Spn

gi 13622369 gb AAK34097.1	gi 13622471 gb AAK34189.1
gi 13622370 gb AAK34098.1	gi 13622473 gb AAK34191.1
gi 13622371 gb AAK34099.1	gi 13622474 gb AAK34192.1
gi 13622372 gb AAK34100.1	gi 13622477 gb AAK34195.1
gi 13622373 gb AAK34101.1	gi 13622478 gb AAK34196.1
gi 13622374 gb AAK34102.1	gi 13622479 gb AAK34197.1
gi 13622375 gb AAK34103.1	gi 13622481 gb AAK34198.1
gi 13622376 gb AAK34104.1	gi 13622482 gb AAK34199.1
gi 13622377 gb AAK34105.1	gi 13622483 gb AAK34200.1
gi 13622378 gb AAK34106.1	gi 13622484 gb AAK34201.1
gi 13622380 gb AAK34107.1	gi 13622485 gb AAK34202.1
gi 13622383 gb AAK34110.1	gi 13622486 gb AAK34203.1
gi 13622384 gb AAK34111.1	gi 13622491 gb AAK34207.1
gi 13622387 gb AAK34114.1	gi 13622492 gb AAK34208.1
gi 13622389 gb AAK34116.1	gi 13622493 gb AAK34209.1
gi 13622394 gb AAK34120.1	gi 13622494 gb AAK34210.1
gi 13622395 gb AAK34121.1	gi 13622495 gb AAK34211.1
gi 13622396 gb AAK34122.1	gi 13622496 gb AAK34212.1
gi 13622398 gb AAK34124.1	gi 13622497 gb AAK34213.1
gi 13622399 gb AAK34125.1	gi 13622499 gb AAK34214.1
gi 13622400 gb AAK34126.1	gi 13622500 gb AAK34215.1
gi 13622401 gb AAK34127.1	gi 13622501 gb AAK34216.1
gi 13622403 gb AAK34128.1	gi 13622506 gb AAK34221.1
gi 13622405 gb AAK34130.1	gi 13622507 gb AAK34222.1
gi 13622406 gb AAK34131.1	gi 13622508 gb AAK34223.1
gi 13622407 gb AAK34132.1	gi 13622509 gb AAK34224.1
gi 13622408 gb AAK34133.1	gi 13622511 gb AAK34225.1
gi 13622415 gb AAK34139.1	gi 13622512 gb AAK34226.1
gi 13622416 gb AAK34140.1	gi 13622513 gb AAK34227.1
gi 13622417 gb AAK34141.1	gi 13622515 gb AAK34229.1
gi 13622419 gb AAK34143.1	gi 13622516 gb AAK34230.1
gi 13622420 gb AAK34144.1	gi 13622517 gb AAK34231.1
gi 13622424 gb AAK34147.1	gi 13622518 gb AAK34232.1
gi 13622425 gb AAK34148.1	gi 13622520 gb AAK34233.1
gi 13622431 gb AAK34153.1	gi 13622521 gb AAK34234.1
gi 13622432 gb AAK34154.1	gi 13622523 gb AAK34236.1
gi 13622433 gb AAK34155.1	gi 13622524 gb AAK34237.1
gi 13622434 gb AAK34156.1	gi 13622525 gb AAK34238.1
gi 13622435 gb AAK34157.1	gi 13622526 gb AAK34239.1
gi 13622436 gb AAK34158.1	gi 13622527 gb AAK34240.1
gi 13622437 gb AAK34159.1	gi 13622579 gb AAK34289.1
gi 13622444 gb AAK34165.1	gi 13622583 gb AAK34292.1
gi 13622447 gb AAK34168.1	gi 13622585 gb AAK34294.1
gi 13622450 gb AAK34170.1	gi 13622587 gb AAK34296.1
gi 13622451 gb AAK34171.1	gi 13622588 gb AAK34297.1
gi 13622455 gb AAK34175.1	gi 13622590 gb AAK34299.1
gi 13622457 gb AAK34177.1	gi 13622591 gb AAK34300.1
gi 13622458 gb AAK34178.1	gi 13622593 gb AAK34301.1
gi 13622460 gb AAK34179.1	gi 13622595 gb AAK34303.1
gi 13622461 gb AAK34180.1	gi 13622596 gb AAK34304.1
gi 13622462 gb AAK34181.1	gi 13622597 gb AAK34305.1
gi 13622463 gb AAK34182.1	gi 13622598 gb AAK34306.1
gi 13622464 gb AAK34183.1	gi 13622599 gb AAK34307.1
gi 13622465 gb AAK34184.1	gi 13622600 gb AAK34308.1
gi 13622467 gb AAK34186.1	gi 13622601 gb AAK34309.1
gi 13622468 gb AAK34187.1	gi 13622603 gb AAK34310.1

Table 33: List of GAS ORFs which are shared with GBS and Spn

gi 13622604 gb AAK34311.1	gi 13622711 gb AAK34408.1
gi 13622606 gb AAK34313.1	gi 13622713 gb AAK34410.1
gi 13622607 gb AAK34314.1	gi 13622714 gb AAK34411.1
gi 13622608 gb AAK34315.1	gi 13622715 gb AAK34412.1
gi 13622609 gb AAK34316.1	gi 13622718 gb AAK34414.1
gi 13622610 gb AAK34317.1	gi 13622719 gb AAK34415.1
gi 13622611 gb AAK34318.1	gi 13622720 gb AAK34416.1
gi 13622612 gb AAK34319.1	gi 13622721 gb AAK34417.1
gi 13622615 gb AAK34321.1	gi 13622722 gb AAK34418.1
gi 13622616 gb AAK34322.1	gi 13622723 gb AAK34419.1
gi 13622617 gb AAK34323.1	gi 13622727 gb AAK34422.1
gi 13622618 gb AAK34324.1	gi 13622728 gb AAK34423.1
gi 13622621 gb AAK34327.1	gi 13622729 gb AAK34424.1
gi 13622622 gb AAK34328.1	gi 13622730 gb AAK34425.1
gi 13622623 gb AAK34329.1	gi 13622731 gb AAK34426.1
gi 13622624 gb AAK34330.1	gi 13622733 gb AAK34428.1
gi 13622625 gb AAK34331.1	gi 13622734 gb AAK34429.1
gi 13622626 gb AAK34332.1	gi 13622735 gb AAK34430.1
gi 13622628 gb AAK34333.1	gi 13622736 gb AAK34431.1
gi 13622629 gb AAK34334.1	gi 13622737 gb AAK34432.1
gi 13622630 gb AAK34335.1	gi 13622740 gb AAK34434.1
gi 13622631 gb AAK34336.1	gi 13622741 gb AAK34435.1
gi 13622632 gb AAK34337.1	gi 13622742 gb AAK34436.1
gi 13622634 gb AAK34339.1	gi 13622744 gb AAK34438.1
gi 13622636 gb AAK34341.1	gi 13622745 gb AAK34439.1
gi 13622640 gb AAK34344.1	gi 13622746 gb AAK34440.1
gi 13622641 gb AAK34345.1	gi 13622749 gb AAK34442.1
gi 13622652 gb AAK34355.1	gi 13622750 gb AAK34443.1
gi 13622653 gb AAK34356.1	gi 13622751 gb AAK34444.1
gi 13622654 gb AAK34357.1	gi 13622752 gb AAK34445.1
gi 13622656 gb AAK34359.1	gi 13622753 gb AAK34446.1
gi 13622660 gb AAK34363.1	gi 13622754 gb AAK34447.1
gi 13622665 gb AAK34367.1	gi 13622760 gb AAK34452.1
gi 13622668 gb AAK34370.1	gi 13622762 gb AAK34454.1
gi 13622675 gb AAK34376.1	gi 13622763 gb AAK34455.1
gi 13622676 gb AAK34377.1	gi 13622764 gb AAK34456.1
gi 13622683 gb AAK34383.1	gi 13622765 gb AAK34457.1
gi 13622684 gb AAK34384.1	gi 13622766 gb AAK34458.1
gi 13622685 gb AAK34385.1	gi 13622767 gb AAK34459.1
gi 13622688 gb AAK34387.1	gi 13622768 gb AAK34460.1
gi 13622689 gb AAK34388.1	gi 13622770 gb AAK34462.1
gi 13622690 gb AAK34389.1	gi 13622771 gb AAK34463.1
gi 13622691 gb AAK34390.1	gi 13622774 gb AAK34465.1
gi 13622692 gb AAK34391.1	gi 13622775 gb AAK34466.1
gi 13622693 gb AAK34392.1	gi 13622776 gb AAK34467.1
gi 13622694 gb AAK34393.1	gi 13622777 gb AAK34468.1
gi 13622695 gb AAK34394.1	gi 13622778 gb AAK34469.1
gi 13622696 gb AAK34395.1	gi 13622779 gb AAK34470.1
gi 13622698 gb AAK34396.1	gi 13622780 gb AAK34471.1
gi 13622699 gb AAK34397.1	gi 13622781 gb AAK34472.1
gi 13622700 gb AAK34398.1	gi 13622782 gb AAK34473.1
gi 13622701 gb AAK34399.1	gi 13622783 gb AAK34474.1
gi 13622702 gb AAK34400.1	gi 13622785 gb AAK34475.1
gi 13622703 gb AAK34401.1	gi 13622787 gb AAK34477.1
gi 13622704 gb AAK34402.1	gi 13622789 gb AAK34479.1
gi 13622705 gb AAK34403.1	gi 13622790 gb AAK34480.1

Table 33: List of GAS ORFs which are shared with GBS and Spn

gi 13622791 gb AAK34481.1	gi 13622870 gb AAK34553.1
gi 13622792 gb AAK34482.1	gi 13622873 gb AAK34555.1
gi 13622793 gb AAK34483.1	gi 13622875 gb AAK34557.1
gi 13622794 gb AAK34484.1	gi 13622876 gb AAK34558.1
gi 13622795 gb AAK34485.1	gi 13622877 gb AAK34559.1
gi 13622796 gb AAK34486.1	gi 13622878 gb AAK34560.1
gi 13622798 gb AAK34487.1	gi 13622879 gb AAK34561.1
gi 13622799 gb AAK34488.1	gi 13622880 gb AAK34562.1
gi 13622800 gb AAK34489.1	gi 13622881 gb AAK34563.1
gi 13622801 gb AAK34490.1	gi 13622882 gb AAK34564.1
gi 13622802 gb AAK34491.1	gi 13622885 gb AAK34566.1
gi 13622803 gb AAK34492.1	gi 13622886 gb AAK34567.1
gi 13622804 gb AAK34493.1	gi 13622887 gb AAK34568.1
gi 13622805 gb AAK34494.1	gi 13622888 gb AAK34569.1
gi 13622806 gb AAK34495.1	gi 13622890 gb AAK34571.1
gi 13622807 gb AAK34496.1	gi 13622893 gb AAK34574.1
gi 13622808 gb AAK34497.1	gi 13622896 gb AAK34576.1
gi 13622809 gb AAK34498.1	gi 13622898 gb AAK34578.1
gi 13622810 gb AAK34499.1	gi 13622899 gb AAK34579.1
gi 13622812 gb AAK34500.1	gi 13622900 gb AAK34580.1
gi 13622813 gb AAK34501.1	gi 13622901 gb AAK34581.1
gi 13622814 gb AAK34502.1	gi 13622903 gb AAK34583.1
gi 13622815 gb AAK34503.1	gi 13622905 gb AAK34585.1
gi 13622818 gb AAK34506.1	gi 13622906 gb AAK34586.1
gi 13622821 gb AAK34509.1	gi 13622907 gb AAK34587.1
gi 13622822 gb AAK34510.1	gi 13622908 gb AAK34588.1
gi 13622823 gb AAK34511.1	gi 13622910 gb AAK34589.1
gi 13622825 gb AAK34512.1	gi 13622911 gb AAK34590.1
gi 13622826 gb AAK34513.1	gi 13622912 gb AAK34591.1
gi 13622827 gb AAK34514.1	gi 13622913 gb AAK34592.1
gi 13622828 gb AAK34515.1	gi 13622914 gb AAK34593.1
gi 13622829 gb AAK34516.1	gi 13622915 gb AAK34594.1
gi 13622830 gb AAK34517.1	gi 13622917 gb AAK34596.1
gi 13622833 gb AAK34520.1	gi 13622918 gb AAK34597.1
gi 13622838 gb AAK34524.1	gi 13622919 gb AAK34598.1
gi 13622839 gb AAK34525.1	gi 13622921 gb AAK34599.1
gi 13622840 gb AAK34526.1	gi 13622922 gb AAK34600.1
gi 13622841 gb AAK34527.1	gi 13622924 gb AAK34602.1
gi 13622847 gb AAK34532.1	gi 13622925 gb AAK34603.1
gi 13622848 gb AAK34533.1	gi 13622926 gb AAK34604.1
gi 13622849 gb AAK34534.1	gi 13622927 gb AAK34605.1
gi 13622853 gb AAK34537.1	gi 13622928 gb AAK34606.1
gi 13622854 gb AAK34538.1	gi 13622929 gb AAK34607.1
gi 13622856 gb AAK34540.1	gi 13622930 gb AAK34608.1
gi 13622857 gb AAK34541.1	gi 13622931 gb AAK34609.1
gi 13622858 gb AAK34542.1	gi 13622933 gb AAK34610.1
gi 13622860 gb AAK34543.1	gi 13622941 gb AAK34617.1
gi 13622861 gb AAK34544.1	gi 13622944 gb AAK34620.1
gi 13622862 gb AAK34545.1	gi 13622945 gb AAK34621.1
gi 13622863 gb AAK34546.1	gi 13622947 gb AAK34623.1
gi 13622864 gb AAK34547.1	gi 13622948 gb AAK34624.1
gi 13622865 gb AAK34548.1	gi 13622949 gb AAK34625.1
gi 13622866 gb AAK34549.1	gi 13622950 gb AAK34626.1
gi 13622867 gb AAK34550.1	gi 13622952 gb AAK34627.1
gi 13622868 gb AAK34551.1	gi 13622955 gb AAK34630.1
gi 13622869 gb AAK34552.1	gi 13622956 gb AAK34631.1

Table 33: List of GAS ORFs which are shared with GBS and Spn

gi 13622959 gb AAK34634.1	gi 13623083 gb AAK34746.1
gi 13622961 gb AAK34636.1	gi 13623085 gb AAK34747.1
gi 13622963 gb AAK34638.1	gi 13623086 gb AAK34748.1
gi 13622964 gb AAK34639.1	gi 13623088 gb AAK34750.1
gi 13622967 gb AAK34641.1	gi 13623089 gb AAK34751.1
gi 13622969 gb AAK34643.1	gi 13623090 gb AAK34752.1
gi 13622971 gb AAK34645.1	gi 13623091 gb AAK34753.1
gi 13622973 gb AAK34647.1	gi 13623093 gb AAK34755.1
gi 13622974 gb AAK34648.1	gi 13623095 gb AAK34756.1
gi 13622977 gb AAK34651.1	gi 13623096 gb AAK34757.1
gi 13622981 gb AAK34654.1	gi 13623098 gb AAK34759.1
gi 13622982 gb AAK34655.1	gi 13623099 gb AAK34760.1
gi 13622983 gb AAK34656.1	gi 13623100 gb AAK34761.1
gi 13622984 gb AAK34657.1	gi 13623102 gb AAK34763.1
gi 13622985 gb AAK34658.1	gi 13623103 gb AAK34764.1
gi 13622989 gb AAK34661.1	gi 13623105 gb AAK34766.1
gi 13622990 gb AAK34662.1	gi 13623107 gb AAK34767.1
gi 13622991 gb AAK34663.1	gi 13623128 gb AAK34787.1
gi 13622992 gb AAK34664.1	gi 13623129 gb AAK34788.1
gi 13622995 gb AAK34666.1	gi 13623131 gb AAK34790.1
gi 13622996 gb AAK34667.1	gi 13623132 gb AAK34791.1
gi 13622998 gb AAK34669.1	gi 13623133 gb AAK34792.1
gi 13622999 gb AAK34670.1	gi 13623134 gb AAK34793.1
gi 13623000 gb AAK34671.1	gi 13623136 gb AAK34794.1
gi 13623001 gb AAK34672.1	gi 13623138 gb AAK34796.1
gi 13623002 gb AAK34673.1	gi 13623139 gb AAK34797.1
gi 13623004 gb AAK34674.1	gi 13623150 gb AAK34807.1
gi 13623005 gb AAK34675.1	gi 13623151 gb AAK34808.1
gi 13623006 gb AAK34676.1	gi 13623152 gb AAK34809.1
gi 13623007 gb AAK34677.1	gi 13623154 gb AAK34811.1
gi 13623009 gb AAK34679.1	gi 13623155 gb AAK34812.1
gi 13623019 gb AAK34688.1	gi 13623156 gb AAK34813.1
gi 13623020 gb AAK34689.1	gi 13623157 gb AAK34814.1
gi 13623030 gb AAK34698.1	gi 13623159 gb AAK34815.1
gi 13623031 gb AAK34699.1	gi 13623161 gb AAK34817.1
gi 13623032 gb AAK34700.1	gi 13623162 gb AAK34818.1
gi 13623033 gb AAK34701.1	gi 13623163 gb AAK34819.1
gi 13623038 gb AAK34705.1	gi 13623165 gb AAK34821.1
gi 13623045 gb AAK34712.1	gi 13623166 gb AAK34822.1
gi 13623046 gb AAK34713.1	gi 13623167 gb AAK34823.1
gi 13623047 gb AAK34714.1	gi 13623168 gb AAK34824.1
gi 13623049 gb AAK34715.1	gi 13623170 gb AAK34826.1
gi 13623050 gb AAK34716.1	gi 13623171 gb AAK34827.1
gi 13623051 gb AAK34717.1	gi 13623175 gb AAK34830.1
gi 13623052 gb AAK34718.1	gi 13623176 gb AAK34831.1
gi 13623053 gb AAK34719.1	gi 13623177 gb AAK34832.1
gi 13623054 gb AAK34720.1	gi 13623179 gb AAK34834.1
gi 13623056 gb AAK34722.1	gi 13623180 gb AAK34835.1
gi 13623058 gb AAK34724.1	gi 13623182 gb AAK34836.1
gi 13623062 gb AAK34727.1	gi 13623183 gb AAK34837.1
gi 13623064 gb AAK34729.1	gi 13623184 gb AAK34838.1
gi 13623065 gb AAK34730.1	gi 13623185 gb AAK34839.1
gi 13623069 gb AAK34733.1	gi 13623186 gb AAK34840.1
gi 13623074 gb AAK34738.1	gi 13623187 gb AAK34841.1
gi 13623081 gb AAK34744.1	
gi 13623082 gb AAK34745.1	

Table 34: List of GAS ORF's which are shared with GBS but not with Spn

gi 13621381 gb AAK33195.1	gi 13621988 gb AAK33748.1
gi 13621423 gb AAK33233.1	gi 13622014 gb AAK33772.1
gi 13621440 gb AAK33249.1	gi 13622015 gb AAK33773.1
gi 13621443 gb AAK33251.1	gi 13622022 gb AAK33779.1
gi 13621453 gb AAK33260.1	gi 13622023 gb AAK33780.1
gi 13621454 gb AAK33261.1	gi 13622028 gb AAK33784.1
gi 13621479 gb AAK33284.1	gi 13622029 gb AAK33785.1
gi 13621482 gb AAK33287.1	gi 13622037 gb AAK33792.1
gi 13621492 gb AAK33296.1	gi 13622038 gb AAK33793.1
gi 13621493 gb AAK33297.1	gi 13622040 gb AAK33795.1
gi 13621497 gb AAK33300.1	gi 13622057 gb AAK33811.1
gi 13621498 gb AAK33301.1	gi 13622061 gb AAK33814.1
gi 13621512 gb AAK33314.1	gi 13622063 gb AAK33816.1
gi 13621514 gb AAK33316.1	gi 13622066 gb AAK33819.1
gi 13621556 gb AAK33354.1	gi 13622067 gb AAK33820.1
gi 13621570 gb AAK33366.1	gi 13622076 gb AAK33828.1
gi 13621587 gb AAK33382.1	gi 13622078 gb AAK33830.1
gi 13621610 gb AAK33403.1	gi 13622084 gb AAK33835.1
gi 13621613 gb AAK33405.1	gi 13622098 gb AAK33848.1
gi 13621626 gb AAK33418.1	gi 13622099 gb AAK33849.1
gi 13621632 gb AAK33423.1	gi 13622100 gb AAK33850.1
gi 13621635 gb AAK33426.1	gi 13622104 gb AAK33854.1
gi 13621643 gb AAK33433.1	gi 13622110 gb AAK33859.1
gi 13621655 gb AAK33444.1	gi 13622116 gb AAK33865.1
gi 13621656 gb AAK33445.1	gi 13622124 gb AAK33873.1
gi 13621659 gb AAK33448.1	gi 13622159 gb AAK33905.1
gi 13621673 gb AAK33461.1	gi 13622193 gb AAK33936.1
gi 13621686 gb AAK33473.1	gi 13622194 gb AAK33937.1
gi 13621696 gb AAK33482.1	gi 13622195 gb AAK33938.1
gi 13621703 gb AAK33488.1	gi 13622196 gb AAK33939.1
gi 13621712 gb AAK33497.1	gi 13622202 gb AAK33944.1
gi 13621728 gb AAK33511.1	gi 13622203 gb AAK33945.1
gi 13621738 gb AAK33520.1	gi 13622206 gb AAK33948.1
gi 13621739 gb AAK33521.1	gi 13622210 gb AAK33951.1
gi 13621740 gb AAK33522.1	gi 13622221 gb AAK33961.1
gi 13621772 gb AAK33551.1	gi 13622231 gb AAK33971.1
gi 13621776 gb AAK33555.1	gi 13622234 gb AAK33973.1
gi 13621791 gb AAK33569.1	gi 13622238 gb AAK33977.1
gi 13621798 gb AAK33575.1	gi 13622245 gb AAK33984.1
gi 13621801 gb AAK33578.1	gi 13622246 gb AAK33985.1
gi 13621803 gb AAK33580.1	gi 13622248 gb AAK33986.1
gi 13621804 gb AAK33581.1	gi 13622249 gb AAK33987.1
gi 13621832 gb AAK33606.1	gi 13622251 gb AAK33989.1
gi 13621833 gb AAK33607.1	gi 13622254 gb AAK33992.1
gi 13621896 gb AAK33665.1	gi 13622267 gb AAK34004.1
gi 13621897 gb AAK33666.1	gi 13622291 gb AAK34026.1
gi 13621906 gb AAK33674.1	gi 13622302 gb AAK34036.1
gi 13621911 gb AAK33679.1	gi 13622303 gb AAK34037.1
gi 13621949 gb AAK33713.1	gi 13622304 gb AAK34038.1
gi 13621951 gb AAK33715.1	gi 13622327 gb AAK34059.1
gi 13621962 gb AAK33724.1	gi 13622344 gb AAK34074.1
gi 13621963 gb AAK33725.1	gi 13622345 gb AAK34075.1
gi 13621964 gb AAK33726.1	gi 13622346 gb AAK34076.1
gi 13621971 gb AAK33732.1	gi 13622347 gb AAK34077.1
gi 13621976 gb AAK33737.1	gi 13622348 gb AAK34078.1
gi 13621983 gb AAK33744.1	gi 13622349 gb AAK34079.1

Table 34: List of GAS ORF's which are shared with GBS but not with Spn

gi 13622382 gb AAK34109.1	gi 13622816 gb AAK34504.1
gi 13622386 gb AAK34113.1	gi 13622817 gb AAK34505.1
gi 13622391 gb AAK34118.1	gi 13622846 gb AAK34531.1
gi 13622392 gb AAK34119.1	gi 13622852 gb AAK34536.1
gi 13622397 gb AAK34123.1	gi 13622874 gb AAK34556.1
gi 13622404 gb AAK34129.1	gi 13622889 gb AAK34570.1
gi 13622412 gb AAK34136.1	gi 13622891 gb AAK34572.1
gi 13622413 gb AAK34137.1	gi 13622892 gb AAK34573.1
gi 13622414 gb AAK34138.1	gi 13622897 gb AAK34577.1
gi 13622418 gb AAK34142.1	gi 13622902 gb AAK34582.1
gi 13622430 gb AAK34152.1	gi 13622904 gb AAK34584.1
gi 13622446 gb AAK34167.1	gi 13622916 gb AAK34595.1
gi 13622449 gb AAK34169.1	gi 13622923 gb AAK34601.1
gi 13622453 gb AAK34173.1	gi 13622934 gb AAK34611.1
gi 13622470 gb AAK34188.1	gi 13622953 gb AAK34628.1
gi 13622487 gb AAK34204.1	gi 13622954 gb AAK34629.1
gi 13622490 gb AAK34206.1	gi 13622960 gb AAK34635.1
gi 13622502 gb AAK34217.1	gi 13622968 gb AAK34642.1
gi 13622503 gb AAK34218.1	gi 13622980 gb AAK34653.1
gi 13622514 gb AAK34228.1	gi 13622987 gb AAK34659.1
gi 13622528 gb AAK34241.1	gi 13623012 gb AAK34682.1
gi 13622540 gb AAK34252.1	gi 13623013 gb AAK34683.1
gi 13622541 gb AAK34253.1	gi 13623014 gb AAK34684.1
gi 13622544 gb AAK34255.1	gi 13623015 gb AAK34685.1
gi 13622545 gb AAK34256.1	gi 13623016 gb AAK34686.1
gi 13622546 gb AAK34257.1	gi 13623018 gb AAK34687.1
gi 13622547 gb AAK34258.1	gi 13623022 gb AAK34691.1
gi 13622548 gb AAK34259.1	gi 13623029 gb AAK34697.1
gi 13622550 gb AAK34261.1	gi 13623037 gb AAK34704.1
gi 13622551 gb AAK34262.1	gi 13623055 gb AAK34721.1
gi 13622552 gb AAK34263.1	gi 13623060 gb AAK34725.1
gi 13622556 gb AAK34267.1	gi 13623061 gb AAK34726.1
gi 13622557 gb AAK34268.1	gi 13623063 gb AAK34728.1
gi 13622558 gb AAK34269.1	gi 13623066 gb AAK34731.1
gi 13622559 gb AAK34270.1	gi 13623068 gb AAK34732.1
gi 13622563 gb AAK34273.1	gi 13623092 gb AAK34754.1
gi 13622571 gb AAK34281.1	gi 13623097 gb AAK34758.1
gi 13622576 gb AAK34286.1	gi 13623104 gb AAK34765.1
gi 13622581 gb AAK34290.1	gi 13623126 gb AAK34785.1
gi 13622582 gb AAK34291.1	gi 13623130 gb AAK34789.1
gi 13622586 gb AAK34295.1	gi 13623137 gb AAK34795.1
gi 13622589 gb AAK34298.1	gi 13623153 gb AAK34810.1
gi 13622605 gb AAK34312.1	gi 13623164 gb AAK34820.1
gi 13622633 gb AAK34338.1	gi 13623178 gb AAK34833.1
gi 13622635 gb AAK34340.1	
gi 13622637 gb AAK34342.1	
gi 13622638 gb AAK34343.1	
gi 13622657 gb AAK34360.1	
gi 13622707 gb AAK34404.1	
gi 13622716 gb AAK34413.1	
gi 13622724 gb AAK34420.1	
gi 13622732 gb AAK34427.1	
gi 13622743 gb AAK34437.1	
gi 13622761 gb AAK34453.1	
gi 13622773 gb AAK34464.1	
gi 13622788 gb AAK34478.1	

**Table 35: GAS ORF's which are shared with pneumococcus
but not with GBS**

gi 13621338 gb AAK33157.1	gi 13623027 gb AAK34695.1
gi 13621352 gb AAK33168.1	gi 13623087 gb AAK34749.1
gi 13621410 gb AAK33221.1	gi 13623101 gb AAK34762.1
gi 13621433 gb AAK33242.1	gi 13623144 gb AAK34802.1
gi 13621445 gb AAK33253.1	gi 13623146 gb AAK34804.1
gi 13621446 gb AAK33254.1	gi 13623147 gb AAK34805.1
gi 13621447 gb AAK33255.1	
gi 13621448 gb AAK33256.1	
gi 13621449 gb AAK33257.1	
gi 13621451 gb AAK33259.1	
gi 13621460 gb AAK33267.1	
gi 13621466 gb AAK33272.1	
gi 13621489 gb AAK33293.1	
gi 13621490 gb AAK33294.1	
gi 13621519 gb AAK33320.1	
gi 13621520 gb AAK33321.1	
gi 13621653 gb AAK33443.1	
gi 13621722 gb AAK33506.1	
gi 13621723 gb AAK33507.1	
gi 13621724 gb AAK33508.1	
gi 13621805 gb AAK33582.1	
gi 13621900 gb AAK33669.1	
gi 13622011 gb AAK33769.1	
gi 13622212 gb AAK33953.1	
gi 13622280 gb AAK34016.1	
gi 13622381 gb AAK34108.1	
gi 13622409 gb AAK34134.1	
gi 13622410 gb AAK34135.1	
gi 13622423 gb AAK34146.1	
gi 13622428 gb AAK34151.1	
gi 13622441 gb AAK34162.1	
gi 13622442 gb AAK34163.1	
gi 13622454 gb AAK34174.1	
gi 13622456 gb AAK34176.1	
gi 13622619 gb AAK34325.1	
gi 13622642 gb AAK34346.1	
gi 13622643 gb AAK34347.1	
gi 13622664 gb AAK34366.1	
gi 13622666 gb AAK34368.1	
gi 13622667 gb AAK34369.1	
gi 13622671 gb AAK34372.1	
gi 13622672 gb AAK34373.1	
gi 13622673 gb AAK34374.1	
gi 13622674 gb AAK34375.1	
gi 13622679 gb AAK34380.1	
gi 13622680 gb AAK34381.1	
gi 13622682 gb AAK34382.1	
gi 13622755 gb AAK34448.1	
gi 13622758 gb AAK34450.1	
gi 13622759 gb AAK34451.1	
gi 13622835 gb AAK34521.1	
gi 13622837 gb AAK34523.1	
gi 13622937 gb AAK34614.1	
gi 13622942 gb AAK34618.1	
gi 13622946 gb AAK34622.1	
gi 13622978 gb AAK34652.1	

Table 36: Spn ORF's are shared with GBS and GAS

SP0001	SP0158	SP0254	SP0385
SP0002	SP0173	SP0259	SP0386
SP0003	SP0179	SP0261	SP0387
SP0004	SP0180	SP0262	SP0400
SP0005	SP0184	SP0263	SP0401
SP0006	SP0185	SP0264	SP0402
SP0007	SP0186	SP0265	SP0403
SP0008	SP0187	SP0266	SP0404
SP0010	SP0189	SP0268	SP0405
SP0011	SP0192	SP0271	SP0406
SP0013	SP0194	SP0272	SP0408
SP0014	SP0197	SP0273	SP0410
SP0019	SP0199	SP0274	SP0411
SP0021	SP0202	SP0280	SP0412
SP0024	SP0204	SP0281	SP0415
SP0027	SP0205	SP0282	SP0416
SP0032	SP0208	SP0283	SP0417
SP0033	SP0209	SP0284	SP0418
SP0034	SP0210	SP0285	SP0419
SP0035	SP0211	SP0286	SP0420
SP0036	SP0212	SP0287	SP0421
SP0037	SP0213	SP0289	SP0422
SP0042	SP0214	SP0290	SP0423
SP0044	SP0215	SP0291	SP0424
SP0045	SP0216	SP0292	SP0425
SP0046	SP0217	SP0294	SP0426
SP0047	SP0218	SP0295	SP0427
SP0048	SP0219	SP0303	SP0433
SP0051	SP0220	SP0310	SP0434
SP0053	SP0221	SP0314	SP0435
SP0054	SP0222	SP0317	SP0436
SP0056	SP0224	SP0318	SP0437
SP0063	SP0225	SP0319	SP0438
SP0073	SP0226	SP0320	SP0439
SP0074	SP0227	SP0321	SP0441
SP0078	SP0228	SP0322	SP0442
SP0079	SP0229	SP0323	SP0443
SP0083	SP0230	SP0324	SP0452
SP0084	SP0231	SP0325	SP0453
SP0085	SP0232	SP0327	SP0454
SP0095	SP0233	SP0330	SP0457
SP0105	SP0234	SP0334	SP0458
SP0106	SP0235	SP0336	SP0459
SP0111	SP0236	SP0337	SP0461
SP0112	SP0240	SP0338	SP0466
SP0118	SP0242	SP0340	SP0467
SP0120	SP0243	SP0342	SP0474
SP0121	SP0245	SP0369	SP0477
SP0122	SP0246	SP0370	SP0478
SP0127	SP0247	SP0371	SP0483
SP0128	SP0248	SP0373	SP0486
SP0129	SP0249	SP0374	SP0488
SP0148	SP0250	SP0381	SP0489
SP0149	SP0251	SP0382	SP0493
SP0151	SP0252	SP0383	SP0494
SP0152	SP0253	SP0384	SP0499

Table 36: Spn ORF's are shared with GBS and GAS

SP0500	SP0652	SP0787	SP0895
SP0501	SP0657	SP0788	SP0896
SP0502	SP0660	SP0792	SP0897
SP0515	SP0662	SP0793	SP0904
SP0516	SP0663	SP0797	SP0905
SP0517	SP0665	SP0798	SP0908
SP0519	SP0668	SP0799	SP0909
SP0521	SP0669	SP0801	SP0912
SP0522	SP0671	SP0802	SP0923
SP0523	SP0672	SP0803	SP0927
SP0526	SP0673	SP0805	SP0928
SP0549	SP0674	SP0806	SP0929
SP0550	SP0675	SP0807	SP0931
SP0552	SP0676	SP0816	SP0932
SP0553	SP0678	SP0817	SP0933
SP0554	SP0680	SP0820	SP0935
SP0555	SP0681	SP0822	SP0936
SP0556	SP0687	SP0823	SP0937
SP0557	SP0688	SP0824	SP0938
SP0563	SP0689	SP0825	SP0943
SP0567	SP0690	SP0828	SP0944
SP0568	SP0701	SP0829	SP0945
SP0576	SP0702	SP0831	SP0946
SP0577	SP0709	SP0835	SP0947
SP0578	SP0713	SP0837	SP0948
SP0579	SP0726	SP0838	SP0954
SP0581	SP0727	SP0839	SP0955
SP0588	SP0729	SP0841	SP0959
SP0589	SP0735	SP0843	SP0960
SP0591	SP0736	SP0844	SP0961
SP0592	SP0741	SP0845	SP0962
SP0593	SP0744	SP0846	SP0964
SP0603	SP0745	SP0847	SP0966
SP0604	SP0746	SP0848	SP0967
SP0605	SP0756	SP0851	SP0968
SP0608	SP0757	SP0852	SP0969
SP0610	SP0758	SP0855	SP0970
SP0611	SP0760	SP0856	SP0971
SP0613	SP0761	SP0862	SP0972
SP0614	SP0762	SP0864	SP0974
SP0615	SP0764	SP0865	SP0975
SP0616	SP0765	SP0867	SP0976
SP0618	SP0766	SP0868	SP0978
SP0620	SP0767	SP0869	SP0979
SP0622	SP0768	SP0870	SP0980
SP0623	SP0770	SP0871	SP0981
SP0624	SP0771	SP0872	SP0984
SP0626	SP0775	SP0873	SP0985
SP0630	SP0776	SP0875	SP0987
SP0631	SP0778	SP0876	SP0988
SP0636	SP0779	SP0877	SP0989
SP0637	SP0780	SP0878	SP0991
SP0638	SP0782	SP0880	SP0992
SP0645	SP0784	SP0881	SP0993
SP0646	SP0785	SP0893	SP1002
SP0647	SP0786	SP0894	SP1003

Table 36: Spn ORF's are shared with GBS and GAS

SP1004	SP1117	SP1242	SP1387
SP1008	SP1118	SP1244	SP1388
SP1010	SP1119	SP1245	SP1389
SP1012	SP1128	SP1246	SP1390
SP1016	SP1151	SP1247	SP1393
SP1017	SP1152	SP1248	SP1394
SP1018	SP1155	SP1249	SP1395
SP1020	SP1156	SP1260	SP1396
SP1021	SP1157	SP1263	SP1397
SP1022	SP1159	SP1266	SP1398
SP1024	SP1160	SP1275	SP1399
SP1025	SP1161	SP1276	SP1400
SP1026	SP1162	SP1277	SP1402
SP1029	SP1163	SP1278	SP1403
SP1033	SP1164	SP1279	SP1404
SP1034	SP1167	SP1280	SP1405
SP1035	SP1168	SP1283	SP1406
SP1045	SP1169	SP1284	SP1407
SP1056	SP1174	SP1285	SP1408
SP1067	SP1175	SP1286	SP1409
SP1068	SP1176	SP1287	SP1411
SP1069	SP1177	SP1288	SP1412
SP1070	SP1178	SP1289	SP1413
SP1071	SP1179	SP1290	SP1414
SP1072	SP1180	SP1291	SP1415
SP1073	SP1182	SP1293	SP1416
SP1074	SP1184	SP1297	SP1420
SP1076	SP1185	SP1298	SP1421
SP1079	SP1187	SP1299	SP1427
SP1081	SP1190	SP1308	SP1428
SP1082	SP1191	SP1316	SP1429
SP1083	SP1192	SP1324	SP1434
SP1084	SP1193	SP1329	SP1435
SP1087	SP1197	SP1330	SP1445
SP1088	SP1200	SP1331	SP1446
SP1089	SP1202	SP1336	SP1448
SP1090	SP1204	SP1341	SP1449
SP1093	SP1205	SP1354	SP1450
SP1094	SP1207	SP1355	SP1452
SP1095	SP1208	SP1357	SP1453
SP1096	SP1212	SP1358	SP1456
SP1097	SP1213	SP1359	SP1457
SP1098	SP1218	SP1362	SP1458
SP1099	SP1219	SP1368	SP1460
SP1100	SP1220	SP1370	SP1461
SP1102	SP1225	SP1371	SP1462
SP1105	SP1226	SP1372	SP1465
SP1106	SP1227	SP1374	SP1466
SP1107	SP1228	SP1375	SP1469
SP1110	SP1229	SP1376	SP1470
SP1111	SP1230	SP1377	SP1473
SP1112	SP1231	SP1378	SP1474
SP1113	SP1232	SP1380	SP1475
SP1114	SP1233	SP1381	SP1478
SP1115	SP1238	SP1383	SP1479
SP1116	SP1241	SP1386	SP1482

Table 36: Spn ORF's are shared with GBS and GAS

SP1483	SP1580	SP1685	SP1857
SP1485	SP1583	SP1688	SP1858
SP1489	SP1584	SP1689	SP1860
SP1491	SP1586	SP1697	SP1861
SP1498	SP1587	SP1698	SP1865
SP1500	SP1588	SP1699	SP1871
SP1501	SP1589	SP1702	SP1873
SP1502	SP1590	SP1709	SP1874
SP1504	SP1591	SP1711	SP1875
SP1505	SP1597	SP1712	SP1876
SP1507	SP1598	SP1713	SP1877
SP1508	SP1599	SP1714	SP1878
SP1509	SP1602	SP1717	SP1879
SP1510	SP1603	SP1721	SP1880
SP1511	SP1606	SP1722	SP1881
SP1512	SP1608	SP1724	SP1883
SP1513	SP1609	SP1725	SP1884
SP1517	SP1610	SP1726	SP1887
SP1518	SP1615	SP1727	SP1888
SP1519	SP1616	SP1732	SP1889
SP1521	SP1617	SP1733	SP1890
SP1522	SP1624	SP1734	SP1895
SP1523	SP1625	SP1735	SP1896
SP1529	SP1626	SP1736	SP1900
SP1530	SP1631	SP1737	SP1901
SP1534	SP1633	SP1738	SP1902
SP1535	SP1638	SP1739	SP1903
SP1536	SP1644	SP1742	SP1906
SP1537	SP1645	SP1743	SP1908
SP1538	SP1646	SP1744	SP1909
SP1539	SP1647	SP1746	SP1916
SP1540	SP1648	SP1747	SP1918
SP1541	SP1649	SP1748	SP1922
SP1542	SP1650	SP1749	SP1940
SP1544	SP1652	SP1750	SP1942
SP1547	SP1653	SP1752	SP1944
SP1549	SP1655	SP1759	SP1953
SP1551	SP1659	SP1776	SP1957
SP1552	SP1661	SP1780	SP1960
SP1553	SP1662	SP1781	SP1961
SP1554	SP1664	SP1782	SP1963
SP1557	SP1665	SP1785	SP1964
SP1558	SP1666	SP1790	SP1966
SP1559	SP1667	SP1795	SP1967
SP1560	SP1668	SP1799	SP1968
SP1561	SP1670	SP1804	SP1969
SP1563	SP1671	SP1816	SP1970
SP1564	SP1672	SP1817	SP1972
SP1565	SP1674	SP1825	SP1973
SP1566	SP1675	SP1839	SP1974
SP1568	SP1676	SP1840	SP1975
SP1569	SP1677	SP1845	SP1976
SP1571	SP1681	SP1847	SP1979
SP1574	SP1682	SP1848	SP1980
SP1575	SP1683	SP1851	SP1981
SP1577	SP1684	SP1855	SP1982

Table 36: Spn ORF's are shared with GBS and GAS

SP1983	SP2085	SP2206
SP1984	SP2086	SP2207
SP1985	SP2087	SP2208
SP1987	SP2088	SP2209
SP1989	SP2090	SP2210
SP1990	SP2091	SP2214
SP1991	SP2092	SP2215
SP1993	SP2094	SP2216
SP1994	SP2099	SP2219
SP1996	SP2100	SP2220
SP1997	SP2101	SP2221
SP1998	SP2106	SP2222
SP1999	SP2107	SP2224
SP2006	SP2108	SP2225
SP2007	SP2109	SP2226
SP2010	SP2110	SP2227
SP2011	SP2112	SP2228
SP2012	SP2113	SP2229
SP2020	SP2114	SP2230
SP2021	SP2119	SP2231
SP2022	SP2121	SP2233
SP2027	SP2129	SP2234
SP2028	SP2131	SP2235
SP2030	SP2135	SP2238
SP2031	SP2142	SP2239
SP2032	SP2148	SP2240
SP2033	SP2150	
SP2034	SP2151	
SP2035	SP2152	
SP2036	SP2153	
SP2037	SP2156	
SP2038	SP2161	
SP2040	SP2162	
SP2041	SP2169	
SP2042	SP2170	
SP2044	SP2171	
SP2045	SP2172	
SP2048	SP2173	
SP2052	SP2174	
SP2053	SP2175	
SP2054	SP2176	
SP2055	SP2184	
SP2056	SP2185	
SP2057	SP2186	
SP2058	SP2187	
SP2063	SP2188	
SP2065	SP2189	
SP2069	SP2191	
SP2070	SP2192	
SP2072	SP2193	
SP2073	SP2194	
SP2075	SP2195	
SP2077	SP2202	
SP2078	SP2203	
SP2082	SP2204	
SP2083	SP2205	

Table 37: Spn ORF's which are shared with GBS but not with GAS

SP0012	SP0725	SP1360	SP1927
SP0020	SP0730	SP1361	SP1928
SP0039	SP0739	SP1365	SP1943
SP0050	SP0749	SP1382	SP1959
SP0082	SP0750	SP1384	SP2001
SP0107	SP0751	SP1392	SP2002
SP0113	SP0752	SP1447	SP2009
SP0119	SP0753	SP1451	SP2026
SP0146	SP0754	SP1463	SP2029
SP0150	SP0769	SP1464	SP2039
SP0175	SP0789	SP1471	SP2061
SP0176	SP0791	SP1472	SP2064
SP0177	SP0826	SP1524	SP2066
SP0178	SP0900	SP1527	SP2079
SP0237	SP0913	SP1600	SP2084
SP0255	SP0914	SP1605	SP2095
SP0260	SP0939	SP1607	SP2096
SP0267	SP0941	SP1632	SP2098
SP0278	SP0942	SP1634	SP2103
SP0288	SP0953	SP1651	SP2127
SP0346	SP0973	SP1673	SP2128
SP0347	SP0977	SP1680	SP2130
SP0348	SP1011	SP1695	SP2134
SP0349	SP1013	SP1700	SP2137
SP0366	SP1027	SP1701	SP2138
SP0376	SP1054	SP1720	SP2157
SP0413	SP1055	SP1729	SP2196
SP0445	SP1080	SP1740	
SP0462	SP1086	SP1741	
SP0463	SP1121	SP1745	
SP0479	SP1122	SP1751	
SP0480	SP1123	SP1757	
SP0482	SP1124	SP1758	
SP0484	SP1126	SP1761	
SP0537	SP1127	SP1762	
SP0538	SP1137	SP1763	
SP0566	SP1166	SP1764	
SP0580	SP1173	SP1765	
SP0585	SP1194	SP1766	
SP0599	SP1195	SP1767	
SP0600	SP1215	SP1768	
SP0601	SP1240	SP1770	
SP0606	SP1256	SP1771	
SP0607	SP1261	SP1772	
SP0609	SP1271	SP1783	
SP0617	SP1272	SP1802	
SP0627	SP1273	SP1828	
SP0655	SP1274	SP1856	
SP0656	SP1306	SP1867	
SP0710	SP1310	SP1869	
SP0711	SP1332	SP1870	
SP0717	SP1333	SP1872	
SP0718	SP1334	SP1891	
SP0720	SP1346	SP1907	
SP0723	SP1348	SP1910	
SP0724	SP1350	SP1911	

Table 38: Spn ORF's which are shared with GAS but no with GBS

SP0065	SP1754
SP0075	SP1797
SP0090	SP1798
SP0091	SP1800
SP0092	SP1885
SP0099	SP1919
SP0100	SP1923
SP0153	SP1941
SP0155	SP1950
SP0156	SP2016
SP0200	SP2017
SP0306	SP2051
SP0313	SP2060
SP0341	SP2111
SP0476	SP2143
SP0496	SP2144
SP0509	SP2201
SP0527	SP2236
SP0648	
SP0658	
SP0659	
SP0661	
SP0677	
SP0715	
SP0742	
SP0743	
SP0858	
SP0859	
SP0860	
SP0910	
SP0986	
SP0994	
SP0999	
SP1000	
SP1001	
SP1023	
SP1075	
SP1129	
SP1147	
SP1171	
SP1186	
SP1315	
SP1317	
SP1319	
SP1320	
SP1321	
SP1322	
SP1438	
SP1442	
SP1525	
SP1546	
SP1570	
SP1572	
SP1578	
SP1604	
SP1715	

Table 40: Comparative Sequences relating to SAG0635

SEQ ID NO 4001 : SAG0653 FROM THE 2603 V/R GBS TYPE V STRAIN
 ATGAAGAAAGTGTAGTGTAGTCTTTTGGTTTATAGGGATTACGATA
 ACGTTACAAACAGTAGTTGAGGCTAAGGGGCCAAAAGTAGCTTATACACAAGAGGGAATG
 ACTGCTCTTTTCGGACACAAATAAAGATAAAGTCACTACTATTTCTATTGACGAGATTCAA
 AAAAGCTTAGAAGGTAAAGAGCCGATTACTGTTAGTTTGTATTTGATGATACACTGCTT
 TTCAGTAGTCAATATTTTCAATATGGTAAAGAATATGTAACCTCTGGATCGTTTGATT
 CTTCAATAACAAAAATTCGCGGATCTTGTGCAAAACGAGGAGATCAAGATTCATTCCC
 AAGAATATGCTAAAAAATTAATTGCTATGCATCAAAACGAGGAGATAAAATTGTTTTT
 ATAACAGGTAGGACAAGAGGGTCAATGTATAAGGAGGGCGAGGTGATAAAACAGCTAAA
 GCCTTAGCTAAAGATTTTAAATTAGACAAACCAATTGCTGTAAATTATACAGGCGATAAA
 CCTAAAAAGCCATACAAATATGATAAATCATATTATATTAAGAAATATGGTTCAGACATT
 CATTTAGGAGATAGTATGACGATATTCATGCAGCTAGGGAGGCGGTGCTAGACCAATT
 AGAATTTTAAGAGCACCTAATTCTACAAATCTACCTTTACCAGAAGCTGAGGCTACGGT
 GAAGAGTTCTCGAAAATTCAGCTTAC

SEQ ID NO 4002 : SAG0653 FROM THE 090 GBS TYPE III STRAIN
 AAGGGGCCAAAAGTAGCTTATACACAAGAGGGAATGAC
 TGCTCTTTTCGGACACAAATAAAGATAAAGTCACTACTATTTCTATTGACG
 AGATTCAAAAAGCTTAGAAGGTAAAGAGCCGATTACTGTTAGTTTGTAT
 ATTGATGATACACTACTTTTTCAGTAGTCAATATTTTCAATATGTTAAAGA
 ATATGTAACCTCTGGATCGTTTGATTCTTCTATAACAAAAATTCGCG
 ATCTTGTGCAAAACGAGGAGATCAAGATTCATTCCCAAGAAATATGCT
 AAAAAATTAATTGCTATGCATCAAAACGAGGAGATAAAATTGTTTTTAT
 AACAGGTAGGACAAGAGGGTCAATGTATAAGGAGGGCGAGGTGATAAA
 CAGCTAAAGCCTTAGCTAAAGATTTTAAATTAGACAAACCAATTGCTGTA
 AATTATACAGGCGATAAACCTAAAAAGCCATACAAATATGATAAATCATA
 TTATATTAAAGAAATATGGTTCAGACATTTCATTATGGAGATAGTGATGACG
 ATATTCTGCAGCTAGGGAGGCGGTGCTAGACCAATTAGAATTTTAAGA
 GCACCTAATTCTACAAATCTACCTTTACCAGAAGCTGGAGGCTACGGTGA
 AGAGGTTCTCGAAAATTCAGCTTAC

SEQ ID NO 4003 : SAG0653 FROM THE A909 GBS TYPE Ia STRAIN
 AAGGGGCCAAAAGTAGCTTATACACA
 AGAGGGAATGACTGCTCTTTTCGGACACAAATAAAGATAAAGTCACTACTA
 TTTCTATTGACGAGATTCAAAAAGCTTAGAAGGTAAAGAGCCGATTACT
 GTTAGTTTGTATATTGATGATACACTGCTTTTTCAGTAGTCAATATTTTCA
 ATATGGTAAAGAATATGTAACCTCTGGATCGTTTGATTCTTCTATAAAC
 AAAAAATTCGCGGATCTTGTGCAAAACGAGGAGATCAAGATTCATTCCC
 AAAGAATATGCTAAAAAATTAATTGCTATGCATCAAAACGAGGAGATAA
 AATTGTTTTTATAACAGGTAGGACAAGAGGGTCAATGTATAAGGAGGCG
 AGGTGATAAAACAGCTAAAGCCTTAGCTAAAGATTTTAAATTAGACAAA
 CCAATTGCTGTAAATTATACAGGCGATAAACCTAAAAAGCCATACAAATA
 TGATAAATCATATTATATTAAAGAAATATGGTTCAGACATTCAATTATGGAG
 ATAGTGATGACGATATTCTATGCAGCTAGGGAGGCGGTGCTAGACCAATT
 AGAATTTTAAGAGCACCTAATTCTACAAATCTACCTTTACCAGAAGCTGG
 AGGCTACGGTGAAGAGGTTCTCGAAAATTCAGCTTAC

SEQ ID NO 4004 : SAG0653 FROM THE 18RS21 GBS TYPE II STRAIN
 AAGGGGCCAAAAGTAGCTTATACACAAGA
 GGAATGACTGCTCTTTTCGGACACAAATAAAGATAAAGTCACTACTATTT
 CTATTGACGAGATTCAAAAAGCTTAGAAGGTAAAGAGCCGATTACTGTT
 AGTTTTGATATTGATGATACACTGCTTTTTCAGTAGTCAATATTTTCAATA
 TGGTAAAGAATATGTAACCTCTGGATCGTTTGATTCTTCTATAAACAAA
 AATTCTGGGATCTTGTGCAAAACGAGGAGATCAAGATTCATTCCCAAA
 GAATATGCTAAAAAATTAATTGCTATGCATCAAAACGAGGAGATAAAAT
 TGTTTTTATAACAGGTAGGACAAGAGGGTCAATGTATAAGGAGGCGAGG
 TTGATAAAACAGCTAAAGCCTTAGCTAAAGATTTTAAATTAGACAAACCA
 ATTGCTGTAAATTATACAGGCGATAAACCTAAAAAGCCATACAAATATGA
 TAAATCATATTATATTAAAGAAATATGGTTCAGACATTCAATTATGGAGATA
 GTGATGACGATATTCTATGCAGCTAGGGAGGCGGTGCTAGACCAATTAGA
 ATTTTAAGAGCACCTAATTCTACAAATCTACCTTTACCAGAAGCTGGAGG
 CTACGGTGAAGAGGTTCTCGAAAATTCAGCTTAC

SEQ ID NO 4005 : SAG0653 FROM THE M732 GBS TYPE III STRAIN
 AAGGGGCCAAAAGTAGCTTATACACAAGA
 GGAATGACTGCTCTTTTCGGACACAAATAAAGATAAAGTCACTACTATTT
 CTATTGACGAGATTCAAAAAGCTTAGAAGGTAAAGAGCCGATTACTGTT
 AGTTTTGATATTGATGATACACTGCTTTTTCAGTAGTCAATATTTTCAATA
 TGGTAAAGAATATGTAACCTCTGGATCGTTTGATTCTTCTATAAACAAA
 AATTCTGGGATCTTGTGCAAAACGAGGAGATCAAGATTCATTCCCAAA
 GAATATGCTAAAAAATTAATTGCTATGCATCAAAACGAGGAGATAAAAT
 TGTTTTTATAACAGGTAGGACAAGAGGGTCAATGTATAAGGAGGCGAGG
 TTGATAAAACAGCTAAAGCCTTAGCTAAAGATTTTAAATTAGACAAACCA
 ATTGCTGTAAATTATACAGGCGATAAACCTAAAAAGCCATACAAATATGA
 TAAATCATATTATATTAAAGAAATATGGTTCAGACATTCAATTATGGAGATA
 GTGATGACGATATTCTATGCAGCTAGGGAGGCGGTGCTAGACCAATTAGA
 ATTTTAAGAGCACCTAATTCTACAAATCTACCTTTACCAGAAGCTGGAGG
 CTACGGTGAAGAGGTTCTCGAAAATTCAGCTTAC

SEQ ID NO 4006 : SAG0653 FROM THE COH1 GBS TYPE III STRAIN
 AAGGGGCCAAAAGTAGCTTATACACAAGAGGGAATGACT
 GCTCTTTTCGGACACAAATAAAGATAAAGTCACTACTATTTCTATTGACGA
 GATTCAAAAAGCTTAGAAGGTAAAGAGCCGATTACTGTTAGTTTGTATA

Table 40: Comparative Sequences relating to SAG0635

TTGATGATACACTGCTTTTCAGTAGTCAATATTTTCAATATGGTAAAGAA
 TATGTAACTCCTGGATCGTTTGATTTTCTTCATAAACAATAATTCGGGA
 TCTTGTGCAAAACGAGGAGATCAAGATTCATTCCTAAAGAAATATGCTA
 AAAAAATTAATTGCTATGCAATCAAAACGAGGAGATAAAATTTGTTTTATA
 ACAGGTAGGACAGAGGGTCAATGTATAAGGAGGGCGAGGTTGATAAAC
 AGCTAAAGCCTTAGCTAAAGATTTTAAATTAGACAAACCAATTGCTGTAA
 ATTATACAGGCGATAAACCTAAAAAGCCATACAAATATGATAAATCATAT
 TATATTAAGAAATATGGTTGAGACATTCATTATGGAGATAGTGACGA
 TATTCATGCAGCTAGGGAGGCCGGTGTAGACCAATTAGAATTTTAAGAG
 CACCTAATTCTACAAATCTACCTTTACCAGAAGCTGGAGGCTACGGTGAA
 GAGGTTCTCGAAATTCAGCTTAC

SEQ ID NO 4007 : SAG0653 FROM THE M781 GBS TYPE III STRAIN

AAGGGGCCAAAAGTAGCTTATACACA
 AGAGGGAATGACTGCTCTTTTCGGACACAAATAAAGATAAAGTCACTACTA
 TTTCTATTGACGAGATTCAAAAAGCTTAGAAGGTAAGAAGCCGATTACT
 GTTAGTTTGTATATTGATGATACACTGCTTTTCAGTAGTCAATATTTTCA
 ATATGGTAAAGATATGTAACCTCTGGATCGTTTGATTTTCTTCATAAAC
 AAAAAATTCGGGATCTTGTGCAAAACGAGGAGATCAAGATTCATTCCC
 AAAGAATATGCTAAAAAATTAATTGCTATGCATCAAAAACGAGGAGATAA
 AATTGTTTTATACAGGTAGGACAGAGGGTCAATGTATAAGGAGGGCG
 AGGTTGATAAAACAGCTAAAGCCTTAGCTAAAGATTTTAAATTAGACAAA
 CCAATGCTGTAAATTATACAGGCGATAAACCTAAAAAGCCATACAAATA
 TGATAAATCATATTATATTAAGAAATATGGTTGAGACATTCATTATGGAG
 ATAGTGATGACGATATTCTAGCAGCTAGGGAGGCCGGTGTAGACCAATT
 AGAATTTTAAGAGCACCTAATTCTACAAATCTACCTTTACCAGAAGCTGG
 AGGCTACGGTGAAGAGGTTCTCGAAATTCAGCTTAC

SEQ ID NO 4008 : SAG0653 FROM THE CJB110 GBS NONTYPEABLE STRAIN

AAGGGGCCAAAAGTAGCTTATACACAAGA
 GGGGAATGACTGCTCTTTTCGGACACAAATAAAGATAAAGTCACTACTATTT
 CTATTGACGAGATTCAAAAAGCTTAGAAGGTAAGAAGCCGATTACTGTT
 AGTTTTGATATTGATGATACACTGCTTTTCAGTAGTCAATATTTTCAATA
 TGGTAAAGAATATGTAACCTCTGGATCGTTTGATTTTCTTCATAAACAAA
 AATTCGGGATCTTGTGCAAAACGAGGAGATCAAGATTCATTCCC
 GAATATGCTAAAAAATTAATTGCTATGCATCAAAAACGAGGAGATAAAAT
 TGTTTTTATAACAGGTAGGACAGAGGGTCAATGTATAAGGAGGGCGAGG
 TTGATAAAACAGCTAAAGCCTTAGCTAAAGATTTTAAATTAGACAAACCA
 ATTGCTGTAAATTTATACAGGCGATAAACCTAAAAAGCCATACAAATATGA
 TAAATCATATTATATTAAGAAATATGGTTGAGACATTCATTATGGAGATA
 GTGATGACGATATTCTAGCAGCTAGGGAGGCCGGTGTAGACCAATTAGA
 ATTTTAAGAGCACCTAATTCTACAAATCTACCTTTACCAGAAGCTGGAGG
 CTACGGTGAAGAGGTTCTCGAAATTCAGCTTAC

SEQ ID NO 4009 : SAG0653 FROM THE JM9130013 GBS TYPE VIII STRAIN

AAGGGGCCAAAAGTAGCTTATACACAAGAGGAAT
 GACTGCTCTTTTCGGACACAAATAAAGATAAAGTCACTACTATTTCTATTG
 ACGAGATTCAAAAAGCTTAGAAGGTAAGAAGCCGATTACTGTTAGTTTT
 GATATTGATGATACACTGCTTTTCAGTAGTCAATATTTTCAATATGGTAA
 AGAATATGTAACCTCTGGATCGTTTGATTTCTTCATAAACAATAATCT
 GGGATCTTGTGCAAAACGAGGAGATCAAGATTCATTCCCAGAAATAT
 GCTAAAAAATTAATTGCTATGCATCAAAAACGAGGAGATAAAATTTGTTTT
 TATAACAGGTAGGACAGAGGGTCAATGTATAAGGAGGGCGAGGTTGATA
 AAACAGCTAAAGCCTTAGCTAAAGATTTTAAATTAGACAAACCAATTGCT
 GTAAATTATACAGGCGATAAACCTAAAAAGCCATACAAATATGATAAATC
 ATATATATTAAGAAATATGGTTGAGACATTCATTATGGAGATAGTGATG
 ACGATATTCTAGCAGCTAGGGAGGCCGGTGTAGACCAATTAGAATTTTA
 AGAGCACCTAATTCTACAAATCTACCTTTACCAGAAGCTGGAGGCTACGG
 TGAAGAGGTTCTCGAAATTCAGCTTAC

Table 40: Comparative Sequences relating to SAG0635

PRETTY of: /biotmp/msa20031.2{*} August 5, 2002 07:05 ..

	1		50
msa20031.2{100_18RS21}	AAGGGGCCAA	AAGTAGCTTA	TACACAAGAG
msa20031.2{100_2603}	AAGGGGCCAA	AAGTAGCTTA	TACACAAGAG
msa20031.2{100_A909}	AAGGGGCCAA	AAGTAGCTTA	TACACAAGAG
msa20031.2{100_CJB110}	AAGGGGCCAA	AAGTAGCTTA	TACACAAGAG
msa20031.2{100_COH1}	AAGGGGCCAA	AAGTAGCTTA	TACACAAGAG
msa20031.2{100_JM9130013}	AAGGGGCCAA	AAGTAGCTTA	TACACAAGAG
msa20031.2{100_M732}	AAGGGGCCAA	AAGTAGCTTA	TACACAAGAG
msa20031.2{100_M781}	AAGGGGCCAA	AAGTAGCTTA	TACACAAGAG
msa20031.2{100_090}	AAGGGGCCAA	AAGTAGCTTA	TACACAAGAG
Consensus	*****	*****	*****
	51		100
msa20031.2{100_18RS21}	CACAAATAAA	GATAAAGTCA	CTACTATTTC
msa20031.2{100_2603}	CACAAATAAA	GATAAAGTCA	CTACTATTTC
msa20031.2{100_A909}	CACAAATAAA	GATAAAGTCA	CTACTATTTC
msa20031.2{100_CJB110}	CACAAATAAA	GATAAAGTCA	CTACTATTTC
msa20031.2{100_COH1}	CACAAATAAA	GATAAAGTCA	CTACTATTTC
msa20031.2{100_JM9130013}	CACAAATAAA	GATAAAGTCA	CTACTATTTC
msa20031.2{100_M732}	CACAAATAAA	GATAAAGTCA	CTACTATTTC
msa20031.2{100_M781}	CACAAATAAA	GATAAAGTCA	CTACTATTTC
msa20031.2{100_090}	CACAAATAAA	GATAAAGTCA	CTACTATTTC
Consensus	*****	*****	*****
	101		150
msa20031.2{100_18RS21}	GCTTAGAAGG	TAAGAAGCCG	ATTACTGTGA
msa20031.2{100_2603}	GCTTAGAAGG	TAAGAAGCCG	ATTACTGTGA
msa20031.2{100_A909}	GCTTAGAAGG	TAAGAAGCCG	ATTACTGTGA
msa20031.2{100_CJB110}	GCTTAGAAGG	TAAGAAGCCG	ATTACTGTGA
msa20031.2{100_COH1}	GCTTAGAAGG	TAAGAAGCCG	ATTACTGTGA
msa20031.2{100_JM9130013}	GCTTAGAAGG	TAAGAAGCCG	ATTACTGTGA
msa20031.2{100_M732}	GCTTAGAAGG	TAAGAAGCCG	ATTACTGTGA
msa20031.2{100_M781}	GCTTAGAAGG	TAAGAAGCCG	ATTACTGTGA
msa20031.2{100_090}	GCTTAGAAGG	TAAGAAGCCG	ATTACTGTGA
Consensus	*****	*****	*****
	151		200
msa20031.2{100_18RS21}	CTgCTTTTCA	GTAAGTCAATA	TTTTCAATAT
msa20031.2{100_2603}	CTgCTTTTCA	GTAAGTCAATA	TTTTCAATAT
msa20031.2{100_A909}	CTgCTTTTCA	GTAAGTCAATA	TTTTCAATAT
msa20031.2{100_CJB110}	CTgCTTTTCA	GTAAGTCAATA	TTTTCAATAT
msa20031.2{100_COH1}	CTgCTTTTCA	GTAAGTCAATA	TTTTCAATAT
msa20031.2{100_JM9130013}	CTgCTTTTCA	GTAAGTCAATA	TTTTCAATAT
msa20031.2{100_M732}	CTgCTTTTCA	GTAAGTCAATA	TTTTCAATAT
msa20031.2{100_M781}	CTgCTTTTCA	GTAAGTCAATA	TTTTCAATAT
msa20031.2{100_090}	CTgCTTTTCA	GTAAGTCAATA	TTTTCAATAT
Consensus	*****	*****	*****
	201		250
msa20031.2{100_18RS21}	TGGATCGTTT	GATTTTCTTC	ATAAACAAAA
msa20031.2{100_2603}	TGGATCGTTT	GATTTTCTTC	ATAAACAAAA
msa20031.2{100_A909}	TGGATCGTTT	GATTTTCTTC	ATAAACAAAA
msa20031.2{100_CJB110}	TGGATCGTTT	GATTTTCTTC	ATAAACAAAA
msa20031.2{100_COH1}	TGGATCGTTT	GATTTTCTTC	ATAAACAAAA
msa20031.2{100_JM9130013}	TGGATCGTTT	GATTTTCTTC	ATAAACAAAA
msa20031.2{100_M732}	TGGATCGTTT	GATTTTCTTC	ATAAACAAAA
msa20031.2{100_M781}	TGGATCGTTT	GATTTTCTTC	ATAAACAAAA
msa20031.2{100_090}	TGGATCGTTT	GATTTTCTTC	ATAAACAAAA
Consensus	*****	*****	*****
	251		300
msa20031.2{100_18RS21}	AACGAGGAGA	TCAAGATTCC	ATTCCCAAAG
msa20031.2{100_2603}	AACGAGGAGA	TCAAGATTCC	ATTCCCAAAG
msa20031.2{100_A909}	AACGAGGAGA	TCAAGATTCC	ATTCCCAAAG
msa20031.2{100_CJB110}	AACGAGGAGA	TCAAGATTCC	ATTCCCAAAG
msa20031.2{100_COH1}	AACGAGGAGA	TCAAGATTCC	ATTCCCAAAG
msa20031.2{100_JM9130013}	AACGAGGAGA	TCAAGATTCC	ATTCCCAAAG
msa20031.2{100_M732}	AACGAGGAGA	TCAAGATTCC	ATTCCCAAAG
msa20031.2{100_M781}	AACGAGGAGA	TCAAGATTCC	ATTCCCAAAG
msa20031.2{100_090}	AACGAGGAGA	TCAAGATTCC	ATTCCCAAAG
Consensus	*****	*****	*****
	301		350
msa20031.2{100_18RS21}	GCTATGCATC	AAAAACGAGG	AGATAAAATT
msa20031.2{100_2603}	GCTATGCATC	AAAAACGAGG	AGATAAAATT
msa20031.2{100_A909}	GCTATGCATC	AAAAACGAGG	AGATAAAATT
msa20031.2{100_CJB110}	GCTATGCATC	AAAAACGAGG	AGATAAAATT
msa20031.2{100_COH1}	GCTATGCATC	AAAAACGAGG	AGATAAAATT
msa20031.2{100_JM9130013}	GCTATGCATC	AAAAACGAGG	AGATAAAATT
msa20031.2{100_M732}	GCTATGCATC	AAAAACGAGG	AGATAAAATT
msa20031.2{100_M781}	GCTATGCATC	AAAAACGAGG	AGATAAAATT
msa20031.2{100_090}	GCTATGCATC	AAAAACGAGG	AGATAAAATT
Consensus	*****	*****	*****

Table 40: Comparative Sequences relating to SAG0635

msa20031.2{100_090}	GCTATGCATC	AAAAACGAGG	AGATAAAATT	GT'TTTTATAA	CAGGTAGGAC
Consensus	*****	*****	*****	*****	*****
msa20031.2{100_18RS21}	351				400
msa20031.2{100_2603}	AAGAGGGTCA	ATGTATAAGG	AGGGCGAGGT	TGATAAAACA	GCTAAAGCCT
msa20031.2{100_A909}	AAGAGGGTCA	ATGTATAAGG	AGGGCGAGGT	TGATAAAACA	GCTAAAGCCT
msa20031.2{100_CJB110}	AAGAGGGTCA	ATGTATAAGG	AGGGCGAGGT	TGATAAAACA	GCTAAAGCCT
msa20031.2{100_COH1}	AAGAGGGTCA	ATGTATAAGG	AGGGCGAGGT	TGATAAAACA	GCTAAAGCCT
msa20031.2{100_JM9130013}	AAGAGGGTCA	ATGTATAAGG	AGGGCGAGGT	TGATAAAACA	GCTAAAGCCT
msa20031.2{100_M732}	AAGAGGGTCA	ATGTATAAGG	AGGGCGAGGT	TGATAAAACA	GCTAAAGCCT
msa20031.2{100_M781}	AAGAGGGTCA	ATGTATAAGG	AGGGCGAGGT	TGATAAAACA	GCTAAAGCCT
msa20031.2{100_090}	AAGAGGGTCA	ATGTATAAGG	AGGGCGAGGT	TGATAAAACA	GCTAAAGCCT
Consensus	*****	*****	*****	*****	*****
msa20031.2{100_18RS21}	401				450
msa20031.2{100_2603}	TAGCTAAAGA	TTTAAATTA	GACAAACCAA	TTGCTGTAAA	TTATACAGGC
msa20031.2{100_A909}	TAGCTAAAGA	TTTAAATTA	GACAAACCAA	TTGCTGTAAA	TTATACAGGC
msa20031.2{100_CJB110}	TAGCTAAAGA	TTTAAATTA	GACAAACCAA	TTGCTGTAAA	TTATACAGGC
msa20031.2{100_COH1}	TAGCTAAAGA	TTTAAATTA	GACAAACCAA	TTGCTGTAAA	TTATACAGGC
msa20031.2{100_JM9130013}	TAGCTAAAGA	TTTAAATTA	GACAAACCAA	TTGCTGTAAA	TTATACAGGC
msa20031.2{100_M732}	TAGCTAAAGA	TTTAAATTA	GACAAACCAA	TTGCTGTAAA	TTATACAGGC
msa20031.2{100_M781}	TAGCTAAAGA	TTTAAATTA	GACAAACCAA	TTGCTGTAAA	TTATACAGGC
msa20031.2{100_090}	TAGCTAAAGA	TTTAAATTA	GACAAACCAA	TTGCTGTAAA	TTATACAGGC
Consensus	*****	*****	*****	*****	*****
msa20031.2{100_18RS21}	451				500
msa20031.2{100_2603}	GATAAACCTA	AAAAGCCATA	CAAATATGAT	AAATCATATT	ATATTAAGAA
msa20031.2{100_A909}	GATAAACCTA	AAAAGCCATA	CAAATATGAT	AAATCATATT	ATATTAAGAA
msa20031.2{100_CJB110}	GATAAACCTA	AAAAGCCATA	CAAATATGAT	AAATCATATT	ATATTAAGAA
msa20031.2{100_COH1}	GATAAACCTA	AAAAGCCATA	CAAATATGAT	AAATCATATT	ATATTAAGAA
msa20031.2{100_JM9130013}	GATAAACCTA	AAAAGCCATA	CAAATATGAT	AAATCATATT	ATATTAAGAA
msa20031.2{100_M732}	GATAAACCTA	AAAAGCCATA	CAAATATGAT	AAATCATATT	ATATTAAGAA
msa20031.2{100_M781}	GATAAACCTA	AAAAGCCATA	CAAATATGAT	AAATCATATT	ATATTAAGAA
msa20031.2{100_090}	GATAAACCTA	AAAAGCCATA	CAAATATGAT	AAATCATATT	ATATTAAGAA
Consensus	*****	*****	*****	*****	*****
msa20031.2{100_18RS21}	501				550
msa20031.2{100_2603}	ATATGGTTCA	GACATTCATT	ATGGAGATAG	TGATGACGAT	ATTCATGCAG
msa20031.2{100_A909}	ATATGGTTCA	GACATTCATT	ATGGAGATAG	TGATGACGAT	ATTCATGCAG
msa20031.2{100_CJB110}	ATATGGTTCA	GACATTCATT	ATGGAGATAG	TGATGACGAT	ATTCATGCAG
msa20031.2{100_COH1}	ATATGGTTCA	GACATTCATT	ATGGAGATAG	TGATGACGAT	ATTCATGCAG
msa20031.2{100_JM9130013}	ATATGGTTCA	GACATTCATT	ATGGAGATAG	TGATGACGAT	ATTCATGCAG
msa20031.2{100_M732}	ATATGGTTCA	GACATTCATT	ATGGAGATAG	TGATGACGAT	ATTCATGCAG
msa20031.2{100_M781}	ATATGGTTCA	GACATTCATT	ATGGAGATAG	TGATGACGAT	ATTCATGCAG
msa20031.2{100_090}	ATATGGTTCA	GACATTCATT	ATGGAGATAG	TGATGACGAT	ATTCATGCAG
Consensus	*****	*****	*****	*****	*****
msa20031.2{100_18RS21}	551				600
msa20031.2{100_2603}	CTAGGGAGGC	CGGTGCTAGA	CCAATTAGAA	TTTAAAGAGC	ACCTAATTCT
msa20031.2{100_A909}	CTAGGGAGGC	CGGTGCTAGA	CCAATTAGAA	TTTAAAGAGC	ACCTAATTCT
msa20031.2{100_CJB110}	CTAGGGAGGC	CGGTGCTAGA	CCAATTAGAA	TTTAAAGAGC	ACCTAATTCT
msa20031.2{100_COH1}	CTAGGGAGGC	CGGTGCTAGA	CCAATTAGAA	TTTAAAGAGC	ACCTAATTCT
msa20031.2{100_JM9130013}	CTAGGGAGGC	CGGTGCTAGA	CCAATTAGAA	TTTAAAGAGC	ACCTAATTCT
msa20031.2{100_M732}	CTAGGGAGGC	CGGTGCTAGA	CCAATTAGAA	TTTAAAGAGC	ACCTAATTCT
msa20031.2{100_M781}	CTAGGGAGGC	CGGTGCTAGA	CCAATTAGAA	TTTAAAGAGC	ACCTAATTCT
msa20031.2{100_090}	CTAGGGAGGC	CGGTGCTAGA	CCAATTAGAA	TTTAAAGAGC	ACCTAATTCT
Consensus	*****	*****	*****	*****	*****
msa20031.2{100_18RS21}	601				650
msa20031.2{100_2603}	ACAAATCTAC	CTTTACCAGA	AGCTGGAGGC	TACGGTGAAG	AGGTTCTCGA
msa20031.2{100_A909}	ACAAATCTAC	CTTTACCAGA	AGCTGGAGGC	TACGGTGAAG	AGGTTCTCGA
msa20031.2{100_CJB110}	ACAAATCTAC	CTTTACCAGA	AGCTGGAGGC	TACGGTGAAG	AGGTTCTCGA
msa20031.2{100_COH1}	ACAAATCTAC	CTTTACCAGA	AGCTGGAGGC	TACGGTGAAG	AGGTTCTCGA
msa20031.2{100_JM9130013}	ACAAATCTAC	CTTTACCAGA	AGCTGGAGGC	TACGGTGAAG	AGGTTCTCGA
msa20031.2{100_M732}	ACAAATCTAC	CTTTACCAGA	AGCTGGAGGC	TACGGTGAAG	AGGTTCTCGA
msa20031.2{100_M781}	ACAAATCTAC	CTTTACCAGA	AGCTGGAGGC	TACGGTGAAG	AGGTTCTCGA
msa20031.2{100_090}	ACAAATCTAC	CTTTACCAGA	AGCTGGAGGC	TACGGTGAAG	AGGTTCTCGA
Consensus	*****	*****	*****	*****	*****
msa20031.2{100_18RS21}	651	663			
msa20031.2{100_2603}	AAATTCAGCT	TAC			
msa20031.2{100_A909}	AAATTCAGCT	TAC			
msa20031.2{100_CJB110}	AAATTCAGCT	TAC			
msa20031.2{100_COH1}	AAATTCAGCT	TAC			
msa20031.2{100_JM9130013}	AAATTCAGCT	TAC			
msa20031.2{100_M732}	AAATTCAGCT	TAC			

Table 40: Comparative Sequences relating to SAG0635

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msa20031.2{100_M781} AAATTCAGCT TAC
msa20031.2{100_090} AAATTCAGCT TAC
Consensus ***** ***

SEQ ID NO 4010 : SAG0653 FROM THE 2603 V/R GBS TYPE V STRAIN
KGPKVAYTQEGMTALSDTNKDKVTTISIDEIQKSLEGKKPITVSFDIDDTLLFSSQYFQY
GKEYVTPGSDFDLHKQKFWDLVAKRGDQDSIPKEYAKKLIAMHQKRGDKIVFITGRTRGS
MYKEGEVDKTAALAKDFKLDKPIAVNYTGDKPKPKPYKYDKSYYIKKYGSDIHYGSDDD
IHAAREAGARPRIILRAPNSTNLPLPEAGGYGEEVLENSAY

SEQ ID NO 4011 : SAG0653 FROM THE 090 GBS TYPE III STRAIN
KGPKVAYTQEGMTALSDTNKDKVTTISIDEIQKSLEGKKPITVSFDIDDTLLFSSQYFQY
GKEYVTPGSDFDLHKQKFWDLVAKRGDQDSIPKEYAKKLIAMHQKRGDKIVFITGRTRGS
MYKEGEVDKTAALAKDFKLDKPIAVNYTGDKPKPKPYKYDKSYYIKKYGSDIHYGSDDD
IHAAREAGARPRIILRAPNSTNLPLPEAGGYGEEVLENSAY

SEQ ID NO 4012 : SAG0653 FROM THE A909 GBS TYPE Ia STRAIN
KGPKVAYTQEGMTALSDTNKDKVTTISIDEIQKSLEGKKPITVSFDIDDTLLFSSQYFQY
GKEYVTPGSDFDLHKQKFWDLVAKRGDQDSIPKEYAKKLIAMHQKRGDKIVFITGRTRGS
MYKEGEVDKTAALAKDFKLDKPIAVNYTGDKPKPKPYKYDKSYYIKKYGSDIHYGSDDD
IHAAREAGARPRIILRAPNSTNLPLPEAGGYGEEVLENSAY

SEQ ID NO 4013 : SAG0653 FROM THE 18RS21 GBS TYPE II STRAIN
KGPKVAYTQEGMTALSDTNKDKVTTISIDEIQKSLEGKKPITVSFDIDDTLLFSSQYFQY
GKEYVTPGSDFDLHKQKFWDLVAKRGDQDSIPKEYAKKLIAMHQKRGDKIVFITGRTRGS
MYKEGEVDKTAALAKDFKLDKPIAVNYTGDKPKPKPYKYDKSYYIKKYGSDIHYGSDDD
IHAAREAGARPRIILRAPNSTNLPLPEAGGYGEEVLENSAY

SEQ ID NO 4014 : SAG0653 FROM THE COH1 GBS TYPE III STRAIN
KGPKVAYTQEGMTALSDTNKDKVTTISIDEIQKSLEGKKPITVSFDIDDTLLFSSQYFQY
GKEYVTPGSDFDLHKQKFWDLVAKRGDQDSIPKEYAKKLIAMHQKRGDKIVFITGRTRGS
MYKEGEVDKTAALAKDFKLDKPIAVNYTGDKPKPKPYKYDKSYYIKKYGSDIHYGSDDD
IHAAREAGARPRIILRAPNSTNLPLPEAGGYGEEVLENSAY

SEQ ID NO 4015 : SAG0653 FROM THE M781 GBS TYPE III STRAIN
KGPKVAYTQEGMTALSDTNKDKVTTISIDEIQKSLEGKKPITVSFDIDDTLLFSSQYFQY
GKEYVTPGSDFDLHKQKFWDLVAKRGDQDSIPKEYAKKLIAMHQKRGDKIVFITGRTRGS
MYKEGEVDKTAALAKDFKLDKPIAVNYTGDKPKPKPYKYDKSYYIKKYGSDIHYGSDDD
IHAAREAGARPRIILRAPNSTNLPLPEAGGYGEEVLENSAY

SEQ ID NO 4016 : SAG0653 FROM THE CJB110 GBS NONTYPEABLE STRAIN
KGPKVAYTQEGMTALSDTNKDKVTTISIDEIQKSLEGKKPITVSFDIDDTLLFSSQYFQY
GKEYVTPGSDFDLHKQKFWDLVAKRGDQDSIPKEYAKKLIAMHQKRGDKIVFITGRTRGS
MYKEGEVDKTAALAKDFKLDKPIAVNYTGDKPKPKPYKYDKSYYIKKYGSDIHYGSDDD
IHAAREAGARPRIILRAPNSTNLPLPEAGGYGEEVLENSAY

SEQ ID NO 4017 : SAG0653 FROM THE JM9130013 GBS TYPE VIII STRAIN
KGPKVAYTQEGMTALSDTNKDKVTTISIDEIQKSLEGKKPITVSFDIDDTLLFSSQYFQY
GKEYVTPGSDFDLHKQKFWDLVAKRGDQDSIPKEYAKKLIAMHQKRGDKIVFITGRTRGS
MYKEGEVDKTAALAKDFKLDKPIAVNYTGDKPKPKPYKYDKSYYIKKYGSDIHYGSDDD
IHAAREAGARPRIILRAPNSTNLPLPEAGGYGEEVLENSAY

SEQ ID NO 4018 : SAG0653 FROM THE M732 GBS TYPE III STRAIN
KGPKVAYTQEGMTALSDTNKDKVTTISIDEIQKSLEGKKPITVSFDIDDTLLFSSQYFQY
GKEYVTPGSDFDLHKQKFWDLVAKRGDQDSIPKEYAKKLIAMHQKRGDKIVFITGRTRGS
MYKEGEVDKTAALAKDFKLDKPIAVNYTGDKPKPKPYKYDKSYYIKKYGSDIHYGSDDD
IHAAREAGARPRIILRAPNSTNLPLPEAGGYGEEVLENSAY

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Table 40: Comparative Sequences relating to SAG0635

PRETTY of: /biotmp/msa25122.2{*} August 5, 2002 07:09 ..

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1                                     50
msa25122.2{100_090} KGPVKVAYTQE GMTALSDTNK DKVTTISIDE IQKSLEGKKP ITVSFDIDDT
msa25122.2{100_18RS21} KGPVKVAYTQE GMTALSDTNK DKVTTISIDE IQKSLEGKKP ITVSFDIDDT
msa25122.2{100_2603} KGPVKVAYTQE GMTALSDTNK DKVTTISIDE IQKSLEGKKP ITVSFDIDDT
msa25122.2{100_A909} KGPVKVAYTQE GMTALSDTNK DKVTTISIDE IQKSLEGKKP ITVSFDIDDT
msa25122.2{100_CJB110} KGPVKVAYTQE GMTALSDTNK DKVTTISIDE IQKSLEGKKP ITVSFDIDDT
msa25122.2{100_COH1} KGPVKVAYTQE GMTALSDTNK DKVTTISIDE IQKSLEGKKP ITVSFDIDDT
msa25122.2{100_JM9130013} KGPVKVAYTQE GMTALSDTNK DKVTTISIDE IQKSLEGKKP ITVSFDIDDT
msa25122.2{100_M732} KGPVKVAYTQE GMTALSDTNK DKVTTISIDE IQKSLEGKKP ITVSFDIDDT
msa25122.2{100_M781} KGPVKVAYTQE GMTALSDTNK DKVTTISIDE IQKSLEGKKP ITVSFDIDDT
Consensus *****

51                                     100
msa25122.2{100_090} LLFSSQYFQY GKEYVTPGSF DFLHKQKFWD LVAKRGDQDS IPKEYAKKLI
msa25122.2{100_18RS21} LLFSSQYFQY GKEYVTPGSF DFLHKQKFWD LVAKRGDQDS IPKEYAKKLI
msa25122.2{100_2603} LLFSSQYFQY GKEYVTPGSF DFLHKQKFWD LVAKRGDQDS IPKEYAKKLI
msa25122.2{100_A909} LLFSSQYFQY GKEYVTPGSF DFLHKQKFWD LVAKRGDQDS IPKEYAKKLI
msa25122.2{100_CJB110} LLFSSQYFQY GKEYVTPGSF DFLHKQKFWD LVAKRGDQDS IPKEYAKKLI
msa25122.2{100_COH1} LLFSSQYFQY GKEYVTPGSF DFLHKQKFWD LVAKRGDQDS IPKEYAKKLI
msa25122.2{100_JM9130013} LLFSSQYFQY GKEYVTPGSF DFLHKQKFWD LVAKRGDQDS IPKEYAKKLI
msa25122.2{100_M732} LLFSSQYFQY GKEYVTPGSF DFLHKQKFWD LVAKRGDQDS IPKEYAKKLI
msa25122.2{100_M781} LLFSSQYFQY GKEYVTPGSF DFLHKQKFWD LVAKRGDQDS IPKEYAKKLI
Consensus *****

101                                    150
msa25122.2{100_090} AMHQKRGDKI VFITGRTRGS MYKEGEVDKT AKALAKDFKL DKPIAVNYTG
msa25122.2{100_18RS21} AMHQKRGDKI VFITGRTRGS MYKEGEVDKT AKALAKDFKL DKPIAVNYTG
msa25122.2{100_2603} AMHQKRGDKI VFITGRTRGS MYKEGEVDKT AKALAKDFKL DKPIAVNYTG
msa25122.2{100_A909} AMHQKRGDKI VFITGRTRGS MYKEGEVDKT AKALAKDFKL DKPIAVNYTG
msa25122.2{100_CJB110} AMHQKRGDKI VFITGRTRGS MYKEGEVDKT AKALAKDFKL DKPIAVNYTG
msa25122.2{100_COH1} AMHQKRGDKI VFITGRTRGS MYKEGEVDKT AKALAKDFKL DKPIAVNYTG
msa25122.2{100_JM9130013} AMHQKRGDKI VFITGRTRGS MYKEGEVDKT AKALAKDFKL DKPIAVNYTG
msa25122.2{100_M732} AMHQKRGDKI VFITGRTRGS MYKEGEVDKT AKALAKDFKL DKPIAVNYTG
msa25122.2{100_M781} AMHQKRGDKI VFITGRTRGS MYKEGEVDKT AKALAKDFKL DKPIAVNYTG
Consensus *****

151                                    200
msa25122.2{100_090} DKPKKPYKYD KSYIICKYGS DIHYGDSDDD IHAAREAGAR PIRILRAPNS
msa25122.2{100_18RS21} DKPKKPYKYD KSYIICKYGS DIHYGDSDDD IHAAREAGAR PIRILRAPNS
msa25122.2{100_2603} DKPKKPYKYD KSYIICKYGS DIHYGDSDDD IHAAREAGAR PIRILRAPNS
msa25122.2{100_A909} DKPKKPYKYD KSYIICKYGS DIHYGDSDDD IHAAREAGAR PIRILRAPNS
msa25122.2{100_CJB110} DKPKKPYKYD KSYIICKYGS DIHYGDSDDD IHAAREAGAR PIRILRAPNS
msa25122.2{100_COH1} DKPKKPYKYD KSYIICKYGS DIHYGDSDDD IHAAREAGAR PIRILRAPNS
msa25122.2{100_JM9130013} DKPKKPYKYD KSYIICKYGS DIHYGDSDDD IHAAREAGAR PIRILRAPNS
msa25122.2{100_M732} DKPKKPYKYD KSYIICKYGS DIHYGDSDDD IHAAREAGAR PIRILRAPNS
msa25122.2{100_M781} DKPKKPYKYD KSYIICKYGS DIHYGDSDDD IHAAREAGAR PIRILRAPNS
Consensus *****

201                                    221
msa25122.2{100_090} TNLPLPEAGG YGEEVLENSA Y
msa25122.2{100_18RS21} TNLPLPEAGG YGEEVLENSA Y
msa25122.2{100_2603} TNLPLPEAGG YGEEVLENSA Y
msa25122.2{100_A909} TNLPLPEAGG YGEEVLENSA Y
msa25122.2{100_CJB110} TNLPLPEAGG YGEEVLENSA Y
msa25122.2{100_COH1} TNLPLPEAGG YGEEVLENSA Y
msa25122.2{100_JM9130013} TNLPLPEAGG YGEEVLENSA Y
msa25122.2{100_M732} TNLPLPEAGG YGEEVLENSA Y
msa25122.2{100_M781} TNLPLPEAGG YGEEVLENSA Y
Consensus *****

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Table 41: Comparative Sequences relating to SAG0649

SEQ ID NO. 4101: SAG0649 FROM 2603 V/R GBS TYPE V STRAIN
 ATGAAAAAGAGACAAAAATA
 TGGAGAGGGTTATCACTTACTTAACTCCTGTCCCAAATTCATTGGGTATATGGTA
 CAAGGTGAACCCCAAGATACCAATCAAGCACTTGGAAAAAGTAATGTAAAAAACCGGA
 GACAAATGCTACACCAATTAGGCAAGCGACTTTTGTGTTAAAAAATGACAAATGATAAGTCA
 GAAACAAAGTCACGAAACCGGTAGAGGGTTCTGGAGAAGCAACCTTTGAAAAACATAAAACCT
 GGAGACTACACATTAAAGAGAAGAAACAGCAACCAATTTGGTTATAAAAAAATGATAAAACC
 TGGAAAGTTAAAGTTGCAGATAACGGAGCAACAATAATCGAGGGTATGGATGCAGATAAA
 GCAGAGAAACGAAAGAAAGTTTGAATGCCCAATATCCAAATCAGCTATTTATGAGGAT
 ACAAAGAAAATTACCCATTAGTTAATGTAGAGGGTTCCAAAGTTGGTGAACAATACAAA
 GCATTGAATCCAATAAATGAAAAAGATGGTGAAGAGAGATTGCTGAAGGTTGGTTATCA
 AAAAAAATACAGGGGTCATGATCTCGATAAGAAATAAATAAATAAATGAATTAACCTGTT
 GAGGGTAAAAACCACTGTTGAAACGAAAGAACTTAATCAACCACTAGATGTCGTTGTGCTA
 TTAGATAATTCAAATAGTATGAATAATGAAAGAGCCAAATAATCTCAAGAGCATTAAAA
 GCTGGGGAAGCAGTTGAAAGCTGATTGATAAAATTACATCAAATAAAGACAATAGAGTA
 GCTCTGTGACATATGCCCTCAACCAATTTTGTATGGTACTGAAGCGACCGTATCAAAGGGA
 GTTGGCGATCAAAATGGTAAAGCGCTGAATGATAGTGTATCATGGGATTATCATAAAACT
 ACTTTTACAGCAACTACACATAATTACAGTTATTTAAATTTAACAAGATGCTAACGAA
 GTTAATATTCTAAAGTCAAGAAATCCAAAGGAAGCGGAGCATATAAATGGGGATCGCAGC
 CTCTATCAATTTGGTGGCAGATTACTCAAAAAGCTCTAATGAAAGCAATGAATTTTA
 GAGACACAAGTTCTAATGCTAGAAAAAACTTATTTTACGTTAATGATGGTGTCCCT
 ACGATGCTTATGCCATAAATTTTAACTCTTATATATCAACATCTTACCAAAACCACTTT
 AATTCTTTTAAATAAAAATACAGATAGAAGTGGTATTCTCCAAGAGGATTTATAATC
 AATGGTGTATGATTATCAATAGTAAAGGAGATGGAGAGAGTTTAACTGTTTTCGGAT
 AGAAAAGTTCCTGTTTACTGGAGGAACGACACAAGCAGCTTATCGAGTACCGCAAAATCAA
 CTCTCTGATAGTATGAGGGATATGCAATTAATAGTGGATATATTTATCTCTATTTGG
 AGGATTACAACCTGGGTCATATCCATTGTATCCCTAAGACAAGAAAGTTTCTGCAACGAAA
 CAAATCAAACTCATGGTGAAGCAACCACTTATCTTTAATGGAAATATAAGACCTAAA
 GGTATGACATTTTACTGTTGGGATTTGGTGTAAACGGAGATCCTGGTGAACCTCTCTT
 GAAGCTGAGAAATTTATGCAATCAATATCAAGTAAACAGAAAAATTAATACTAATGTTGAT
 GATACAAATAAAATTTATGATGAGCTAAATAAATACTTTAAAAACAATTTGTTGAGGAAAA
 CATTCTATTTGTTGATGGAAATGTGACTGATCCTATGGGAGAGATGATGAATTTCAATTA
 AAAAAATGGTCAAAGTTTACACATGATGATTACGTTTGGTTGGAATGATGGCAGTCAA
 TTAATAAAATGGTGTGGCTCTTGGTGGACCAACAGTGTGGGGAAATTTTAAAGATGTT
 ACAGTGATCTTATGATAAGACATCTCAACCATCAAAATCAATCATTTGAACCTTAGGAAGT
 GGACAAAAAGTAGTTCTTACCTATGATGATGCTTTAAAGATAACTATATAAGTAACAAA
 TTTTACAATACAATAATCGTACAACGCTAAGTCCGAAGAGTGAAGAAAGAACCAATACT
 ATTCGTGATTTCCCAATTTCCCAAAATTCGTGATGTTCTGTGAGTTTCCGGTACTAACCATC
 AGTAATCAGAAGAAATGGGTGAGGTTGAATTTATTAAGTTAATAAAGACAACCAATCA
 GAATCGCTTTTGGAGCTAAGTTTCAACTTCAGATAGAAAAAGATTTTCTGGGTATAAG
 CAATTTGTTCCAGAGGGAAGTGTATGATACAAACAAAGATGATGGTAAAAATTTATTTAAA
 GCACCTCAAGATGGTAACTATAAATTATATGAAATTTCAAGTCCAGATGGCTATATAGAG
 GTTAAACGAAACCTGTTGTGACATTACAATTCAAATGGAGAAAGTTACGAACCTGAAA
 GCAGATCCAAATGCTAATAAAAAATCAAATCGGGTATCTTGAAGGAAATGGTAAACATCTT
 ATTACCAACACTCCCAACGCCCAACAGGTGTTTCTTAAACAGGGGGAATGGGTACA
 ATTTGCTATATATAGTTGGTTTACTTTTATGATACCTTACCATTGTTCTTTCCGTGCT
 AAACAATTG

SEQ ID NO. 4102: SAG0649 FROM 090 GBS TYPE Ia STRAIN
 GGTGAACCCCAAGATACCAATCAAGCACTTGGAAAAAG
 TAATTTGTTAAAAAACCGGAGACAATGCTACACCAATTAGGCAAGCGACT
 TTTGTTGTTAAAAAATGACAAATGATAAGTCAGAAACAAGTCACGAAACGGT
 AGAGGGTTCTGGAGAAGCAACCTTTGAAAAACATAAAACCTGGAGACTACA
 CATTAAAGAGAAGAAACAGCAACCAATTTGGTTATAAAAAAATGATAAAACC
 TGGAAAGTTAAAGTTGCAGATAACGGAGCAACAATAATCGAGGGTATGGA
 TGCAGATAAAGCAGAGAAACGAAAGAAAGTTTGAATGCCCAATATCCAA
 AATCAGCTATTTATGAGGATACAAAAGAAATTTACCCATTAGTTAATGTA
 GAGGGTTCCAAAGTTGGTGAACAAATACAAAGCAATGAATCCAATAAATGG
 AAAAGATGGTGAAGAGAGATTGCTGAAGGTTGGTTATCAAAAAAATTA
 CAGGGGTCAATGATCTCGATAAGAAATAAATAAATTTGAATTAACGTGT
 GAGGGTAAAAACCACTGTTGAAACGAAAGAACTTAATCAACCACTAGATGT
 CGTTGTGCTATTAGATAAATCAAATAGTATGAATAATGAAGAGCCAATA
 ATTTCTCAAGAGCATTAAAAAGCTGGGAAGCAGTTGAAAGCTGATTGAT
 AAAATTACATCAAATAAAGCAATAGAGTAGCTCTTGTGACATATGCCCTC
 AACCATTTTGTATGGTACTGAAGCGACCGGTATCAAGGGAGTTGCCGATC
 AAAATGGTAAAGCGCTGAATGATAGTGTATCATGGGATTATCATAAAACT
 ACTTTTACAGCAACTACACATAATTACAGTTATTTAAATTTAACAATGA
 TGCTAACGAAGTTAATATTCTAAGTCAAGAAATTCAAAGGAAGCGGAGC
 ATATAAATGGGGATCGCAGCTCTATCAATTTGGTGGCAGATTACTCAA
 AAGCTCTAATGAAAGCAATGAATTTTATAGACACAAAGTTCTAATGTC
 TAGAAAAAACTTATTTTACGTAACCTGATGGTGTCCCTACGATGTCCT
 ATGCCATAAATTTAATCCTTATATATCAACATCTTACCAAAACCACTTT
 AATTCTTTTAAATAAATAAACCAGATAGAAGTGGTATTCTCAAGAGGA
 TTTTATAATCAATGGTGTATGATTCAATAGTAAAGGAGATGGAGAGA
 GTTTTAACTGTTTTCGGATAGAAAAGTTCTGTACTGGAGGAACGACA
 CAAGCAGCTTATCGAGTACCGCAAAATCAACTCTCTGTAATGAGTAATGA
 GGGATATGAATTAATAGTGGATATATTtCTCTATTGGAGAGATTACA
 ACTGGGTCTATCCATTGATCCTAAGACAAGAAAGTTCTGCAACGAAA
 CAAATCAAACTCATGGTGAAGCAACCACTTATCTTTAATGGAATAT
 AAGACCTAAAGGTTATGACATTTTACTGTTGGGATTTGGTGTAAACGGAG
 ATCTTGGTGCAACTCTCTTGAAGCTGAGAAATTTATGCAATCAATATCA
 AGTAAACAGAAATTTATACTAATGTTGATGATACAAATAAATTTATGA
 TGAGCTAAATAAATACCTTTTAAACAATTTGTTGAGGAAAAACATTTCTATTG

Table 41: Comparative Sequences relating to SAG0649

TTGATGGAAATGTGACTGATCCTATGGGAGAGATGATTGAATTCGAATTA
 AAAAAATGGTCAAAGTTTACACATGATGATTACGCTTTGGGCTGGAAATGA
 tGGCAGTCAATTAAAAAATGGTGTGGCTCTTGGTGGACCAACAGTGTATG
 GGGGAATTTTAAAAAGATGTTACAGTGACTTATGATAAGACATCTCAAACC
 ATCAAAATCAATCATTTGAACCTAGGAAGTGGACAAAAGTAGTTCTTAC
 CTATGATGTACGTTTAAAAAGATACTATATAAGTAACAAATTTTACAATA
 CAAATTAATCGTACAACGCTAAGTCCGAAGAGTGAAGAAACCAAAATACT
 ATTCTGTGATTTCCCAATTCCCAAAATTCGTGATGTTCTGTGAGTTTCCGGT
 ACTAACCATCAGTAATCAGAAGAAAATGGGTGAGGTGGAATTTATTAAAG
 TTAATAAAGACAAACATTCAGAAATCGCTTTTGGGAGCTAAGTTTCAACTT
 CAGATAGAAAAAGATTTTCTGGGTATAAGCAATTTGTTCCAGAGGGAAG
 TGATGTTACAACAAAGATGATGGTAAAAATTTATTTTAAAGCACTTCAAG
 ATGGTAACTATAAATTATATGAATTTCAAGTCCAGATGGCTATATAGAG
 GTTAAAAAGAAACCTGTGTGACATTTACAAATCAAATGGAGAAGTTAC
 GAACCTGAAAGCAGATCCAAATGCTAATAAAAAATCAAATCGGGTATCTTG
 AAGGAAATGGTAAACATCTTATTACCAACACTCCCAACGCCACCAGGT
 GTT

SEQ ID NO. 4103: SAG0649 FROM A909 GBS TYPE 1a STRAIN

GGTGAACCCCAAGATACCAATCAAGCACTTGGAAAA
 GTAATTGTAAAAAAGCGGGGACCAATGCTACACCATTAGGCAAAGCGAC
 TTTTGTGTTAAAAAATGACAAATGATAAGTCAGAAACAAAGTCAAGAAACGG
 TAGAGGGTTCTGGAGAAgCAACCTTTGAAAACATAAAACCTGGAGACTAC
 ACATTAAGAGAAGAAACAGCAACCAATTTGGTTATAAAAAAATGATAAAAC
 CTGGAAGATTAAAGTTGCAGATAACGGAGCAACAATAATCGAGGGTATGG
 ATGCAGATAAAGCAGAGAAACGAAAAGAGTTTGAATGCCCAATATCCA
 AATCAGCTATTTATGAGGATACAAAAGAAAATTAACCATTAgtTAAATGT
 AGAGGGTTCCAAAGTTGGTGAACAATAACAAGCATTGAATCCAAATAAATG
 GAAAAGATGGTCGAAGAGAGATTGCTGAAGGTTGGTTATCAAAAAAATTT
 ACAGGGGTCAATGATCTCGATAAGAAATAAATATAAAATTTGAATTAATCTG
 TGAGGGTAAACCACTGTTGAAACGAAAGAACTTAATCAACCACTAGATG
 TCGTTGTGCTATTAGATAAATCAAAATAGTATGAATAATGAAGAGCCAAT
 AATTTCTAAAGAGCATTAAAAGCTGGGGAAGCAGTTGAAAAGCTGATTGA
 TAAAAATACATCAAAATAAGACAAATAGAGTAGCTCTTGTGACATATGCCT
 CAACCATTTTGTGATGGTACTGAAGCGACCGTATCAAGGGAGTTTCCGGAT
 CAAAATGGTAAAGCGCTGAATGATAGTGTATCATGGGATTTATCATAAAAAC
 TACTTTTACAGCAACTACACATAATTACAGTTATTTAAATTTAAACAAATG
 ATGCTAACGAAGTTAATATTCTAAAGTCAAGAATTTCCAAAGGAAGCGGAG
 CATATAAATGGGATCGCAGCTCTATCAATTTGGTGGCAGATTTACTCA
 AAAAGCTCTAATGAAGCAAAATGAAATTTTAGAGACACAAAGTTCTAATG
 CTAGAAAAAACTTTATTTTCAAGTAACTGATGGTGTCCCTACGATGTCT
 TATGCCATAAATTTAATCCTTATATATCAACATCTTACCAAAACCAAGTT
 TAATTTCTTTTAAATAAAATACAGATAGAAGTGGTATTCTCCAGAGGG
 ATTTTATAATCAATGGTGTGATGATTATCAAAATAGTAAAGGAGATGGAGAG
 AGTTTAAACTGTTTTCCGGATAGAAAAAGTTCTCTTACTGGAGGAACGAC
 ACAAGCAGCTTATCGAGTACCGCAAAATCAACTCTCTGTAATGAGTAATG
 AGGGATATGCAATTAAATAGTGGATATATTTATCTCTATTGGAGAGATTAC
 AACTGGGTCTATCCATTGATCTTAAGACAAAGAAAGTTCTGCAACGAA
 ACAAAATCAAACCTCATGGTGAAGCCAAACATTATACTTTAAATGGAATA
 TAAGACCTAAAGGTTATGACATTTTACTGTGTGGATTGGTGTAAACGGA
 GATCCTGGTGCAACTCTCTTGAAGCTGAGAAATTTATGCAATCAATATC
 AAGTAAACAGAAAATTTATACTAATGTTGATGATACAAATAAAATTTATG
 ATGAGCTAAATAAATCTTTAAAAACAATTTGTTGAGGAAAAACATTCTATT
 GTTGATGGAATGTGACTGATCTTATGGGAGAGATGATTGAATTTCAATTT
 AAAAAATGGTCAAAGTTTACACATGATGATTACGCTTTTGGTGGAAATG
 AtGGCAGTCAATTAAAAAATGGTGTGGCTCTTGGTGGACCAACAGTGAT
 GGGGGAATTTTAAAGATGTTACAGTGACTTATGATAAGACATCTCAAC
 CATCAAAATCAATCATTTGAACCTAGGAAGTGGACAAAAGTAGTTCTTA
 CCTATGATGTACGTTTAAAGATAACTATATAAGTAACAAATTTTACAAT
 ACAAAATATCGTACAACGCTAAGTCCGAAGAGTGAAGAAACCAAAATAC
 TATTCTGTGATTTCCCAATTCCCAAAATTCGTGATGTTCTGTGAGTTTCCGG
 TACTAACCATCAGTAATCAGAAGAAAATGGGTGAGGTGGAATTTATTAA
 GTTAATAAAGACAAACATTCAGAAATCGCTTTTGGGAGCTAAGTTTCAACT
 TCAGATAGAAAAAGATTTTCTGGGTATAAGCAATTTGTTCCAGAGGGA
 GTGATGTTACAACAAAGAAATGATGGTAAAAATTTATTTTAAAGCACTTCAA
 GATGGTAACTATAAATTATATGAATTTCAAGTCCAGATGGCTATATAGA
 GGTTAAACGAAACCTGTTGTGACATTTACAATCAAATGGAGAAGTTA
 CGAACCTGAAAGCAGATCCAAATGCTAATAAAAAATCAAATCGGGTATCTT
 GAAGGAAATGGTAAACATCTTATTACCAACACTCCCAACGCCACCAGG
 TGT

SEQ ID NO. 4104: SAG0649 FROM 18RS21 GBS TYPE II STRAIN

GGTGAACCCCAAGATACCAATCAAGCAC
 TTGGAAGTAATTTGTTAAAAAAGCGGGAGACAAAGTACACCATTAGGC
 AAAGCGACTTTTGTGTTAAAAAATGACAAATGATAAGTCAGAAACAAAGTCA
 CGAAACGGTAGAGGGTTCTGGAGAAgCAACCTTTGAAAACATAAAACCTG
 GAGACTACACATTAAGAGAAGAAACAGCAACCAATTTGGTTATAAAAAAAT
 GATAAAACCTGGAAGTTAAAGTTGCAGATAACGGAGCAACAATAATCGA
 GGGTATGGATGCAGATAAAGCAGAGAAACGAAaAGAAGTTTGAATGCC
 AATATCAAAATCAGCTATTATGAGGATACAAAAGAAAATTAACCATTA
 GTTAATGTAGAGGGTTCCAAAGTTGGTGAACAATAACAAGCATTGAATCC
 AATAAATGGAAAGATGGTCGAAGAGAGATTGCTGAAGGTGGTTATCAA
 AAAAAATTaCaGGGGTCAATGATCTCGATAAGAAATAAATAAATTTGAA

Table 41: Comparative Sequences relating to SAG0649

TTAACTGTTGAGGGTAAACCACTGTTGAAACGAAAGAACTTAATCAACC
 ACTAGATGTCGTTGTGCTATTAGATAATTCAAATAGTATGAATAATGAAA
 GAGCCAAATATTCTCAAGAGCATTAAAGCTGGGAGCAGTTGAAAAG
 CTGATTGATAAAATTACATCAAATAAAGCAATAGAGTAGCTCTTGTGAC
 ATATGCTCAACCATTTTGTATGTTACTGAAGCGACCGTATCAAGGGGAG
 TTGCCGATCAAAATGGTAAAGCGCTGAATGATAGTGTATCATGGGATTAT
 CATAAACTACTTTTACAGCACTACACATAATTACAGTTATTTAAATTT
 AACAAATGATGCTAACGAAGTTAATATTCTAAAGTCAAGAATTCCAAAGG
 AAGCGGAGCATATAAATGGGGATCGCACGCTCTATCAATTTGGTGCGACA
 TTACTCAAAAAGCTCTAATGAAGCAAAATGAAATTTTAGAGACACAAAG
 TTCTAATGCTAGAAAAAACTTATTTTTCACGTAACCTGATGGTGTCCCTA
 CGATGCTTATGCCATAAATTTAATCCTTATATATCAACATCTTACCAA
 AACCAATTTAATTTCTTTTAAATAAATAACCAGATAGAAGTGGTATTCT
 CCAAGAGGATTTTATAATCAATGGTGTATGATTATCAAATAGTAAAAGGAG
 ATGGAGAGAGTTTAAACTGTTTTTCGGATAGAAAAGTTCCTGTTACTGGA
 GGAACGACACAAGCAGCTTATCGAGTACCGCAAAATCAACTCTCTGTAAT
 GAGTAATGAGGGATATGCAATTAATAGTGGATATTTATCTCTATTGGA
 GAGATTACAACCTGGGTCTATCCATTTGATCCTAAGACAAAGAAAGTTCT
 GCAACGAAACAAATCAAACTCATGGTGAGCCAACACATTATACCTTTAA
 TGGAAATATAAGACCTAAAGGTTATGACATTTTACTGTTGGGATTTGGTG
 TAAACGGAGATCCTGGTGCAACTCCTCTGAAGCTGAGAAATTTATGCAA
 TCAATATCAAGTAAACAGAAAATATATACTAATGTTGATGATACAAATAA
 AATTTATGATGAGCTAAATAAATACTTTAAACAATTTGTTGAGGAAAAAC
 ATTCTATGTTGATGGAATGTGACTGATCCTATGGGAGAGATGATTGAA
 TTCCAATTAATAAATGGTCAAAGTTTACACATGATGATTACGTTTGGT
 TGGAAATGATGGCAGTCAATTAATAAATGGTGTGGCTCTTGGTGGACCA
 ACAGTATGAGGGGAAATTTAAAGATGTTACAGTGACTTATGATAAGACA
 TCTCAAAACCATCAAAATCAATCATTTGAACCTAGGAAGTGGACAAAAAGT
 AGTTCTTACCTATGATGACGTTTAAAGATACTATATAAGTAACAAAT
 TTTACAATACAAAATAATCGTACACGCTAAGTCCGAAGAGTGAAGAAAGAA
 CCAATACTATt cGtgATTt CCCAATTCCTCAAAATTCGTGATGTTCTGTA
 GTTTCGGTACTAACCATCAGTAATCAGAAGAAAATGGGTGAGGTTGAAT
 TTATTAAAGTTAATAAAGACAAACATTCAAGATCGCTTTTGGGAGCTAAG
 TTTCAACTTCAGATAGAAAAGATTTTCTGGGTATAAGCAATTTGTTCC
 AGAGGGAAGTGAATGTTACAACAAAGAAATGATGGTAAATTTATTTTAAAG
 CACTTCAAGATGGTAACTATAAATATATGAAATTTCAAGTCCAGATGGC
 TATATAGAGGTTAAACGAAACCTGTTGTGACATTTCAATTCAAAATGG
 AGAAGTTACGAACCTGAAAGCAGATCCAAATGCTAATAAATAAATCAATCG
 GGTATCTGAAGGAAATGGTAAACATCTTATTACCAACACTCCCAACGCG
 CCACCAGGTGT

SEQ ID NO. 4105: SAG0649 FROM M732 GBS TYPE III STRAIN
 GGTGAACCCCAAGATACCAATCAAGCACT

TGGAAAAGTAATTTGTTAAAAAACGGGAGACAAaTGCTACACCATTAGGCA
 AAGCGACTTTTGTGTTAAAAAATGACAATGATAAGTCAGAAACAAAGTCAC
 GAAACCGTAGAGGGTTCTGGAGAGCAACCTTTGAAAACATAAAACCTGG
 AGACTACACATTAAGAGAAGAAACAGCACCAATGGTTATAAAAAAACTG
 ATAAACCTGGAAAGTTAAAGTTGCAGATAACGGAGCAACAAATATCGAG
 GGTATGGATGCAGATAAAGCAGAGAAACGAAAAGAAAGTTTGAATGCCCA
 ATATCCAAATCAGCTATTATGAGGATACAAAAGAAAATTACCAATTAG
 TTAATGTAGAGGGTCCAAAGTTGGTGAAACAAATACAAGCATGGAATCCA
 ATAAATGGAAAAGATGGTGAAGAGAGATTGCTGAAGGTTGGTTATCAAA
 AAAAAaTaCaGGGGTCAATGATCTCGATAAGAATAAATATAAATTTGAAT
 TAATGTTGAGGGTAAACCACTGTTGAAAACGAAAGAACTTAATCAACCA
 CTAGATGTCGTTGTGCTATTAGATAAATCAAATAGTATGAATAATGAAAG
 AGCCAATAATTTCTCAAGAGCATTAAAGCTGGGGAAGCAGTTGAAAAGC
 TGATTGATAAAATTACATCAAAATAAGACAAATAGAGTAGCTCTTGTGACA
 TATGCCCTCAACCATTTTGTATGTTACTGAAGCGACCGTATCAAGGGGAGT
 TGCCGATCAAAATGGTAAAGCGCTGAATGATAGTGTATCATGGGATTATC
 ATAAACTACTTTTACAGCAACTACACATAATTACAGTTATTTAAATTTA
 ACAATGATGCTAACGAAGTTAATATTCTAAAGTCAAGAATTCCAAAGGA
 AGCGGAGCATATAAATGGGGATCGCACGCTCTATCAATTTGGTGCGACAT
 TTACTCAAAAAGCTCTAATGAAAGCAAATGAAATTTTAGAGACACAAAGT
 TCTAATGCTAGAAAAAACTTATTTTTCACGTAACCTGATGGTGTCCCTAC
 GATGTCCTATGCCATAAATTTAATCCTTATATATCAACATCTTACCAA
 ACCAGTTTAATTTCTTTTAAATAAATAACCAGATAGAAGTGGTATTCTC
 CAAGAGGATTTTATAATCAATGGTGTATGATTATCAAATAGTAAAAGGAGA
 TGAGAGAGGTTTAAACTGTTTTTCGGATAGAAAAGTTCCTGTTACTGGAG
 GAACGACACAAGCAGCTTATCGAGTACCGCAAAATCAACTCTCTGTAATG
 AGTAATGAGGGATATGCAATTAATAGTGGATATATTTATCTCTATTGGAG
 AGATTACAACCTGGGTCTATCCATTTGATCCTAAGACAAAGAAAGTTCTG
 CAACGAAACAAATCAAACTCATGGTGAGCCAACACATTATACCTTTAAT
 GGAATATAAGACCTAAAGGTTATGACATTTTACTGTTGGGATTTGGTGT
 AAACGGAGATCCTGGTGCAACTCCTCTGAAGCTGAGAAATTTATGCAAT
 CAATATCAAGTAAACAGAAAATTATACTAATGTTGATGATACAAATAAA
 ATTTATGATGAGCTAAATAAATACTTTAAACAATTTGTTGAGGAAAAACA
 TTCTATTTGTTGATGGAATGTGACTGATCCTATGGGAGAGATGATTGAAT
 TCCAATTAATAAATGGTCAAAGTTTACACATGATGATTACGCTTTGGCT
 TCGAAATGATGGCAGTCAATTAATAAATGGTGTGGCTCTTGGTGGACCAA
 CAGTGTGGGGGAATTTAAAGATGTTACAGTGACTTATGATAAGACAT
 CTCAACCATCAAAATCAATCATTTGAACCTAGGAAGTGGACAAAAAGTA
 GTTCTTACCTATGATGTACGTTTAAAGATAACTATATAAGTAACAAAT
 TTACAATACAAAATCGTACAaCGCTAAGTCCGAAGAGTGAAGAAAGAAC

Table 41: Comparative Sequences relating to SAG0649

CAAACTACTATTCGTGATTCCCAATTCCTCAAAATTCGTGATGTTCTGTGAG
 TTTCCTGGTACTAACCATCAGTAATCAGAAAGAAATGGGTGAGGTTGAAAT
 TATTAAAGTTAATAAGACAAACATTGCAATCGCTTTGGGAGCTAAGT
 TTCACTTCAGATAGAAAAGATTCTCTGGGTATAAGCAATTTGTTCCA
 GAGGGAAGTGATGTTACACAAAGAATGATGGTAAAAATTTATTTTAAAGC
 ACTTCAAGATGGTAACATATAAATTATATGAAATTTCAAGTCCAGATGGCT
 ATATAGAGGTTAAACGAAACCTGTGTGACATTACAAATCAAATGGA
 GAAGTTACGAACCTGAAAGCAGATCCAATGCTAATAAAAAATCAAATCGG
 GTATCTTGAAGGAATGGTAAACATCTTATTACCAACACTCCCAACGCC
 CACCAGGTGTT

SEQ ID NO. 4106: SAG0649 FROM COH1 GBS TYPE III STRAIN

GGTGAACCCAGATACCAATCAAGCACTTGGAAAAG
 TAATTGTTAAAAAACCGGAGACaTGCTACACCAATTAGGCAAGCGACT
 TTTGTGTTAAAAATGCAATGATAAGTCAGAAACAAGTCACGAAACGGT
 AGAGGGTTCTGGATAGCAACCTTTGAAAAATAAAACCTGGAGACTACA
 CATTAAAGAGAAGAAACAGCAACCAATTGGTTATAAAAAAACTGATAAAACC
 TGGAAAGTTAAAGTTGAGATAACGGAGCAACAATAATCGAGGGTATGGA
 TGCAGATAAAGCAGAGAAACGAAAAGAGTTTGAATGCCCAATATCCAA
 AATCAGCTATTTATGAGGATACAAAAGAAAATTACCCATTAgTTAATGTA
 GAGGGTTCCAAAGTTGGTGAACAAATaCAAAGCATTGAATCCAATAAATGG
 AAAAGATGGTCCGAGAGAGATTGCTGAAGGTTGGTTATCAAAAAAAATA
 CAGGGGTCAATGATCTCgATAAGAATAAATATAAAATGAATTAACGTGT
 GAGGGTAAAAACCACTGTTGAAACGAAAGAACTTAATCAACCACTAGATGT
 CGTTGTGCTATTAGATAATTCAAATAGTATGAATAATGAAAGAGCCAATA
 ATTCTCAAGAGCATTAAAAGCTGGGGAAGCAGTTGAAAAGCTGATTGAT
 AAAATTACATCAATAAAGACAATAGAGTAGCTCTTGTGACATATGCCTC
 AACCATTTTGTAGGTACTGAAGCGACCGTATCAAAGGGAGTTGCCGATC
 AAAATGGTAAAGCGCTGAATGATAGTGTATCATGGGATTATCATAAAACT
 ACTTTTACGCAACTACACATAATTACAGTTATTAAATTTAAACAAATGA
 TGCTAACGAAGTTAATATTCTAAAGTCAAGAAATCCAAAGGAAGCGGAGC
 ATATAAATGGGATCGCAGCTCTATCAATTTGGTGGCAGATTTACTCAA
 AAAAGCTCTAATGAAAGCAATGAAATTTAGAGACACAAAGTTCTAATGC
 TAGAAAAAACTTATTTTACGTAACATGATGGTGTCCCTACGATGTCTT
 ATGCCATAAAATTTTAACTCCTTATATATCAACATCTTACCAAAACCACTT
 AATTCTTTTAAATAAAATACCAGATAGAAAGTGGTATTCTCCAAGAGGA
 TTTTATAATCAATGGTGATGATTATCAAATAGTAAAGGAGATGGAGAGA
 GTTTTAAACGTCTTTCGGATAGAAAAGTTCCTGTTACTGGAGGAACGACA
 CAGCAGCTTATCGATACCGCAAAATCAACTCTCTGTAATGAGTAATGA
 GGGATATGCAATTAAATAGTGGATATATTATCTCTATTGGAGAGATTACA
 ACTGGGTCTATCCATTGATCCTAAGACAAAGAAAGTTTCTGCAACGAAA
 CAAATCAAACTCATGGTGAGCCAAACAATTATACCTTAAATGGAAATAT
 AAGACCTAAAGGTTATGACATTTTACTGTTGGGATTGGTGTAAACGGAG
 ATCTGGTGCACTCTCTTGAAGCTGAGAAATTTATGCAATCAATATCA
 AGTAAACAGAAAATTATACTAATGTTGATGATACAAATAAAATTTATGA
 TGAGCTAAATAAATACCTTTAAACCAATTTGTTGAGGAAAAACATTCTATTG
 TTGATGGAAATGTGACTGATCCTATGGGAGAGATGATTGAATTTCAATTA
 AAAAAATGGTCAAAGTTTACACATGATGATTACGTTTGGTTGGAAATGA
 TGGCACTCAATTAAAAAATGGTGTGGCTCTTGGTGGACCAACAGTGATG
 GGGGAATTTTAAAGATGTTACAGTGACTTATGATAAGACATCTCAAACC
 ATCAAAATCAATCATTGAACCTAGGAAGTGGACAAAAGTAGTTCTTAC
 CTATGATGTACGTTTAAAGATAACTATATAAGTAACAAATTTTACAATA
 CAAATAATCGTACAACGCTAAGTCCGAAGAGTGAAGAAAGAACCAATACT
 ATTCTGTGATTCCCAATTTCCCAAAATTCGTGATGTTCTGTGAGTTTCCGGT
 ACTAACCATCAGTAATCAGAAAGAAATGGGTGAGGTTGAATTTATTAAG
 TTAATAAAGACAAACATTCgAATCGCTTTTGGGAGCTAAGTTTCAACT
 CAGATAGAAAAGATTCTTCTGGGTATAAGCAATTTGTTCCAGAGGGGAAG
 TGATGTTACAAACAAAGAAATGATGGTAAAAATTTATTTTAAAGCACTTCAAG
 ATGGTAACTATAAATTATATGAAATTTCAAGTCCAATGGCTATATAGAG
 GTTAAAAAGAAACCTGTTGTGACATTTACAATCAAATGGAGAAAGTTAC
 GAACCTGAAAGCAGATCCAATGCTAATAAAAAATCAAATCGGGTATCTTG
 AAGGAAATGGTAAACATCTTATTACCAACACTCCCAACGCCACCAGGT
 GTT

SEQ ID NO. 4107: SAG0649 FROM M781 GBS TYPE III STRAIN

TTGGAAAAGTAATTGTTAAAAAACCGGAGACACTGCTACACCATTAGGC
 AAAGCGACTTTTGTGTTAAAAATGCAATGATAAGTCAGAAACAAGTCA
 CGAAACGGTAGAGGGTTCTGGAAAAGCAACCTTTGAAAACATAAAACCTG
 GAGACTACACATTAAGAGAAGAAACAGCACCAATGGTTATAAAAAAACT
 GATAAAACCTGGAAGGTTAAAGTTGCAGATAACGGAGCAmCAATAATCGA
 GGGTATGGATGCAGATAAAGCAGAGAAACGAAAAGAGTTTGAATGCC
 AATATCCAAATCAGCTATTATGAGGATACAAAAGAAAATTACCCATTA
 GTTAATGTAGAGGGTTCCAAAGTTGGTGAACAAATCAAAAGCATTGAATCC
 AATAAATGGAAAAGATGGTCgAAGAGAGATTGCTGAAGGTTGGTTATCAA
 AAAAAATTACaGGGGTCAATGATCTCGATAAGAAATAAATATAAAATGAA
 TTAACGTTGAGGGTAAAAACCACTGTTGAAACgAAAGAACTTAATCAACC
 ACTAGATGTCGTTGTGCTATTAGATAATTCAAATAGTATGAATAATGAAA
 GAGCCAATAATTCTCAAGAGCATTAAAAGCTGGGGAAGCAGTTGAAAAG
 CTGATTGATAAAATTACATCAATAAAGCAATAGAGTAGCTCTTGTGAC
 ATATGCCCTCAACCATTTTGTGATGTTACTGAAGCGACCGTATCAAGGGAG
 TTGCCGATCAAAATGGTAAAGCGCTGAATGATAGTGTATCATGGGATTAT
 CATAAAACTACTTTTACAGCACTACACATAATTACAGTTATTAAATTT
 AACAAATGATGCTAACGAAGTTAATATTCTAAAGTCAAGAAATCCAAAGG

Table 41: Comparative Sequences relating to SAG0649

AAGCGGAGCATATAAATGGGGATCGCACGCTCTATCAATTTGGTGCGACA
 TTACTCTAAAGAGCTCTAATGAAGCAAATGAAATTTAGAGACACAAAG
 TTCTAATGCTAGAAAAAACTTATTTTTCACGTAACGTGATGGTGTCCCTA
 CGATGTCTTATGCCATAAATTTTAACTCTTATATATCAACATCTTACCAA
 AACAGGATTTAATCTCTTTTAAATAAAATACCAGATAGAAAGTGGTATCT
 CCAAGAGGATTTTATAATCAATGGTGATGATTATCAAAATAGTAAAAGGAG
 ATGGAGAGAGTTTAACTGTTTTCGGATAGAAAAGTTCCTGTTACTGGA
 GGAACGACACAAAGCAGCTTATCGAGTACCGCAAATCAACTCTCTGTAAT
 GAGTAATGAGGGATATGCAATTAATAGTGGATATATTTATCTCTATGGA
 GAGATTACAACTGGGTCTATCCATTTGATCCTAAGACAAAGAAAGTTTCT
 GCAACGAAAACAAATCAAACTCATGGTGAGCCAAACATTATATCTTTAA
 TGGAAATATAAGACCTAAAGGTTATGACATTTTACTGTTGGGATGGTG
 TAAACGGAGATCCTGGTGCACTCTCTTGAAGCTGAGAAATTTATGCAA
 TCAATATCAAGTAAACAGAAAATTTATACTAATGTTGATGATACAAATAA
 AATTTATGATGAGCTAAATAAATCTTTAAACAAATTTGTTGAGGAAAAAC
 ATCTTATTTGTTGATGGAATGTGACTGATCCTATGGGAGAGATGATTGAA
 TTCCAATTAATAAATGGTCAAGTTTACACATGATGATTACGTTTGGT
 TGGAAATGATGGCAGTCAATTAATAAATGGTGTGGCTCTTGGTGGACCAA
 ACAGTATGGGGAAATTTTAAAGATGTTACAGTGACTTATGATAAGACA
 TCTCAACCATCAAAATCAATCTTTGAACCTTAGGAAGTGGACAAAAAGT
 AGTTCTTACCTATGATGATCGTTTAAAGATAACTATATAAGTAACAAAT
 TTTACATAACAAATAATCGTACAAACGCTAAGTCCGAAGAGTGAATAAGAA
 CCAATACTATTCTGTGATTTCCCAATTTCCCAAAATTCGTGATGTTCTGTA
 GTTTCGGTACTAACCATCAGTAATCAGAAGAAATGGGTGAGGTTGAAT
 TTATTAAGTTAATAAAGACAAACATTGAGTAATCGCTTTTGGGAGCTAAG
 TTTCACTTCAGATAGAAAAGATTTTCTGGGTATAAGCAATTTGTTCC
 AGAGGGAAGTGTGTACACAAAGAAATGATGGTAAATTTATTTTAAAG
 CACTTCAAGATGGTAACATATAAATTTATATGAAATTTCAAGTCCAGATGGC
 TATATAGAGGTTAAACGAAACCTGTTGTGACATTTCAATTTCAAAATGG
 AGAAGTTACGAACCTGAAAGCAGATCCAAATGCTAATAAATAAATCAATCG
 GGTATCTGAAGGAAATGGTAAACATCTTATTACCAACACTCCCAACGC
 CCACCAGGTGT

SEQ ID NO. 4108: SAG0649 FROM CJB GBS NONTYPEABLE STRAIN
 GGTGAACCCCAAGATACCAATCAAGCACTTGGAAAAAGT

AATTGTTAAAAAACGGGAGACaTGCTACACCATTAGGCAAGCGACIT
 TTGTGTTAAAAATGACAAATGATAAGTCAGAAACAAGTCAGAAACGGTA
 GAGGGTTCTGGATAAGCAACCTTTGAAAACATAAAACCTGGGAGCTACAC
 ATTAAGAGAGAAACAGCAACCAATTTGTTTATAAAAAAATGATAAAACCT
 GGAAAGTTAAAGTTGAGATAACGGAGCAACATAATCGAGGGTATGGAT
 GCAGATAAAGCAGAGAAACGAAAGAGTTTGAATGCCAATATCCAAA
 ATCAGCTATTATGAGGATACAAAAGAAAATTACCCATTAGTTAATGTAG
 AGGGTTCCAAAGTTGGTGAACAATACAAAGCAATGAATCCATAAATGGA
 AAAGATGGTGAAGAGAGATTTGCTGAAGGTTGGTTATCAAAAAAATTAC
 aGGGGTCAATGATCTCGATAAGAAATAAATAAATAAATGAATTAACGTGT
 AGGGTAAAAACCATGTTGAAACGAAAGAACTTAATCAACCACTAGATGTC
 GTTGTGCTATTAGATAAATCAAAATAGTATGAATAATGAAAGAGCCAAATA
 TTCTCAAGAGCATTAAAGCTGGGGAAGCAGTTGAAAGCTGATTGATA
 AAATTACATCAATAAAGACAATAGAGTAGCTCTGTGACATATGCCTCA
 ACCATTTTGTATGGTACTGAAGCGACCGTATCAAAAGGAGTTGCCGATCA
 AAATGGTTAAAGCGCTGAATGATAGTGTATCATGGGATTATCATAAAACTA
 CTTTTACAGCAACTACACATAATTACAGTTATTTAAATTTAAACAAATGAT
 GCTAAGCAAGTTAATATTCTAAGTCAAGAAATCCAAAGGAAGCGGAGCA
 TATAAATGGGGATCGCACGCTCTATCAATTTGGTGCGACATTTACTCAA
 AAGCTCTAATGAAAGCAAATGAAATTTAGAGACACAAAGTTCTAATGCT
 AGAAAAAACTTATTTTTCACGTAACGTGATGGTGTCCCTACGATGTCTTA
 TGCCATAAATTTTAACTCTTATATATCAACATCTTACCAAAACAGTTTA
 ATTCTTTTAAATAAATAACAGATAGAAAGTGGTATTCTCCAAGAGGAT
 TTTATAATCAATGGTGATGATTATCAAAATAGTAAAAGGAGATGGAGAGAG
 TTTTAAACTGTTTTCGGATAGAAAAGTTCCTGTTACTGGAGGAACGACAC
 AAGCAGCTTATCGAGTACCGCAAATCAACTCTCTGTAATGAGTAATGAG
 GGATATGCAATTAATAGTGGATATATTTATCTCTATTGGAGAGATTACAA
 CTGGGTCTATCCATTTGATCCTAAGACAAAGAAAGTTTCTGCAACGAAAC
 AAATCAAAACTCATGGTGAGCCAAACACATTATACCTTTAATGGAAATATA
 AGACCTAAAGGTTATGACATTTTACTGTTGGGATGGTGTAAACGGGAGA
 TCTGTGTCAACTCCTCTTGAAGCTGAGAAATTTATGCAATCAATATCAA
 GTAAACAGAAAATTTATACTAATGTTGATGATACAAATAAATTTATGAT
 GAGCTAAATAAATCTTTAAACAAATTTGTTGAGGAAAAACATTTCTATTGT
 TGAATGGAAATGTGACTGATCCTATGGGAGAGATGATTGAATTTCAATTA
 AAAATGGTCAAGTTTACACATGATGATTACGTTTGGTTGGGAAATGAT
 GGCAGTCAATTAATAAATGGTGTGGCTCTTGGTGGACCAACAGTGAATGG
 GGAATTTTAAAGATGTTACAGTGACTTATGATAAGACATCTCAAACCA
 TCAAAATCAATCAATTTGAACCTTAGGAAGTGGACAAAAAGTAGTTCTTACC
 TATGATGTACGTTTAAAGATACTATATAAGTAACAAATTTTACAATAC
 AAAATATCGTACACGCTAAGTCCGAAGAGTGAATAAGAAACCAAAATCTA
 TCGTGATTTCCCAATTTCCCAAAATTCGTGATGTTCTGTGAGTTTCCGGTA
 CTAAACATCAGTAATCAGAAGAAATGGGTGAGGTTGAATTTTAAAGT
 TAATAAGACAAACATTGAGAAATCGCTTTTGGGAGCTAAGTTTCAACTTC
 AGATAGAAAAAGATTTTCTGGGTATAAGCAATTTGTTCCAGAGGGAAGT
 GATGTTTACAACAAAGAAATGATGGTAAATTTATTTTAAAGCACTTCAAGA
 TGGTAACATAAATTTATGAAATTTCAAGTCCAGATGGCTATATAGAGG
 TTAACGAAACCTGTTGTGACATTTCAATTTCAAAATGGGAGAGTTTACG
 AACCTGAAAGCAGATCCAAATGCTAATAAATAAATCAATCGGGTATCTTGA

Table 41: Comparative Sequences relating to SAG0649

AGGAAATGGTAAACATCTTATTACCAACACTCCCAAACGCCACCAGGTG
TT

SEQ ID NO. 4109: SAG0649 FROM JM9130013 GBS TYPE VIII STRAIN

GGTGAAACCCCAAGATACCAATCAAGCACTTGGAAAAAG
TAATTGTTAAAAAACGGGAGACAATGCTACACCATTAGGCAAAGCGACT
TTTGTGTTAAAAAATGACAATGATAAGTCAGAAACAAGTCACGAAACGGT
AGAGGGTTCTGGAGAAGCAACCTTTGAAAAATAAAACTGGAGACTACA
CATTAAGAGAAGAAAACAGCACCAATTGGTTATAAAAAAATGATAAAACC
TGGAAAGTTAAAGTTGCAGATAACGGAGCAACAATAATCGAGGGTATGGA
TGCAGATAAAGCAGAGAAACGAAAAGAGTTTGAATGCCCAATATCCAA
AATCAGCTATTTATGAGGATACAAAAGAAAATTACCCATTAGTTAATGTA
GAGGGTTCCAAAGTTGGTGAACAATACAAAGCATTGAATCCAATAAATGG
AAAAGATGGTCGAAGAGAGATTGCTGAAGGTTGGTTATCAAAAAAATTA
CAGGGGTCAATGATCTCGATAAGAATAAATATAAAATTGAATTAACTGTT
GAGGGTAAAACCACTGTTGAAACGAAAGAACTTAATCAACCACTAGATGT
CGTTGTGCTATTAGATAAATCAAAATAGTATGAATAATGAAAGAGCCAATA
ATTCTCAAAGAGCAATTAAAAAGCTGGGGAAGCAGTTGAAAAGCTGATTGAT
AAAATTACATCAAATAAGACAATAGAGTAGCTCTTGTGACATATGCCTC
AACCATTTTTGATGGTACTGAAGCGACCGTATCAAAAGGGAGTTGCCGATC
AAAATGGTAAAGCGCTGAATGATAGTGTATCATGGGATTATCATAAAACT
ACTTTTACAGCACTACACATAATTACAGTTATTATAAATTTAACAAATGA
TGCTAACGAAGTTAATATTCTAAAGTCAAGAATTCCAAGGAAGCGGAGC
ATATAAATGGGGATCGCACGCTCTATCAATTTGGTGCAGACATTTACTCAA
AAGGCTCTAATGAAAGCAAAATGAAATTTTAGAGACACAAGTTCTAATGC
TAGAAAAAATCTTATTTTACGTAACCTGATGGTGTCCCTACGATGTCTT
ATGCCATAAATTTAATCCTTATATATCAACATCTTACCAAAACCAAGTTT
AATTCTTTTAAATAAATAACCAGATAGAAGTGGTATTCTCAAAGAGGA
TTTTATAATCAATGGTGTGATGATTATCAAAATAGTAAAAGGAGATGGAGAGA
GTTTTAACTGTTTTTCGGATAGAAAAGTTCTGTACTGGAGGAACGACA
CAAGCAGCTTATCGAGTACCGCAAAATCAACTCTCTGTATAGTAATGA
GGGATATGCAATTAATAGTGGATATATTTATCTCTATTGGAGAGATTACA
ACTGGGTCTATCCATTGATCCTTAAGACAAGAAAGTTTCTGCAACGAAA
CAAATCAAACCTCATGGTGAGCCAACAACATTATCTTAAATGGAATAT
AAGACCTAAAGGTTATGACATTTTACTGTTGGGATTGGTGTAAACGGAG
ATCCTGGTGCAACTCCTCTTGAAGCTGAGAAATTTATGCAATCAATATCA
AGTAAACAGAAAATTTACTAATGTTGATGATACAAATAAAATTTATGA
TGAGCTAAATAAATACTTTAAAACAATTGTTGAGGAAAAACATTCTATTG
TTGATGGAATGTGACTGATCCTATGGGAGAGATGATTGAATTCCAATTA
AAAAATGGTCAAAGTTTACACATGATGATTACGTTTGGTTGGAAATGA
TGGCAGTCAATTAATAAATGGTGTGGCTCTTGGTGGACCAACAGTGATG
GGGGAATTTAAAGATGTTACAGTGACTTATGATAAGACATCTCAAACC
ATCAAAATCAATCAATTGAACCTTAGGAAGTGGACAAAAAGTAGTTCTTAC
CTATGATGTACGTTTAAAGATAACTATATAAGTAACAAATTTTACAATA
CAAATAATCGTACAACGCTAAGTCCGAAGAGTGAAAAAGAACCAATACT
ATTCTGTGATTTCCCAATTCCTCAAAATTCGTGATGTTCTGTGAGTTTCCGGT
ACTAACCATCAGTAATCAAAAGAAAATGGGTGAGGTTGAATTTATTAAAG
TTAATAAAGACAACATTCAGAATCGCTTTTGGGAGCTAAGTTTCACTT
CAGATAAAAAAGATTTTCTGGGTATAAGCAATTTGTTCCAGAGGGAAG
TGATGTTACAACAAAGAATGATGGTAAAAATTTATTTAAAGCACTTCAAG
ATGGTAACTATAAATATATGAAATTTCAAGTCCAGATGGCTATATAGAG
GTTAAAAAGAAACCTGTTGTGACATTTACAATTCAAAATGGAGAAGTTAC
GAACCTGAAAGCAGATCCAAATGCTAATAAAAAATCAAATCGGTATCTTG
AA

Table 41: Comparative Sequences relating to SAG0649

PRETTY of: /biotmp/msa178297.2{*} May 12, 2003 09:22 ..

	1				50
msa178297.2{104_090}	-----	-----	-----	-----	-----
msa178297.2{104_18RS21}	-----	-----	-----	-----	-----
msa178297.2{104_2603}	atgaaaaaga	gacaaaaaat	atggagaggg	ttatcagtta	ctttactaat
msa178297.2{104_CJB110}	-----	-----	-----	-----	-----
msa178297.2{104_COH1}	-----	-----	-----	-----	-----
msa178297.2{104_M732}	-----	-----	-----	-----	-----
msa178297.2{104_A909}	-----	-----	-----	-----	-----
msa178297.2{104_M781}	-----	-----	-----	-----	-----
msa178297.2{104_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa178297.2{104_090}	-----	-----	-----	---ggtgaa	acccaagata
msa178297.2{104_18RS21}	-----	-----	-----	---ggtgaa	acccaagata
msa178297.2{104_2603}	cctgtcccaa	attccatttg	gtatatgggt	acaaggtgaa	acccaagata
msa178297.2{104_CJB110}	-----	-----	-----	---ggtgaa	acccaagata
msa178297.2{104_COH1}	-----	-----	-----	---ggtgaa	acccaagata
msa178297.2{104_M732}	-----	-----	-----	---ggtgaa	acccaagata
msa178297.2{104_A909}	-----	-----	-----	---ggtgaa	acccaagata
msa178297.2{104_M781}	-----	-----	-----	---ggtgaa	acccaagata
msa178297.2{104_JM9130013}	-----	-----	-----	---ggtgaa	acccaagata
Consensus	*****	*****	*****	*****	*****
	101				150
msa178297.2{104_090}	ccaatcaagc	actTGGAAAA	GTAATTGTTA	AAAAAACGGG	agACAaTGCT
msa178297.2{104_18RS21}	ccaatcaagc	actTGGAAAA	GTAATTGTTA	AAAAAACGGG	agACAaTGCT
msa178297.2{104_2603}	ccaatcaagc	actTGGAAAA	GTAATTGTTA	AAAAAACGGG	agACAaTGCT
msa178297.2{104_CJB110}	ccaatcaagc	actTGGAAAA	GTAATTGTTA	AAAAAACGGG	agACAaTGCT
msa178297.2{104_COH1}	ccaatcaagc	actTGGAAAA	GTAATTGTTA	AAAAAACGGG	agACAaTGCT
msa178297.2{104_M732}	ccaatcaagc	actTGGAAAA	GTAATTGTTA	AAAAAACGGG	agACAaTGCT
msa178297.2{104_A909}	ccaatcaagc	actTGGAAAA	GTAATTGTTA	AAAAAACGGG	agACAaTGCT
msa178297.2{104_M781}	ccaatcaagc	actTGGAAAA	GTAATTGTTA	AAAAAACGGG	agACAaTGCT
msa178297.2{104_JM9130013}	ccaatcaagc	actTGGAAAA	GTAATTGTTA	AAAAAACGGG	agACAaTGCT
Consensus	-----	---*****	*****	*****	-----*****
	151				200
msa178297.2{104_090}	ACACCATTAG	GCAAAGCGAC	TTTTGTGTTA	AAAAATGACA	ATGATAAGTC
msa178297.2{104_18RS21}	ACACCATTAG	GCAAAGCGAC	TTTTGTGTTA	AAAAATGACA	ATGATAAGTC
msa178297.2{104_2603}	ACACCATTAG	GCAAAGCGAC	TTTTGTGTTA	AAAAATGACA	ATGATAAGTC
msa178297.2{104_CJB110}	ACACCATTAG	GCAAAGCGAC	TTTTGTGTTA	AAAAATGACA	ATGATAAGTC
msa178297.2{104_COH1}	ACACCATTAG	GCAAAGCGAC	TTTTGTGTTA	AAAAATGACA	ATGATAAGTC
msa178297.2{104_M732}	ACACCATTAG	GCAAAGCGAC	TTTTGTGTTA	AAAAATGACA	ATGATAAGTC
msa178297.2{104_A909}	ACACCATTAG	GCAAAGCGAC	TTTTGTGTTA	AAAAATGACA	ATGATAAGTC
msa178297.2{104_M781}	ACACCATTAG	GCAAAGCGAC	TTTTGTGTTA	AAAAATGACA	ATGATAAGTC
msa178297.2{104_JM9130013}	ACACCATTAG	GCAAAGCGAC	TTTTGTGTTA	AAAAATGACA	ATGATAAGTC
Consensus	*****	*****	*****	*****	*****
	201				250
msa178297.2{104_090}	AGAAACAAGT	CACGAAACGG	TAGAGGGTTC	TGGAgAAGCA	ACCTTTGAAA
msa178297.2{104_18RS21}	AGAAACAAGT	CACGAAACGG	TAGAGGGTTC	TGGAgAAGCA	ACCTTTGAAA
msa178297.2{104_2603}	AGAAACAAGT	CACGAAACGG	TAGAGGGTTC	TGGAgAAGCA	ACCTTTGAAA
msa178297.2{104_CJB110}	AGAAACAAGT	CACGAAACGG	TAGAGGGTTC	TGGAgAAGCA	ACCTTTGAAA
msa178297.2{104_COH1}	AGAAACAAGT	CACGAAACGG	TAGAGGGTTC	TGGAgAAGCA	ACCTTTGAAA
msa178297.2{104_M732}	AGAAACAAGT	CACGAAACGG	TAGAGGGTTC	TGGAgAAGCA	ACCTTTGAAA
msa178297.2{104_A909}	AGAAACAAGT	CACGAAACGG	TAGAGGGTTC	TGGAgAAGCA	ACCTTTGAAA
msa178297.2{104_M781}	AGAAACAAGT	CACGAAACGG	TAGAGGGTTC	TGGAgAAGCA	ACCTTTGAAA
msa178297.2{104_JM9130013}	AGAAACAAGT	CACGAAACGG	TAGAGGGTTC	TGGAgAAGCA	ACCTTTGAAA
Consensus	*****	*****	*****	*****	*****
	251				300
msa178297.2{104_090}	ACATAAAACC	TGGAGACTAC	ACATTAAAGAG	AAGAAACAGC	ACCAATTGGT
msa178297.2{104_18RS21}	ACATAAAACC	TGGAGACTAC	ACATTAAAGAG	AAGAAACAGC	ACCAATTGGT
msa178297.2{104_2603}	ACATAAAACC	TGGAGACTAC	ACATTAAAGAG	AAGAAACAGC	ACCAATTGGT
msa178297.2{104_CJB110}	ACATAAAACC	TGGAGACTAC	ACATTAAAGAG	AAGAAACAGC	ACCAATTGGT
msa178297.2{104_COH1}	ACATAAAACC	TGGAGACTAC	ACATTAAAGAG	AAGAAACAGC	ACCAATTGGT
msa178297.2{104_M732}	ACATAAAACC	TGGAGACTAC	ACATTAAAGAG	AAGAAACAGC	ACCAATTGGT
msa178297.2{104_A909}	ACATAAAACC	TGGAGACTAC	ACATTAAAGAG	AAGAAACAGC	ACCAATTGGT
msa178297.2{104_M781}	ACATAAAACC	TGGAGACTAC	ACATTAAAGAG	AAGAAACAGC	ACCAATTGGT
msa178297.2{104_JM9130013}	ACATAAAACC	TGGAGACTAC	ACATTAAAGAG	AAGAAACAGC	ACCAATTGGT
Consensus	*****	*****	*****	*****	*****
	301				350
msa178297.2{104_090}	TATAAAAAAA	CTGATAAAAC	CTGGAAAGTT	AAAGTTGCAG	ATAACGGAGC
msa178297.2{104_18RS21}	TATAAAAAAA	CTGATAAAAC	CTGGAAAGTT	AAAGTTGCAG	ATAACGGAGC
msa178297.2{104_2603}	TATAAAAAAA	CTGATAAAAC	CTGGAAAGTT	AAAGTTGCAG	ATAACGGAGC
msa178297.2{104_CJB110}	TATAAAAAAA	CTGATAAAAC	CTGGAAAGTT	AAAGTTGCAG	ATAACGGAGC
msa178297.2{104_COH1}	TATAAAAAAA	CTGATAAAAC	CTGGAAAGTT	AAAGTTGCAG	ATAACGGAGC
msa178297.2{104_M732}	TATAAAAAAA	CTGATAAAAC	CTGGAAAGTT	AAAGTTGCAG	ATAACGGAGC
msa178297.2{104_A909}	TATAAAAAAA	CTGATAAAAC	CTGGAAAGTT	AAAGTTGCAG	ATAACGGAGC
msa178297.2{104_M781}	TATAAAAAAA	CTGATAAAAC	CTGGAAAGTT	AAAGTTGCAG	ATAACGGAGC

Table 41: Comparative Sequences relating to SAG0649

msal78297.2{104_JM9130013}	TATAAAAAAA	CTGATAAAAC	CTGGAAAGTT	AAAGTTGCAG	ATAACGGAGC
Consensus	*****	*****	*****	*****	*****
	351				400
msal78297.2{104_090}	AaCAATAATC	GAGGGTATGG	ATGCAGATAA	AGCAGAGAAA	CGAAAAGAAG
msal78297.2{104_18RS21}	AaCAATAATC	GAGGGTATGG	ATGCAGATAA	AGCAGAGAAA	CGAAAAGAAG
msal78297.2{104_2603}	AaCAATAATC	GAGGGTATGG	ATGCAGATAA	AGCAGAGAAA	CGAAAAGAAG
msal78297.2{104_CJB110}	AaCAATAATC	GAGGGTATGG	ATGCAGATAA	AGCAGAGAAA	CGAAAAGAAG
msal78297.2{104_COH1}	AaCAATAATC	GAGGGTATGG	ATGCAGATAA	AGCAGAGAAA	CGAAAAGAAG
msal78297.2{104_M732}	AaCAATAATC	GAGGGTATGG	ATGCAGATAA	AGCAGAGAAA	CGAAAAGAAG
msal78297.2{104_A909}	AaCAATAATC	GAGGGTATGG	ATGCAGATAA	AGCAGAGAAA	CGAAAAGAAG
msal78297.2{104_M781}	AmCAATAATC	GAGGGTATGG	ATGCAGATAA	AGCAGAGAAA	CGAAAAGAAG
msal78297.2{104_JM9130013}	AaCAATAATC	GAGGGTATGG	ATGCAGATAA	AGCAGAGAAA	CGAAAAGAAG
Consensus	*-*****	*****	*****	*****	*****
	401				450
msal78297.2{104_090}	TTTTGAATGC	CCAATATCCA	AAATCAGCTA	TTTATGAGGA	TACAAAAGAA
msal78297.2{104_18RS21}	TTTTGAATGC	CCAATATCCA	AAATCAGCTA	TTTATGAGGA	TACAAAAGAA
msal78297.2{104_2603}	TTTTGAATGC	CCAATATCCA	AAATCAGCTA	TTTATGAGGA	TACAAAAGAA
msal78297.2{104_CJB110}	TTTTGAATGC	CCAATATCCA	AAATCAGCTA	TTTATGAGGA	TACAAAAGAA
msal78297.2{104_COH1}	TTTTGAATGC	CCAATATCCA	AAATCAGCTA	TTTATGAGGA	TACAAAAGAA
msal78297.2{104_M732}	TTTTGAATGC	CCAATATCCA	AAATCAGCTA	TTTATGAGGA	TACAAAAGAA
msal78297.2{104_A909}	TTTTGAATGC	CCAATATCCA	AAATCAGCTA	TTTATGAGGA	TACAAAAGAA
msal78297.2{104_M781}	TTTTGAATGC	CCAATATCCA	AAATCAGCTA	TTTATGAGGA	TACAAAAGAA
msal78297.2{104_JM9130013}	TTTTGAATGC	CCAATATCCA	AAATCAGCTA	TTTATGAGGA	TACAAAAGAA
Consensus	*****	*****	*****	*****	*****
	451				500
msal78297.2{104_090}	AATTACCCAT	TAGTTAATGT	AGAGGGTTCC	AAAGTTGGTG	AACAATACAA
msal78297.2{104_18RS21}	AATTACCCAT	TAGTTAATGT	AGAGGGTTCC	AAAGTTGGTG	AACAATACAA
msal78297.2{104_2603}	AATTACCCAT	TAGTTAATGT	AGAGGGTTCC	AAAGTTGGTG	AACAATACAA
msal78297.2{104_CJB110}	AATTACCCAT	TAGTTAATGT	AGAGGGTTCC	AAAGTTGGTG	AACAATACAA
msal78297.2{104_COH1}	AATTACCCAT	TAGTTAATGT	AGAGGGTTCC	AAAGTTGGTG	AACAATACAA
msal78297.2{104_M732}	AATTACCCAT	TAGTTAATGT	AGAGGGTTCC	AAAGTTGGTG	AACAATACAA
msal78297.2{104_A909}	AATTACCCAT	TAGTTAATGT	AGAGGGTTCC	AAAGTTGGTG	AACAATACAA
msal78297.2{104_M781}	AATTACCCAT	TAGTTAATGT	AGAGGGTTCC	AAAGTTGGTG	AACAATACAA
msal78297.2{104_JM9130013}	AATTACCCAT	TAGTTAATGT	AGAGGGTTCC	AAAGTTGGTG	AACAATACAA
Consensus	*****	*****	*****	*****	*****
	501				550
msal78297.2{104_090}	AGCATTGAAT	CCAATAAATG	GAAAAGATGG	TGGAAGAGAG	ATTGCTGAAG
msal78297.2{104_18RS21}	AGCATTGAAT	CCAATAAATG	GAAAAGATGG	TGGAAGAGAG	ATTGCTGAAG
msal78297.2{104_2603}	AGCATTGAAT	CCAATAAATG	GAAAAGATGG	TGGAAGAGAG	ATTGCTGAAG
msal78297.2{104_CJB110}	AGCATTGAAT	CCAATAAATG	GAAAAGATGG	TGGAAGAGAG	ATTGCTGAAG
msal78297.2{104_COH1}	AGCATTGAAT	CCAATAAATG	GAAAAGATGG	TGGAAGAGAG	ATTGCTGAAG
msal78297.2{104_M732}	AGCATTGAAT	CCAATAAATG	GAAAAGATGG	TGGAAGAGAG	ATTGCTGAAG
msal78297.2{104_A909}	AGCATTGAAT	CCAATAAATG	GAAAAGATGG	TGGAAGAGAG	ATTGCTGAAG
msal78297.2{104_M781}	AGCATTGAAT	CCAATAAATG	GAAAAGATGG	TGGAAGAGAG	ATTGCTGAAG
msal78297.2{104_JM9130013}	AGCATTGAAT	CCAATAAATG	GAAAAGATGG	TGGAAGAGAG	ATTGCTGAAG
Consensus	*****	*****	*****	*****	*****
	551				600
msal78297.2{104_090}	GTTGGTTATC	AAAAAAAAT	ACAGGGGTCA	ATGATCTCGA	TAAGAATAAA
msal78297.2{104_18RS21}	GTTGGTTATC	AAAAAAAAT	ACAGGGGTCA	ATGATCTCGA	TAAGAATAAA
msal78297.2{104_2603}	GTTGGTTATC	AAAAAAAAT	ACAGGGGTCA	ATGATCTCGA	TAAGAATAAA
msal78297.2{104_CJB110}	GTTGGTTATC	AAAAAAAAT	ACAGGGGTCA	ATGATCTCGA	TAAGAATAAA
msal78297.2{104_COH1}	GTTGGTTATC	AAAAAAAAT	ACAGGGGTCA	ATGATCTCGA	TAAGAATAAA
msal78297.2{104_M732}	GTTGGTTATC	AAAAAAAAT	ACAGGGGTCA	ATGATCTCGA	TAAGAATAAA
msal78297.2{104_A909}	GTTGGTTATC	AAAAAAAAT	ACAGGGGTCA	ATGATCTCGA	TAAGAATAAA
msal78297.2{104_M781}	GTTGGTTATC	AAAAAAAAT	ACAGGGGTCA	ATGATCTCGA	TAAGAATAAA
msal78297.2{104_JM9130013}	GTTGGTTATC	AAAAAAAAT	ACAGGGGTCA	ATGATCTCGA	TAAGAATAAA
Consensus	*****	*****	*****	*****	*****
	601				650
msal78297.2{104_090}	TATAAAATTG	AATTAAGTGT	TGAGGGTAAA	ACCACTGTTG	AAACGAAAGA
msal78297.2{104_18RS21}	TATAAAATTG	AATTAAGTGT	TGAGGGTAAA	ACCACTGTTG	AAACGAAAGA
msal78297.2{104_2603}	TATAAAATTG	AATTAAGTGT	TGAGGGTAAA	ACCACTGTTG	AAACGAAAGA
msal78297.2{104_CJB110}	TATAAAATTG	AATTAAGTGT	TGAGGGTAAA	ACCACTGTTG	AAACGAAAGA
msal78297.2{104_COH1}	TATAAAATTG	AATTAAGTGT	TGAGGGTAAA	ACCACTGTTG	AAACGAAAGA
msal78297.2{104_M732}	TATAAAATTG	AATTAAGTGT	TGAGGGTAAA	ACCACTGTTG	AAACGAAAGA
msal78297.2{104_A909}	TATAAAATTG	AATTAAGTGT	TGAGGGTAAA	ACCACTGTTG	AAACGAAAGA
msal78297.2{104_M781}	TATAAAATTG	AATTAAGTGT	TGAGGGTAAA	ACCACTGTTG	AAACGAAAGA
msal78297.2{104_JM9130013}	TATAAAATTG	AATTAAGTGT	TGAGGGTAAA	ACCACTGTTG	AAACGAAAGA
Consensus	*****	*****	*****	*****	*****
	651				700
msal78297.2{104_090}	ACTTAATCAA	CCACTAGATG	TCGTTGTGCT	ATTAGATAAT	TCAAATAGTA
msal78297.2{104_18RS21}	ACTTAATCAA	CCACTAGATG	TCGTTGTGCT	ATTAGATAAT	TCAAATAGTA
msal78297.2{104_2603}	ACTTAATCAA	CCACTAGATG	TCGTTGTGCT	ATTAGATAAT	TCAAATAGTA
msal78297.2{104_CJB110}	ACTTAATCAA	CCACTAGATG	TCGTTGTGCT	ATTAGATAAT	TCAAATAGTA
msal78297.2{104_COH1}	ACTTAATCAA	CCACTAGATG	TCGTTGTGCT	ATTAGATAAT	TCAAATAGTA
msal78297.2{104_M732}	ACTTAATCAA	CCACTAGATG	TCGTTGTGCT	ATTAGATAAT	TCAAATAGTA
msal78297.2{104_A909}	ACTTAATCAA	CCACTAGATG	TCGTTGTGCT	ATTAGATAAT	TCAAATAGTA

Table 41: Comparative Sequences relating to SAG0649

msa178297.2{104_M781}	ACITTAATCAA	CCACTAGATG	TCGTTGTGCT	ATTAGATAAT	TCAAATAGTA
msa178297.2{104_JM9130013}	ACITTAATCAA	CCACTAGATG	TCGTTGTGCT	ATTAGATAAT	TCAAATAGTA
Consensus	*****	*****	*****	*****	*****
	701				750
msa178297.2{104_090}	TGAATAATGA	AAGAGCCAAT	AATTCTCAAA	GAGCATTAAA	AGCTGGGGAA
msa178297.2{104_18RS21}	TGAATAATGA	AAGAGCCAAT	AATTCTCAAA	GAGCATTAAA	AGCTGGGGAA
msa178297.2{104_2603}	TGAATAATGA	AAGAGCCAAT	AATTCTCAAA	GAGCATTAAA	AGCTGGGGAA
msa178297.2{104_CJB110}	TGAATAATGA	AAGAGCCAAT	AATTCTCAAA	GAGCATTAAA	AGCTGGGGAA
msa178297.2{104_COH1}	TGAATAATGA	AAGAGCCAAT	AATTCTCAAA	GAGCATTAAA	AGCTGGGGAA
msa178297.2{104_M732}	TGAATAATGA	AAGAGCCAAT	AATTCTCAAA	GAGCATTAAA	AGCTGGGGAA
msa178297.2{104_A909}	TGAATAATGA	AAGAGCCAAT	AATTCTCAAA	GAGCATTAAA	AGCTGGGGAA
msa178297.2{104_M781}	TGAATAATGA	AAGAGCCAAT	AATTCTCAAA	GAGCATTAAA	AGCTGGGGAA
msa178297.2{104_JM9130013}	TGAATAATGA	AAGAGCCAAT	AATTCTCAAA	GAGCATTAAA	AGCTGGGGAA
Consensus	*****	*****	*****	*****	*****
	751				800
msa178297.2{104_090}	GCAGTTGAAA	AGCTGATTGA	TAAAATTACA	TCAAATAAAG	ACAATAGAGT
msa178297.2{104_18RS21}	GCAGTTGAAA	AGCTGATTGA	TAAAATTACA	TCAAATAAAG	ACAATAGAGT
msa178297.2{104_2603}	GCAGTTGAAA	AGCTGATTGA	TAAAATTACA	TCAAATAAAG	ACAATAGAGT
msa178297.2{104_CJB110}	GCAGTTGAAA	AGCTGATTGA	TAAAATTACA	TCAAATAAAG	ACAATAGAGT
msa178297.2{104_COH1}	GCAGTTGAAA	AGCTGATTGA	TAAAATTACA	TCAAATAAAG	ACAATAGAGT
msa178297.2{104_M732}	GCAGTTGAAA	AGCTGATTGA	TAAAATTACA	TCAAATAAAG	ACAATAGAGT
msa178297.2{104_A909}	GCAGTTGAAA	AGCTGATTGA	TAAAATTACA	TCAAATAAAG	ACAATAGAGT
msa178297.2{104_M781}	GCAGTTGAAA	AGCTGATTGA	TAAAATTACA	TCAAATAAAG	ACAATAGAGT
msa178297.2{104_JM9130013}	GCAGTTGAAA	AGCTGATTGA	TAAAATTACA	TCAAATAAAG	ACAATAGAGT
Consensus	*****	*****	*****	*****	*****
	801				850
msa178297.2{104_090}	AGCTCTGTG	ACATATGCCT	CAACCATTTT	TGATGGTACT	GAAGCGACCG
msa178297.2{104_18RS21}	AGCTCTGTG	ACATATGCCT	CAACCATTTT	TGATGGTACT	GAAGCGACCG
msa178297.2{104_2603}	AGCTCTGTG	ACATATGCCT	CAACCATTTT	TGATGGTACT	GAAGCGACCG
msa178297.2{104_CJB110}	AGCTCTGTG	ACATATGCCT	CAACCATTTT	TGATGGTACT	GAAGCGACCG
msa178297.2{104_COH1}	AGCTCTGTG	ACATATGCCT	CAACCATTTT	TGATGGTACT	GAAGCGACCG
msa178297.2{104_M732}	AGCTCTGTG	ACATATGCCT	CAACCATTTT	TGATGGTACT	GAAGCGACCG
msa178297.2{104_A909}	AGCTCTGTG	ACATATGCCT	CAACCATTTT	TGATGGTACT	GAAGCGACCG
msa178297.2{104_M781}	AGCTCTGTG	ACATATGCCT	CAACCATTTT	TGATGGTACT	GAAGCGACCG
msa178297.2{104_JM9130013}	AGCTCTGTG	ACATATGCCT	CAACCATTTT	TGATGGTACT	GAAGCGACCG
Consensus	*****	*****	*****	*****	*****
	851				900
msa178297.2{104_090}	TATCAAAGGG	AGTTGCCGAT	CAAAATGGTA	AAGCGCTGAA	TGATAGTGTA
msa178297.2{104_18RS21}	TATCAAAGGG	AGTTGCCGAT	CAAAATGGTA	AAGCGCTGAA	TGATAGTGTA
msa178297.2{104_2603}	TATCAAAGGG	AGTTGCCGAT	CAAAATGGTA	AAGCGCTGAA	TGATAGTGTA
msa178297.2{104_CJB110}	TATCAAAGGG	AGTTGCCGAT	CAAAATGGTA	AAGCGCTGAA	TGATAGTGTA
msa178297.2{104_COH1}	TATCAAAGGG	AGTTGCCGAT	CAAAATGGTA	AAGCGCTGAA	TGATAGTGTA
msa178297.2{104_M732}	TATCAAAGGG	AGTTGCCGAT	CAAAATGGTA	AAGCGCTGAA	TGATAGTGTA
msa178297.2{104_A909}	TATCAAAGGG	AGTTGCCGAT	CAAAATGGTA	AAGCGCTGAA	TGATAGTGTA
msa178297.2{104_M781}	TATCAAAGGG	AGTTGCCGAT	CAAAATGGTA	AAGCGCTGAA	TGATAGTGTA
msa178297.2{104_JM9130013}	TATCAAAGGG	AGTTGCCGAT	CAAAATGGTA	AAGCGCTGAA	TGATAGTGTA
Consensus	*****	*****	*****	*****	*****
	901				950
msa178297.2{104_090}	TCATGGGATT	ATCATAAAAC	TACTTTTACA	GCAACTACAC	ATAATTACAG
msa178297.2{104_18RS21}	TCATGGGATT	ATCATAAAAC	TACTTTTACA	GCAACTACAC	ATAATTACAG
msa178297.2{104_2603}	TCATGGGATT	ATCATAAAAC	TACTTTTACA	GCAACTACAC	ATAATTACAG
msa178297.2{104_CJB110}	TCATGGGATT	ATCATAAAAC	TACTTTTACA	GCAACTACAC	ATAATTACAG
msa178297.2{104_COH1}	TCATGGGATT	ATCATAAAAC	TACTTTTACA	GCAACTACAC	ATAATTACAG
msa178297.2{104_M732}	TCATGGGATT	ATCATAAAAC	TACTTTTACA	GCAACTACAC	ATAATTACAG
msa178297.2{104_A909}	TCATGGGATT	ATCATAAAAC	TACTTTTACA	GCAACTACAC	ATAATTACAG
msa178297.2{104_M781}	TCATGGGATT	ATCATAAAAC	TACTTTTACA	GCAACTACAC	ATAATTACAG
msa178297.2{104_JM9130013}	TCATGGGATT	ATCATAAAAC	TACTTTTACA	GCAACTACAC	ATAATTACAG
Consensus	*****	*****	*****	*****	*****
	951				1000
msa178297.2{104_090}	TTATTTAAAT	TTAACAAATG	ATGCTAACGA	AGTTAATATT	CTAAAGTCAA
msa178297.2{104_18RS21}	TTATTTAAAT	TTAACAAATG	ATGCTAACGA	AGTTAATATT	CTAAAGTCAA
msa178297.2{104_2603}	TTATTTAAAT	TTAACAAATG	ATGCTAACGA	AGTTAATATT	CTAAAGTCAA
msa178297.2{104_CJB110}	TTATTTAAAT	TTAACAAATG	ATGCTAACGA	AGTTAATATT	CTAAAGTCAA
msa178297.2{104_COH1}	TTATTTAAAT	TTAACAAATG	ATGCTAACGA	AGTTAATATT	CTAAAGTCAA
msa178297.2{104_M732}	TTATTTAAAT	TTAACAAATG	ATGCTAACGA	AGTTAATATT	CTAAAGTCAA
msa178297.2{104_A909}	TTATTTAAAT	TTAACAAATG	ATGCTAACGA	AGTTAATATT	CTAAAGTCAA
msa178297.2{104_M781}	TTATTTAAAT	TTAACAAATG	ATGCTAACGA	AGTTAATATT	CTAAAGTCAA
msa178297.2{104_JM9130013}	TTATTTAAAT	TTAACAAATG	ATGCTAACGA	AGTTAATATT	CTAAAGTCAA
Consensus	*****	*****	*****	*****	*****
	1001				1050
msa178297.2{104_090}	GAATTCCTAA	GGAAGCGGAG	CATATAAATG	GGGATCGCAC	GCTCTATCAA
msa178297.2{104_18RS21}	GAATTCCTAA	GGAAGCGGAG	CATATAAATG	GGGATCGCAC	GCTCTATCAA
msa178297.2{104_2603}	GAATTCCTAA	GGAAGCGGAG	CATATAAATG	GGGATCGCAC	GCTCTATCAA
msa178297.2{104_CJB110}	GAATTCCTAA	GGAAGCGGAG	CATATAAATG	GGGATCGCAC	GCTCTATCAA
msa178297.2{104_COH1}	GAATTCCTAA	GGAAGCGGAG	CATATAAATG	GGGATCGCAC	GCTCTATCAA
msa178297.2{104_M732}	GAATTCCTAA	GGAAGCGGAG	CATATAAATG	GGGATCGCAC	GCTCTATCAA

Table 41: Comparative Sequences relating to SAG0649

msa178297.2{104_A909}	GAATTCCTAAA	GGAAGCGGAG	CATATAAATG	GGGATCGCAC	GCTCTATCAA
msa178297.2{104_M781}	GAATTCCTAAA	GGAAGCGGAG	CATATAAATG	GGGATCGCAC	GCTCTATCAA
msa178297.2{104_JM9130013}	GAATTCCTAAA	GGAAGCGGAG	CATATAAATG	GGGATCGCAC	GCTCTATCAA
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	TTTGGTGCGA	CATTTACTCA	AAAAGCTCTA	ATGAAAGCAA	ATGAAATTTT
msa178297.2{104_18RS21}	TTTGGTGCGA	CATTTACTCA	AAAAGCTCTA	ATGAAAGCAA	ATGAAATTTT
msa178297.2{104_2603}	TTTGGTGCGA	CATTTACTCA	AAAAGCTCTA	ATGAAAGCAA	ATGAAATTTT
msa178297.2{104_CJB110}	TTTGGTGCGA	CATTTACTCA	AAAAGCTCTA	ATGAAAGCAA	ATGAAATTTT
msa178297.2{104_COH1}	TTTGGTGCGA	CATTTACTCA	AAAAGCTCTA	ATGAAAGCAA	ATGAAATTTT
msa178297.2{104_M732}	TTTGGTGCGA	CATTTACTCA	AAAAGCTCTA	ATGAAAGCAA	ATGAAATTTT
msa178297.2{104_A909}	TTTGGTGCGA	CATTTACTCA	AAAAGCTCTA	ATGAAAGCAA	ATGAAATTTT
msa178297.2{104_M781}	TTTGGTGCGA	CATTTACTCA	AAAAGCTCTA	ATGAAAGCAA	ATGAAATTTT
msa178297.2{104_JM9130013}	TTTGGTGCGA	CATTTACTCA	AAAAGCTCTA	ATGAAAGCAA	ATGAAATTTT
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	AGAGACACAA	AGTTCTAATG	CTAGAAAAAA	ACTTATTTTT	CACGTAACCTG
msa178297.2{104_18RS21}	AGAGACACAA	AGTTCTAATG	CTAGAAAAAA	ACTTATTTTT	CACGTAACCTG
msa178297.2{104_2603}	AGAGACACAA	AGTTCTAATG	CTAGAAAAAA	ACTTATTTTT	CACGTAACCTG
msa178297.2{104_CJB110}	AGAGACACAA	AGTTCTAATG	CTAGAAAAAA	ACTTATTTTT	CACGTAACCTG
msa178297.2{104_COH1}	AGAGACACAA	AGTTCTAATG	CTAGAAAAAA	ACTTATTTTT	CACGTAACCTG
msa178297.2{104_M732}	AGAGACACAA	AGTTCTAATG	CTAGAAAAAA	ACTTATTTTT	CACGTAACCTG
msa178297.2{104_A909}	AGAGACACAA	AGTTCTAATG	CTAGAAAAAA	ACTTATTTTT	CACGTAACCTG
msa178297.2{104_M781}	AGAGACACAA	AGTTCTAATG	CTAGAAAAAA	ACTTATTTTT	CACGTAACCTG
msa178297.2{104_JM9130013}	AGAGACACAA	AGTTCTAATG	CTAGAAAAAA	ACTTATTTTT	CACGTAACCTG
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	ATGGTGTCCC	TACGATGTCT	TATGCCATAA	ATTTTAATCC	TTATATATCA
msa178297.2{104_18RS21}	ATGGTGTCCC	TACGATGTCT	TATGCCATAA	ATTTTAATCC	TTATATATCA
msa178297.2{104_2603}	ATGGTGTCCC	TACGATGTCT	TATGCCATAA	ATTTTAATCC	TTATATATCA
msa178297.2{104_CJB110}	ATGGTGTCCC	TACGATGTCT	TATGCCATAA	ATTTTAATCC	TTATATATCA
msa178297.2{104_COH1}	ATGGTGTCCC	TACGATGTCT	TATGCCATAA	ATTTTAATCC	TTATATATCA
msa178297.2{104_M732}	ATGGTGTCCC	TACGATGTCT	TATGCCATAA	ATTTTAATCC	TTATATATCA
msa178297.2{104_A909}	ATGGTGTCCC	TACGATGTCT	TATGCCATAA	ATTTTAATCC	TTATATATCA
msa178297.2{104_M781}	ATGGTGTCCC	TACGATGTCT	TATGCCATAA	ATTTTAATCC	TTATATATCA
msa178297.2{104_JM9130013}	ATGGTGTCCC	TACGATGTCT	TATGCCATAA	ATTTTAATCC	TTATATATCA
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	ACATCTTACC	AAAACCAGTT	TAATTCCTTT	TTAAATAAAA	TACCAGATAG
msa178297.2{104_18RS21}	ACATCTTACC	AAAACCAGTT	TAATTCCTTT	TTAAATAAAA	TACCAGATAG
msa178297.2{104_2603}	ACATCTTACC	AAAACCAGTT	TAATTCCTTT	TTAAATAAAA	TACCAGATAG
msa178297.2{104_CJB110}	ACATCTTACC	AAAACCAGTT	TAATTCCTTT	TTAAATAAAA	TACCAGATAG
msa178297.2{104_COH1}	ACATCTTACC	AAAACCAGTT	TAATTCCTTT	TTAAATAAAA	TACCAGATAG
msa178297.2{104_M732}	ACATCTTACC	AAAACCAGTT	TAATTCCTTT	TTAAATAAAA	TACCAGATAG
msa178297.2{104_A909}	ACATCTTACC	AAAACCAGTT	TAATTCCTTT	TTAAATAAAA	TACCAGATAG
msa178297.2{104_M781}	ACATCTTACC	AAAACCAGTT	TAATTCCTTT	TTAAATAAAA	TACCAGATAG
msa178297.2{104_JM9130013}	ACATCTTACC	AAAACCAGTT	TAATTCCTTT	TTAAATAAAA	TACCAGATAG
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	AAGTGGTATT	CTCCAAGAGG	ATTTTATAAT	CAATGGTGAT	GATTATCAAA
msa178297.2{104_18RS21}	AAGTGGTATT	CTCCAAGAGG	ATTTTATAAT	CAATGGTGAT	GATTATCAAA
msa178297.2{104_2603}	AAGTGGTATT	CTCCAAGAGG	ATTTTATAAT	CAATGGTGAT	GATTATCAAA
msa178297.2{104_CJB110}	AAGTGGTATT	CTCCAAGAGG	ATTTTATAAT	CAATGGTGAT	GATTATCAAA
msa178297.2{104_COH1}	AAGTGGTATT	CTCCAAGAGG	ATTTTATAAT	CAATGGTGAT	GATTATCAAA
msa178297.2{104_M732}	AAGTGGTATT	CTCCAAGAGG	ATTTTATAAT	CAATGGTGAT	GATTATCAAA
msa178297.2{104_A909}	AAGTGGTATT	CTCCAAGAGG	ATTTTATAAT	CAATGGTGAT	GATTATCAAA
msa178297.2{104_M781}	AAGTGGTATT	CTCCAAGAGG	ATTTTATAAT	CAATGGTGAT	GATTATCAAA
msa178297.2{104_JM9130013}	AAGTGGTATT	CTCCAAGAGG	ATTTTATAAT	CAATGGTGAT	GATTATCAAA
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	TAGTAAAAGG	AGATGGAGAG	AGTTTAAAC	TGTTTTCGGA	TAGAAAAGTT
msa178297.2{104_18RS21}	TAGTAAAAGG	AGATGGAGAG	AGTTTAAAC	TGTTTTCGGA	TAGAAAAGTT
msa178297.2{104_2603}	TAGTAAAAGG	AGATGGAGAG	AGTTTAAAC	TGTTTTCGGA	TAGAAAAGTT
msa178297.2{104_CJB110}	TAGTAAAAGG	AGATGGAGAG	AGTTTAAAC	TGTTTTCGGA	TAGAAAAGTT
msa178297.2{104_COH1}	TAGTAAAAGG	AGATGGAGAG	AGTTTAAAC	TGTTTTCGGA	TAGAAAAGTT
msa178297.2{104_M732}	TAGTAAAAGG	AGATGGAGAG	AGTTTAAAC	TGTTTTCGGA	TAGAAAAGTT
msa178297.2{104_A909}	TAGTAAAAGG	AGATGGAGAG	AGTTTAAAC	TGTTTTCGGA	TAGAAAAGTT
msa178297.2{104_M781}	TAGTAAAAGG	AGATGGAGAG	AGTTTAAAC	TGTTTTCGGA	TAGAAAAGTT
msa178297.2{104_JM9130013}	TAGTAAAAGG	AGATGGAGAG	AGTTTAAAC	TGTTTTCGGA	TAGAAAAGTT
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	CCTGTTACTG	GAGGAACGAC	ACAAGCAGCT	TATCGAGTAC	CGCAAAATCA
msa178297.2{104_18RS21}	CCTGTTACTG	GAGGAACGAC	ACAAGCAGCT	TATCGAGTAC	CGCAAAATCA
msa178297.2{104_2603}	CCTGTTACTG	GAGGAACGAC	ACAAGCAGCT	TATCGAGTAC	CGCAAAATCA
msa178297.2{104_CJB110}	CCTGTTACTG	GAGGAACGAC	ACAAGCAGCT	TATCGAGTAC	CGCAAAATCA
msa178297.2{104_COH1}	CCTGTTACTG	GAGGAACGAC	ACAAGCAGCT	TATCGAGTAC	CGCAAAATCA

Table 41: Comparative Sequences relating to SAG0649

msa178297.2{104_M732}	CCTGTTACTG	GAGGAACGAC	ACAAGCAGCT	TATCGAGTAC	CGCAAAATCA
msa178297.2{104_A909}	CCTGTTACTG	GAGGAACGAC	ACAAGCAGCT	TATCGAGTAC	CGCAAAATCA
msa178297.2{104_M781}	CCTGTTACTG	GAGGAACGAC	ACAAGCAGCT	TATCGAGTAC	CGCAAAATCA
msa178297.2{104_JM9130013}	CCTGTTACTG	GAGGAACGAC	ACAAGCAGCT	TATCGAGTAC	CGCAAAATCA
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	ACTCTCTGTA	ATGAGTAATG	AGGGATATGC	AATTAATAGT	GGATATATTT
msa178297.2{104_18RS21}	ACTCTCTGTA	ATGAGTAATG	AGGGATATGC	AATTAATAGT	GGATATATTT
msa178297.2{104_2603}	ACTCTCTGTA	ATGAGTAATG	AGGGATATGC	AATTAATAGT	GGATATATTT
msa178297.2{104_CJB110}	ACTCTCTGTA	ATGAGTAATG	AGGGATATGC	AATTAATAGT	GGATATATTT
msa178297.2{104_COH1}	ACTCTCTGTA	ATGAGTAATG	AGGGATATGC	AATTAATAGT	GGATATATTT
msa178297.2{104_M732}	ACTCTCTGTA	ATGAGTAATG	AGGGATATGC	AATTAATAGT	GGATATATTT
msa178297.2{104_A909}	ACTCTCTGTA	ATGAGTAATG	AGGGATATGC	AATTAATAGT	GGATATATTT
msa178297.2{104_M781}	ACTCTCTGTA	ATGAGTAATG	AGGGATATGC	AATTAATAGT	GGATATATTT
msa178297.2{104_JM9130013}	ACTCTCTGTA	ATGAGTAATG	AGGGATATGC	AATTAATAGT	GGATATATTT
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	ATCTCTATTG	GAGAGATTAC	AACCTGGGTCT	ATCCATTGGA	TCCTAAGACA
msa178297.2{104_18RS21}	ATCTCTATTG	GAGAGATTAC	AACCTGGGTCT	ATCCATTGGA	TCCTAAGACA
msa178297.2{104_2603}	ATCTCTATTG	GAGAGATTAC	AACCTGGGTCT	ATCCATTGGA	TCCTAAGACA
msa178297.2{104_CJB110}	ATCTCTATTG	GAGAGATTAC	AACCTGGGTCT	ATCCATTGGA	TCCTAAGACA
msa178297.2{104_COH1}	ATCTCTATTG	GAGAGATTAC	AACCTGGGTCT	ATCCATTGGA	TCCTAAGACA
msa178297.2{104_M732}	ATCTCTATTG	GAGAGATTAC	AACCTGGGTCT	ATCCATTGGA	TCCTAAGACA
msa178297.2{104_A909}	ATCTCTATTG	GAGAGATTAC	AACCTGGGTCT	ATCCATTGGA	TCCTAAGACA
msa178297.2{104_M781}	ATCTCTATTG	GAGAGATTAC	AACCTGGGTCT	ATCCATTGGA	TCCTAAGACA
msa178297.2{104_JM9130013}	ATCTCTATTG	GAGAGATTAC	AACCTGGGTCT	ATCCATTGGA	TCCTAAGACA
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	AAGAAAGTTT	CTGCAACGAA	ACAAATCAAA	ACTCATGGTG	AGCCAACAAC
msa178297.2{104_18RS21}	AAGAAAGTTT	CTGCAACGAA	ACAAATCAAA	ACTCATGGTG	AGCCAACAAC
msa178297.2{104_2603}	AAGAAAGTTT	CTGCAACGAA	ACAAATCAAA	ACTCATGGTG	AGCCAACAAC
msa178297.2{104_CJB110}	AAGAAAGTTT	CTGCAACGAA	ACAAATCAAA	ACTCATGGTG	AGCCAACAAC
msa178297.2{104_COH1}	AAGAAAGTTT	CTGCAACGAA	ACAAATCAAA	ACTCATGGTG	AGCCAACAAC
msa178297.2{104_M732}	AAGAAAGTTT	CTGCAACGAA	ACAAATCAAA	ACTCATGGTG	AGCCAACAAC
msa178297.2{104_A909}	AAGAAAGTTT	CTGCAACGAA	ACAAATCAAA	ACTCATGGTG	AGCCAACAAC
msa178297.2{104_M781}	AAGAAAGTTT	CTGCAACGAA	ACAAATCAAA	ACTCATGGTG	AGCCAACAAC
msa178297.2{104_JM9130013}	AAGAAAGTTT	CTGCAACGAA	ACAAATCAAA	ACTCATGGTG	AGCCAACAAC
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	ATTATACITT	AATGGAAATA	TAAGACCTAA	AGGTTATGAC	ATTTTACTG
msa178297.2{104_18RS21}	ATTATACITT	AATGGAAATA	TAAGACCTAA	AGGTTATGAC	ATTTTACTG
msa178297.2{104_2603}	ATTATACITT	AATGGAAATA	TAAGACCTAA	AGGTTATGAC	ATTTTACTG
msa178297.2{104_CJB110}	ATTATACITT	AATGGAAATA	TAAGACCTAA	AGGTTATGAC	ATTTTACTG
msa178297.2{104_COH1}	ATTATACITT	AATGGAAATA	TAAGACCTAA	AGGTTATGAC	ATTTTACTG
msa178297.2{104_M732}	ATTATACITT	AATGGAAATA	TAAGACCTAA	AGGTTATGAC	ATTTTACTG
msa178297.2{104_A909}	ATTATACITT	AATGGAAATA	TAAGACCTAA	AGGTTATGAC	ATTTTACTG
msa178297.2{104_M781}	ATTATACITT	AATGGAAATA	TAAGACCTAA	AGGTTATGAC	ATTTTACTG
msa178297.2{104_JM9130013}	ATTATACITT	AATGGAAATA	TAAGACCTAA	AGGTTATGAC	ATTTTACTG
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	TTGGGATTGG	TGTAAACGGA	GATCCTGGTG	CAACTCCTCT	TGAAGCTGAG
msa178297.2{104_18RS21}	TTGGGATTGG	TGTAAACGGA	GATCCTGGTG	CAACTCCTCT	TGAAGCTGAG
msa178297.2{104_2603}	TTGGGATTGG	TGTAAACGGA	GATCCTGGTG	CAACTCCTCT	TGAAGCTGAG
msa178297.2{104_CJB110}	TTGGGATTGG	TGTAAACGGA	GATCCTGGTG	CAACTCCTCT	TGAAGCTGAG
msa178297.2{104_COH1}	TTGGGATTGG	TGTAAACGGA	GATCCTGGTG	CAACTCCTCT	TGAAGCTGAG
msa178297.2{104_M732}	TTGGGATTGG	TGTAAACGGA	GATCCTGGTG	CAACTCCTCT	TGAAGCTGAG
msa178297.2{104_A909}	TTGGGATTGG	TGTAAACGGA	GATCCTGGTG	CAACTCCTCT	TGAAGCTGAG
msa178297.2{104_M781}	TTGGGATTGG	TGTAAACGGA	GATCCTGGTG	CAACTCCTCT	TGAAGCTGAG
msa178297.2{104_JM9130013}	TTGGGATTGG	TGTAAACGGA	GATCCTGGTG	CAACTCCTCT	TGAAGCTGAG
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	AAATTTATGC	AATCAATATC	AAGTAAAACA	GAAAATTATA	CTAATGTTGA
msa178297.2{104_18RS21}	AAATTTATGC	AATCAATATC	AAGTAAAACA	GAAAATTATA	CTAATGTTGA
msa178297.2{104_2603}	AAATTTATGC	AATCAATATC	AAGTAAAACA	GAAAATTATA	CTAATGTTGA
msa178297.2{104_CJB110}	AAATTTATGC	AATCAATATC	AAGTAAAACA	GAAAATTATA	CTAATGTTGA
msa178297.2{104_COH1}	AAATTTATGC	AATCAATATC	AAGTAAAACA	GAAAATTATA	CTAATGTTGA
msa178297.2{104_M732}	AAATTTATGC	AATCAATATC	AAGTAAAACA	GAAAATTATA	CTAATGTTGA
msa178297.2{104_A909}	AAATTTATGC	AATCAATATC	AAGTAAAACA	GAAAATTATA	CTAATGTTGA
msa178297.2{104_M781}	AAATTTATGC	AATCAATATC	AAGTAAAACA	GAAAATTATA	CTAATGTTGA
msa178297.2{104_JM9130013}	AAATTTATGC	AATCAATATC	AAGTAAAACA	GAAAATTATA	CTAATGTTGA
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	TGATACAAAT	AAAATTTATG	ATGAGCTAAA	TAAATACITT	AAAACAATTG
msa178297.2{104_18RS21}	TGATACAAAT	AAAATTTATG	ATGAGCTAAA	TAAATACITT	AAAACAATTG
msa178297.2{104_2603}	TGATACAAAT	AAAATTTATG	ATGAGCTAAA	TAAATACITT	AAAACAATTG
msa178297.2{104_CJB110}	TGATACAAAT	AAAATTTATG	ATGAGCTAAA	TAAATACITT	AAAACAATTG

Table 41: Comparative Sequences relating to SAG0649

msa178297.2{104_COH1}	TGATACAAAT	AAAATTATG	ATGAGCTAAA	TAAATACTTT	AAAACAATTG
msa178297.2{104_M732}	TGATACAAAT	AAAATTATG	ATGAGCTAAA	TAAATACTTT	AAAACAATTG
msa178297.2{104_A909}	TGATACAAAT	AAAATTATG	ATGAGCTAAA	TAAATACTTT	AAAACAATTG
msa178297.2{104_M781}	TGATACAAAT	AAAATTATG	ATGAGCTAAA	TAAATACTTT	AAAACAATTG
msa178297.2{104_JM9130013}	TGATACAAAT	AAAATTATG	ATGAGCTAAA	TAAATACTTT	AAAACAATTG
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	TTGAGGAAAA	ACATTCTATT	GTGATGGAA	ATGTGACTGA	TCCTATGGGA
msa178297.2{104_18RS21}	TTGAGGAAAA	ACATTCTATT	GTGATGGAA	ATGTGACTGA	TCCTATGGGA
msa178297.2{104_2603}	TTGAGGAAAA	ACATTCTATT	GTGATGGAA	ATGTGACTGA	TCCTATGGGA
msa178297.2{104_CJB110}	TTGAGGAAAA	ACATTCTATT	GTGATGGAA	ATGTGACTGA	TCCTATGGGA
msa178297.2{104_COH1}	TTGAGGAAAA	ACATTCTATT	GTGATGGAA	ATGTGACTGA	TCCTATGGGA
msa178297.2{104_M732}	TTGAGGAAAA	ACATTCTATT	GTGATGGAA	ATGTGACTGA	TCCTATGGGA
msa178297.2{104_A909}	TTGAGGAAAA	ACATTCTATT	GTGATGGAA	ATGTGACTGA	TCCTATGGGA
msa178297.2{104_M781}	TTGAGGAAAA	ACATTCTATT	GTGATGGAA	ATGTGACTGA	TCCTATGGGA
msa178297.2{104_JM9130013}	TTGAGGAAAA	ACATTCTATT	GTGATGGAA	ATGTGACTGA	TCCTATGGGA
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	GAGATGATTG	AATTCCAATT	AAAAAATGGT	CAAAGTTTGA	CACATGATGA
msa178297.2{104_18RS21}	GAGATGATTG	AATTCCAATT	AAAAAATGGT	CAAAGTTTGA	CACATGATGA
msa178297.2{104_2603}	GAGATGATTG	AATTCCAATT	AAAAAATGGT	CAAAGTTTGA	CACATGATGA
msa178297.2{104_CJB110}	GAGATGATTG	AATTCCAATT	AAAAAATGGT	CAAAGTTTGA	CACATGATGA
msa178297.2{104_COH1}	GAGATGATTG	AATTCCAATT	AAAAAATGGT	CAAAGTTTGA	CACATGATGA
msa178297.2{104_M732}	GAGATGATTG	AATTCCAATT	AAAAAATGGT	CAAAGTTTGA	CACATGATGA
msa178297.2{104_A909}	GAGATGATTG	AATTCCAATT	AAAAAATGGT	CAAAGTTTGA	CACATGATGA
msa178297.2{104_M781}	GAGATGATTG	AATTCCAATT	AAAAAATGGT	CAAAGTTTGA	CACATGATGA
msa178297.2{104_JM9130013}	GAGATGATTG	AATTCCAATT	AAAAAATGGT	CAAAGTTTGA	CACATGATGA
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	TTACGTTTTG	GTTGGAAATG	ATGGCAGTCA	ATTAAAAAAT	GGTGTGGCTC
msa178297.2{104_18RS21}	TTACGTTTTG	GTTGGAAATG	ATGGCAGTCA	ATTAAAAAAT	GGTGTGGCTC
msa178297.2{104_2603}	TTACGTTTTG	GTTGGAAATG	ATGGCAGTCA	ATTAAAAAAT	GGTGTGGCTC
msa178297.2{104_CJB110}	TTACGTTTTG	GTTGGAAATG	ATGGCAGTCA	ATTAAAAAAT	GGTGTGGCTC
msa178297.2{104_COH1}	TTACGTTTTG	GTTGGAAATG	ATGGCAGTCA	ATTAAAAAAT	GGTGTGGCTC
msa178297.2{104_M732}	TTACGTTTTG	GTTGGAAATG	ATGGCAGTCA	ATTAAAAAAT	GGTGTGGCTC
msa178297.2{104_A909}	TTACGTTTTG	GTTGGAAATG	ATGGCAGTCA	ATTAAAAAAT	GGTGTGGCTC
msa178297.2{104_M781}	TTACGTTTTG	GTTGGAAATG	ATGGCAGTCA	ATTAAAAAAT	GGTGTGGCTC
msa178297.2{104_JM9130013}	TTACGTTTTG	GTTGGAAATG	ATGGCAGTCA	ATTAAAAAAT	GGTGTGGCTC
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	TTGGTGGACC	AAACAGTGAT	GGGGGAATTT	TAAAAGATGT	TACAGTGACT
msa178297.2{104_18RS21}	TTGGTGGACC	AAACAGTGAT	GGGGGAATTT	TAAAAGATGT	TACAGTGACT
msa178297.2{104_2603}	TTGGTGGACC	AAACAGTGAT	GGGGGAATTT	TAAAAGATGT	TACAGTGACT
msa178297.2{104_CJB110}	TTGGTGGACC	AAACAGTGAT	GGGGGAATTT	TAAAAGATGT	TACAGTGACT
msa178297.2{104_COH1}	TTGGTGGACC	AAACAGTGAT	GGGGGAATTT	TAAAAGATGT	TACAGTGACT
msa178297.2{104_M732}	TTGGTGGACC	AAACAGTGAT	GGGGGAATTT	TAAAAGATGT	TACAGTGACT
msa178297.2{104_A909}	TTGGTGGACC	AAACAGTGAT	GGGGGAATTT	TAAAAGATGT	TACAGTGACT
msa178297.2{104_M781}	TTGGTGGACC	AAACAGTGAT	GGGGGAATTT	TAAAAGATGT	TACAGTGACT
msa178297.2{104_JM9130013}	TTGGTGGACC	AAACAGTGAT	GGGGGAATTT	TAAAAGATGT	TACAGTGACT
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	TATGATAAGA	CATCTCAAAC	CATCAAAATC	AATCATTTGA	ACTTAGGAAG
msa178297.2{104_18RS21}	TATGATAAGA	CATCTCAAAC	CATCAAAATC	AATCATTTGA	ACTTAGGAAG
msa178297.2{104_2603}	TATGATAAGA	CATCTCAAAC	CATCAAAATC	AATCATTTGA	ACTTAGGAAG
msa178297.2{104_CJB110}	TATGATAAGA	CATCTCAAAC	CATCAAAATC	AATCATTTGA	ACTTAGGAAG
msa178297.2{104_COH1}	TATGATAAGA	CATCTCAAAC	CATCAAAATC	AATCATTTGA	ACTTAGGAAG
msa178297.2{104_M732}	TATGATAAGA	CATCTCAAAC	CATCAAAATC	AATCATTTGA	ACTTAGGAAG
msa178297.2{104_A909}	TATGATAAGA	CATCTCAAAC	CATCAAAATC	AATCATTTGA	ACTTAGGAAG
msa178297.2{104_M781}	TATGATAAGA	CATCTCAAAC	CATCAAAATC	AATCATTTGA	ACTTAGGAAG
msa178297.2{104_JM9130013}	TATGATAAGA	CATCTCAAAC	CATCAAAATC	AATCATTTGA	ACTTAGGAAG
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	TGGACAAAAA	GTAGTTCCTA	CCTATGATGT	ACGTTTAAAA	GATAACTATA
msa178297.2{104_18RS21}	TGGACAAAAA	GTAGTTCCTA	CCTATGATGT	ACGTTTAAAA	GATAACTATA
msa178297.2{104_2603}	TGGACAAAAA	GTAGTTCCTA	CCTATGATGT	ACGTTTAAAA	GATAACTATA
msa178297.2{104_CJB110}	TGGACAAAAA	GTAGTTCCTA	CCTATGATGT	ACGTTTAAAA	GATAACTATA
msa178297.2{104_COH1}	TGGACAAAAA	GTAGTTCCTA	CCTATGATGT	ACGTTTAAAA	GATAACTATA
msa178297.2{104_M732}	TGGACAAAAA	GTAGTTCCTA	CCTATGATGT	ACGTTTAAAA	GATAACTATA
msa178297.2{104_A909}	TGGACAAAAA	GTAGTTCCTA	CCTATGATGT	ACGTTTAAAA	GATAACTATA
msa178297.2{104_M781}	TGGACAAAAA	GTAGTTCCTA	CCTATGATGT	ACGTTTAAAA	GATAACTATA
msa178297.2{104_JM9130013}	TGGACAAAAA	GTAGTTCCTA	CCTATGATGT	ACGTTTAAAA	GATAACTATA
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	TAAGTAACAA	ATTTTACAAT	ACAAATAATC	GTACAACGCT	AAGTCCGAAG
msa178297.2{104_18RS21}	TAAGTAACAA	ATTTTACAAT	ACAAATAATC	GTACAACGCT	AAGTCCGAAG
msa178297.2{104_2603}	TAAGTAACAA	ATTTTACAAT	ACAAATAATC	GTACAACGCT	AAGTCCGAAG

Table 41: Comparative Sequences relating to SAG0649

msa178297.2{104_CJB110}	TAAGTAACAA	ATTTTACAAT	ACAAATAATC	GTACAACGCT	AAGTCCGAAG
msa178297.2{104_COH1}	TAAGTAACAA	ATTTTACAAT	ACAAATAATC	GTACAACGCT	AAGTCCGAAG
msa178297.2{104_M732}	TAAGTAACAA	ATTTTACAAT	ACAAATAATC	GTACAACGCT	AAGTCCGAAG
msa178297.2{104_A909}	TAAGTAACAA	ATTTTACAAT	ACAAATAATC	GTACAACGCT	AAGTCCGAAG
msa178297.2{104_M781}	TAAGTAACAA	ATTTTACAAT	ACAAATAATC	GTACAACGCT	AAGTCCGAAG
msa178297.2{104_JM9130013}	TAAGTAACAA	ATTTTACAAT	ACAAATAATC	GTACAACGCT	AAGTCCGAAG
Consensus	*****	*****	*****	*****	*****
2101					
msa178297.2{104_090}	AGTGAAAAAG	AACCAAATAC	TATTCGTGAT	TTCCCAATTC	CCAAAAATTCG
msa178297.2{104_18RS21}	AGTGAAAAAG	AACCAAATAC	TATTCGTGAT	TTCCCAATTC	CCAAAAATTCG
msa178297.2{104_2603}	AGTGAAAAAG	AACCAAATAC	TATTCGTGAT	TTCCCAATTC	CCAAAAATTCG
msa178297.2{104_CJB110}	AGTGAAAAAG	AACCAAATAC	TATTCGTGAT	TTCCCAATTC	CCAAAAATTCG
msa178297.2{104_COH1}	AGTGAAAAAG	AACCAAATAC	TATTCGTGAT	TTCCCAATTC	CCAAAAATTCG
msa178297.2{104_M732}	AGTGAAAAAG	AACCAAATAC	TATTCGTGAT	TTCCCAATTC	CCAAAAATTCG
msa178297.2{104_A909}	AGTGAAAAAG	AACCAAATAC	TATTCGTGAT	TTCCCAATTC	CCAAAAATTCG
msa178297.2{104_M781}	AGTGAAAAAG	AACCAAATAC	TATTCGTGAT	TTCCCAATTC	CCAAAAATTCG
msa178297.2{104_JM9130013}	AGTGAAAAAG	AACCAAATAC	TATTCGTGAT	TTCCCAATTC	CCAAAAATTCG
Consensus	*****	*****	*****	*****	*****
2151					
msa178297.2{104_090}	TGATGTTTCGT	GAGTTTCCGG	TACTAACCAT	CAGTAATCag	AAGAAAAATGG
msa178297.2{104_18RS21}	TGATGTTTCGT	GAGTTTCCGG	TACTAACCAT	CAGTAATCag	AAGAAAAATGG
msa178297.2{104_2603}	TGATGTTTCGT	GAGTTTCCGG	TACTAACCAT	CAGTAATCag	AAGAAAAATGG
msa178297.2{104_CJB110}	TGATGTTTCGT	GAGTTTCCGG	TACTAACCAT	CAGTAATCag	AAGAAAAATGG
msa178297.2{104_COH1}	TGATGTTTCGT	GAGTTTCCGG	TACTAACCAT	CAGTAATCag	AAGAAAAATGG
msa178297.2{104_M732}	TGATGTTTCGT	GAGTTTCCGG	TACTAACCAT	CAGTAATCag	AAGAAAAATGG
msa178297.2{104_A909}	TGATGTTTCGT	GAGTTTCCGG	TACTAACCAT	CAGTAATCag	AAGAAAAATGG
msa178297.2{104_M781}	TGATGTTTCGT	GAGTTTCCGG	TACTAACCAT	CAGTAATCag	AAGAAAAATGG
msa178297.2{104_JM9130013}	TGATGTTTCGT	GAGTTTCCGG	TACTAACCAT	CAGTAATCag	AAGAAAAATGG
Consensus	*****	*****	*****	*****	*****
2201					
msa178297.2{104_090}	GTGAGGTTGA	ATTTATTAAA	GTTAATAAAG	ACAAACATTC	AGAATCGCTT
msa178297.2{104_18RS21}	GTGAGGTTGA	ATTTATTAAA	GTTAATAAAG	ACAAACATTC	AGAATCGCTT
msa178297.2{104_2603}	GTGAGGTTGA	ATTTATTAAA	GTTAATAAAG	ACAAACATTC	AGAATCGCTT
msa178297.2{104_CJB110}	GTGAGGTTGA	ATTTATTAAA	GTTAATAAAG	ACAAACATTC	AGAATCGCTT
msa178297.2{104_COH1}	GTGAGGTTGA	ATTTATTAAA	GTTAATAAAG	ACAAACATTC	AGAATCGCTT
msa178297.2{104_M732}	GTGAGGTTGA	ATTTATTAAA	GTTAATAAAG	ACAAACATTC	AGAATCGCTT
msa178297.2{104_A909}	GTGAGGTTGA	ATTTATTAAA	GTTAATAAAG	ACAAACATTC	AGAATCGCTT
msa178297.2{104_M781}	GTGAGGTTGA	ATTTATTAAA	GTTAATAAAG	ACAAACATTC	AGAATCGCTT
msa178297.2{104_JM9130013}	GTGAGGTTGA	ATTTATTAAA	GTTAATAAAG	ACAAACATTC	AGAATCGCTT
Consensus	*****	*****	*****	*****	*****
2251					
msa178297.2{104_090}	TTGGGAGCTA	AGTTTCAACT	TCAGATagAA	AAAGATTITTT	CTGGGTATAAA
msa178297.2{104_18RS21}	TTGGGAGCTA	AGTTTCAACT	TCAGATagAA	AAAGATTITTT	CTGGGTATAAA
msa178297.2{104_2603}	TTGGGAGCTA	AGTTTCAACT	TCAGATagAA	AAAGATTITTT	CTGGGTATAAA
msa178297.2{104_CJB110}	TTGGGAGCTA	AGTTTCAACT	TCAGATagAA	AAAGATTITTT	CTGGGTATAAA
msa178297.2{104_COH1}	TTGGGAGCTA	AGTTTCAACT	TCAGATagAA	AAAGATTITTT	CTGGGTATAAA
msa178297.2{104_M732}	TTGGGAGCTA	AGTTTCAACT	TCAGATagAA	AAAGATTITTT	CTGGGTATAAA
msa178297.2{104_A909}	TTGGGAGCTA	AGTTTCAACT	TCAGATagAA	AAAGATTITTT	CTGGGTATAAA
msa178297.2{104_M781}	TTGGGAGCTA	AGTTTCAACT	TCAGATagAA	AAAGATTITTT	CTGGGTATAAA
msa178297.2{104_JM9130013}	TTGGGAGCTA	AGTTTCAACT	TCAGATagAA	AAAGATTITTT	CTGGGTATAAA
Consensus	*****	*****	*****	*****	*****
2251					
msa178297.2{104_090}	GCAATTGTGT	CCAGAGGGAA	GTGATGTTAC	AACAAGAAT	GATGGTAAAA
msa178297.2{104_18RS21}	GCAATTGTGT	CCAGAGGGAA	GTGATGTTAC	AACAAGAAT	GATGGTAAAA
msa178297.2{104_2603}	GCAATTGTGT	CCAGAGGGAA	GTGATGTTAC	AACAAGAAT	GATGGTAAAA
msa178297.2{104_CJB110}	GCAATTGTGT	CCAGAGGGAA	GTGATGTTAC	AACAAGAAT	GATGGTAAAA
msa178297.2{104_COH1}	GCAATTGTGT	CCAGAGGGAA	GTGATGTTAC	AACAAGAAT	GATGGTAAAA
msa178297.2{104_M732}	GCAATTGTGT	CCAGAGGGAA	GTGATGTTAC	AACAAGAAT	GATGGTAAAA
msa178297.2{104_A909}	GCAATTGTGT	CCAGAGGGAA	GTGATGTTAC	AACAAGAAT	GATGGTAAAA
msa178297.2{104_M781}	GCAATTGTGT	CCAGAGGGAA	GTGATGTTAC	AACAAGAAT	GATGGTAAAA
msa178297.2{104_JM9130013}	GCAATTGTGT	CCAGAGGGAA	GTGATGTTAC	AACAAGAAT	GATGGTAAAA
Consensus	*****	*****	*****	*****	*****
2301					
msa178297.2{104_090}	TTTATTTTAA	AGCACTTCAA	GATGGTAACT	ATAAATTATA	TGAAATTTTCA
msa178297.2{104_18RS21}	TTTATTTTAA	AGCACTTCAA	GATGGTAACT	ATAAATTATA	TGAAATTTTCA
msa178297.2{104_2603}	TTTATTTTAA	AGCACTTCAA	GATGGTAACT	ATAAATTATA	TGAAATTTTCA
msa178297.2{104_CJB110}	TTTATTTTAA	AGCACTTCAA	GATGGTAACT	ATAAATTATA	TGAAATTTTCA
msa178297.2{104_COH1}	TTTATTTTAA	AGCACTTCAA	GATGGTAACT	ATAAATTATA	TGAAATTTTCA
msa178297.2{104_M732}	TTTATTTTAA	AGCACTTCAA	GATGGTAACT	ATAAATTATA	TGAAATTTTCA
msa178297.2{104_A909}	TTTATTTTAA	AGCACTTCAA	GATGGTAACT	ATAAATTATA	TGAAATTTTCA
msa178297.2{104_M781}	TTTATTTTAA	AGCACTTCAA	GATGGTAACT	ATAAATTATA	TGAAATTTTCA
msa178297.2{104_JM9130013}	TTTATTTTAA	AGCACTTCAA	GATGGTAACT	ATAAATTATA	TGAAATTTTCA
Consensus	*****	*****	*****	*****	*****
2351					
msa178297.2{104_090}	AGTCCAGATG	GCTATATAGA	GGTTAAAACG	AAACCTGTTG	TGACATTTCa
msa178297.2{104_18RS21}	AGTCCAGATG	GCTATATAGA	GGTTAAAACG	AAACCTGTTG	TGACATTTCa

Table 41: Comparative Sequences relating to SAG0649

msa178297.2{104_2603}	AGTCCAGATG	GCTATATAGA	GGTTAAAAACG	AAACCTGTTG	TGACATTTAC
msa178297.2{104_CJB110}	AGTCCAGATG	GCTATATAGA	GGTTAAAAACG	AAACCTGTTG	TGACATTTAC
msa178297.2{104_COH1}	AGTCCAGATG	GCTATATAGA	GGTTAAAAACG	AAACCTGTTG	TGACATTTAC
msa178297.2{104_M732}	AGTCCAGATG	GCTATATAGA	GGTTAAAAACG	AAACCTGTTG	TGACATTTAC
msa178297.2{104_A909}	AGTCCAGATG	GCTATATAGA	GGTTAAAAACG	AAACCTGTTG	TGACATTTAC
msa178297.2{104_M781}	AGTCCAGATG	GCTATATAGA	GGTTAAAAACG	AAACCTGTTG	TGACATTTAC
msa178297.2{104_JM9130013}	AGTCCAGATG	GCTATATAGA	GGTTAAAAACG	AAACCTGTTG	TGACATTTAC
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	AATTCAAAAT	GGAGAAGTTA	CGAACCTGAA	AGCAGATCCA	AATGCTAATA
msa178297.2{104_18RS21}	AATTCAAAAT	GGAGAAGTTA	CGAACCTGAA	AGCAGATCCA	AATGCTAATA
msa178297.2{104_2603}	AATTCAAAAT	GGAGAAGTTA	CGAACCTGAA	AGCAGATCCA	AATGCTAATA
msa178297.2{104_CJB110}	AATTCAAAAT	GGAGAAGTTA	CGAACCTGAA	AGCAGATCCA	AATGCTAATA
msa178297.2{104_COH1}	AATTCAAAAT	GGAGAAGTTA	CGAACCTGAA	AGCAGATCCA	AATGCTAATA
msa178297.2{104_M732}	AATTCAAAAT	GGAGAAGTTA	CGAACCTGAA	AGCAGATCCA	AATGCTAATA
msa178297.2{104_A909}	AATTCAAAAT	GGAGAAGTTA	CGAACCTGAA	AGCAGATCCA	AATGCTAATA
msa178297.2{104_M781}	AATTCAAAAT	GGAGAAGTTA	CGAACCTGAA	AGCAGATCCA	AATGCTAATA
msa178297.2{104_JM9130013}	AATTCAAAAT	GGAGAAGTTA	CGAACCTGAA	AGCAGATCCA	AATGCTAATA
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	AAAATCAAAT	CGGGTATCTT	GAAggaaatg	gtaaacatct	tattaccaac
msa178297.2{104_18RS21}	AAAATCAAAT	CGGGTATCTT	GAAggaaatg	gtaaacatct	tattaccaac
msa178297.2{104_2603}	AAAATCAAAT	CGGGTATCTT	GAAggaaatg	gtaaacatct	tattaccaac
msa178297.2{104_CJB110}	AAAATCAAAT	CGGGTATCTT	GAAggaaatg	gtaaacatct	tattaccaac
msa178297.2{104_COH1}	AAAATCAAAT	CGGGTATCTT	GAAggaaatg	gtaaacatct	tattaccaac
msa178297.2{104_M732}	AAAATCAAAT	CGGGTATCTT	GAAggaaatg	gtaaacatct	tattaccaac
msa178297.2{104_A909}	AAAATCAAAT	CGGGTATCTT	GAAggaaatg	gtaaacatct	tattaccaac
msa178297.2{104_M781}	AAAATCAAAT	CGGGTATCTT	GAAggaaatg	gtaaacatct	tattaccaac
msa178297.2{104_JM9130013}	AAAATCAAAT	CGGGTATCTT	GAA-----	-----	-----
Consensus	*****	*****	***-----	-----	-----
msa178297.2{104_090}	actcccaaac	gcccaccagg	tggt-----	-----	-----
msa178297.2{104_18RS21}	actcccaaac	gcccaccagg	tggt-----	-----	-----
msa178297.2{104_2603}	actcccaaac	gcccaccagg	tggttttctct	aaaacagggg	gaattggtac
msa178297.2{104_CJB110}	actcccaaac	gcccaccagg	tggt-----	-----	-----
msa178297.2{104_COH1}	actcccaaac	gcccaccagg	tggt-----	-----	-----
msa178297.2{104_M732}	actcccaaac	gcccaccagg	tggt-----	-----	-----
msa178297.2{104_A909}	actcccaaac	gcccaccagg	tggt-----	-----	-----
msa178297.2{104_M781}	actcccaaac	gcccaccagg	tggt-----	-----	-----
msa178297.2{104_JM9130013}	-----	-----	-----	-----	-----
Consensus	-----	-----	-----	*****	*****
msa178297.2{104_090}	-----	-----	-----	-----	-----
msa178297.2{104_18RS21}	-----	-----	-----	-----	-----
msa178297.2{104_2603}	aattgtctat	atattagttg	gttctacttt	tatgatactt	accatttggt
msa178297.2{104_CJB110}	-----	-----	-----	-----	-----
msa178297.2{104_COH1}	-----	-----	-----	-----	-----
msa178297.2{104_M732}	-----	-----	-----	-----	-----
msa178297.2{104_A909}	-----	-----	-----	-----	-----
msa178297.2{104_M781}	-----	-----	-----	-----	-----
msa178297.2{104_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
msa178297.2{104_090}	-----	-----	-----	-----	-----
msa178297.2{104_18RS21}	-----	-----	-----	-----	-----
msa178297.2{104_2603}	ctttccgtcg	taaacaattg	-----	-----	-----
msa178297.2{104_CJB110}	-----	-----	-----	-----	-----
msa178297.2{104_COH1}	-----	-----	-----	-----	-----
msa178297.2{104_M732}	-----	-----	-----	-----	-----
msa178297.2{104_A909}	-----	-----	-----	-----	-----
msa178297.2{104_M781}	-----	-----	-----	-----	-----
msa178297.2{104_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	-----	-----	-----

Table 41: Comparative Sequences relating to SAG0649

SEQ ID NO. 4110: SAG0649 FROM 2603 V/R GBS TYPE V STRAIN
 MKKRQKIWRGLSVTLILLISQIPFGILVQGETQDTNQAALGKVI VVKKTGDNATPLGKATFVL
 KNDNDKSETSHETVEGSGEATFENIKPGDYTLREETAPIGYKKTDKTWKVKVADNGATII
 EGMADADKAERKEVLNAQYPKSAIYEDTKENYPLVNVEGSKVGEQYKALNPINGKDRRE
 IAEGLWSKKITGVNDLKNKYKIELTVEGKTIVETKELNQPLDVVLLDNSNSMNNERAN
 NSQRAKAGEAVEKLIDKITSNKDNRVALTIVYASTIFDGTEATVSKGVADQNGKALNDSV
 SWDYHKTTFATTTHNYSYLNLTNDANEVNILKSRI PKEAEHINGDRTLYQFGATFTQKAL
 MKANEI LETQSSNARKKLI FHVTDGVPTMSYAINFNPIYSTSYQNQFNSFLNKI PDRSGI
 LQEDFI INGGDDYQIVKGDGESFKLFSDRKVPVTGGTTQAAAYRVPQNQLSVMSNEGYAINS
 GYIYLWYRDYNWVYFPDPKTKKVSATKQIKTHGEPTTLYFNGNIRPKGYDIFTVGIGVNG
 DPGATPLEAEKFMQSISSKTENYTNVDDTNKIYDELNKYFKTIVEEKHSIVDGNVTDPMG
 EMIEFQLKNGQSFTHDDYVLVGNDSGQKNGVALGGPNSDGGILKDVTVTYDKTSQTIKI
 NHLNLGSGQKVVLTYDVRLLKDNYSNKFYNTNNRTTLPKSEKEPNTIRDFPIPKIRDVR
 EFPVLTISNQKKMGEVEFIKVNKDKHSESLGAKFQLQIEKDFSGYKQFVPEGSDVTTKN
 DGKIYFKALQDGNKYLYEISSPDGYIEVKTTPVVTFTIQNGEVTNLKADPNANKNQIGYL
 EGNKGHLITNTPKRPPGVFPKTTGGIGTIVYILVGSFTMILITCSFRRKQL

SEQ ID NO. 4111: SAG0649 FROM 090 GBS TYPE Ia STRAIN
 GETQDTNQAALGKVI VVKKTGDNATPLGKATFVLKNDNDKSETSHETVEGSGEATFENIKPG
 DYTTLREETAPIGYKKTDKTWKVKVADNGATII EGMADADKAERKEVLNAQYPKSAIYEDT
 KENYPLVNVEGSKVGEQYKALNPINGKDRREIAEGLWSKKITGVNDLKNKYKIELTVE
 GKTIVETKELNQPLDVVLLDNSNSMNNERANNSQRAKAGEAVEKLIDKITSNKDNRVA
 LVTYASTIFDGTEATVSKGVADQNGKALNDSVSWDYHKTTFATTTHNYSYLNLTNDANEV
 NILKSRI PKEAEHINGDRTLYQFGATFTQKALMKANEI LETQSSNARKKLI FHVTDGVPT
 MSYAINFNPIYSTSYQNQFNSFLNKI PDRSGILQEDFI INGGDDYQIVKGDGESFKLFSDR
 KVPVTGGTTQAAAYRVPQNQLSVMSNEGYAINS GYIYLWYRDYNWVYFPDPKTKKVSATKQ
 IKTHGEPTTLYFNGNIRPKGYDIFTVGIGVNGDPGATPLEAEKFMQSISSKTENYTNVDD
 TNKIYDELNKYFKTIVEEKHSIVDGNVTDPMGEMIEFQLKNGQSFTHDDYVLVGNDSGQ
 KNGVALGGPNSDGGILKDVTVTYDKTSQTIKINHLNLGSGQKVVLTYDVRLLKDNYSNKF
 YNTNNRTTLPKSEKEPNTIRDFPIPKIRDVREFPVLTI SNQKKMGEVEFIKVNKDKHSE
 SLLGAKFQLQIEKDFSGYKQFVPEGSDVTTKNDGKIYFKALQDGNKYLYEISSPDGYIEV
 KTKPVVTFTIQNGEVTNLKADPNANKNQIGYLEGNGKHLITNTPKRPPGV

SEQ ID NO. 4112: SAG0649 FROM A909 GBS TYPE Ia STRAIN
 GETQDTNQAALGKVI VVKKTGDNATPLGKATFVLKNDNDKSETSHETVEGSGEATFENIKPG
 DYTTLREETAPIGYKKTDKTWKVKVADNGATII EGMADADKAERKEVLNAQYPKSAIYEDT
 KENYPLVNVEGSKVGEQYKALNPINGKDRREIAEGLWSKKITGVNDLKNKYKIELTVE
 GKTIVETKELNQPLDVVLLDNSNSMNNERANNSQRAKAGEAVEKLIDKITSNKDNRVA
 LVTYASTIFDGTEATVSKGVADQNGKALNDSVSWDYHKTTFATTTHNYSYLNLTNDANEV
 NILKSRI PKEAEHINGDRTLYQFGATFTQKALMKANEI LETQSSNARKKLI FHVTDGVPT
 MSYAINFNPIYSTSYQNQFNSFLNKI PDRSGILQEDFI INGGDDYQIVKGDGESFKLFSDR
 KVPVTGGTTQAAAYRVPQNQLSVMSNEGYAINS GYIYLWYRDYNWVYFPDPKTKKVSATKQ
 IKTHGEPTTLYFNGNIRPKGYDIFTVGIGVNGDPGATPLEAEKFMQSISSKTENYTNVDD
 TNKIYDELNKYFKTIVEEKHSIVDGNVTDPMGEMIEFQLKNGQSFTHDDYVLVGNDSGQ
 KNGVALGGPNSDGGILKDVTVTYDKTSQTIKINHLNLGSGQKVVLTYDVRLLKDNYSNKF
 YNTNNRTTLPKSEKEPNTIRDFPIPKIRDVREFPVLTI SNQKKMGEVEFIKVNKDKHSE
 SLLGAKFQLQIEKDFSGYKQFVPEGSDVTTKNDGKIYFKALQDGNKYLYEISSPDGYIEV
 KTKPVVTFTIQNGEVTNLKADPNANKNQIGYLEGNGKHLITNTPKRPPGV

SEQ ID NO. 4113: SAG0649 FROM 18RS21 GBS TYPE II STRAIN
 GETQDTNQAALGKVI VVKKTGDNATPLGKATFVLKNDNDKSETSHETVEGSGEATFENIKPG
 DYTTLREETAPIGYKKTDKTWKVKVADNGATII EGMADADKAERKEVLNAQYPKSAIYEDT
 KENYPLVNVEGSKVGEQYKALNPINGKDRREIAEGLWSKKITGVNDLKNKYKIELTVE
 GKTIVETKELNQPLDVVLLDNSNSMNNERANNSQRAKAGEAVEKLIDKITSNKDNRVA
 LVTYASTIFDGTEATVSKGVADQNGKALNDSVSWDYHKTTFATTTHNYSYLNLTNDANEV
 NILKSRI PKEAEHINGDRTLYQFGATFTQKALMKANEI LETQSSNARKKLI FHVTDGVPT
 MSYAINFNPIYSTSYQNQFNSFLNKI PDRSGILQEDFI INGGDDYQIVKGDGESFKLFSDR
 KVPVTGGTTQAAAYRVPQNQLSVMSNEGYAINS GYIYLWYRDYNWVYFPDPKTKKVSATKQ
 IKTHGEPTTLYFNGNIRPKGYDIFTVGIGVNGDPGATPLEAEKFMQSISSKTENYTNVDD
 TNKIYDELNKYFKTIVEEKHSIVDGNVTDPMGEMIEFQLKNGQSFTHDDYVLVGNDSGQ
 KNGVALGGPNSDGGILKDVTVTYDKTSQTIKINHLNLGSGQKVVLTYDVRLLKDNYSNKF
 YNTNNRTTLPKSEKEPNTIRDFPIPKIRDVREFPVLTI SNQKKMGEVEFIKVNKDKHSE
 SLLGAKFQLQIEKDFSGYKQFVPEGSDVTTKNDGKIYFKALQDGNKYLYEISSPDGYIEV
 KTKPVVTFTIQNGEVTNLKADPNANKNQIGYLEGNGKHLITNTPKRPPGV

SEQ ID NO. 4114: SAG0649 FROM M732 GBS TYPE III STRAIN
 GETQDTNQAALGKVI VVKKTGDNATPLGKATFVLKNDNDKSETSHETVEGSGEATFENIKPG
 DYTTLREETAPIGYKKTDKTWKVKVADNGATII EGMADADKAERKEVLNAQYPKSAIYEDT
 KENYPLVNVEGSKVGEQYKALNPINGKDRREIAEGLWSKKITGVNDLKNKYKIELTVE
 GKTIVETKELNQPLDVVLLDNSNSMNNERANNSQRAKAGEAVEKLIDKITSNKDNRVA
 LVTYASTIFDGTEATVSKGVADQNGKALNDSVSWDYHKTTFATTTHNYSYLNLTNDANEV
 NILKSRI PKEAEHINGDRTLYQFGATFTQKALMKANEI LETQSSNARKKLI FHVTDGVPT
 MSYAINFNPIYSTSYQNQFNSFLNKI PDRSGILQEDFI INGGDDYQIVKGDGESFKLFSDR
 KVPVTGGTTQAAAYRVPQNQLSVMSNEGYAINS GYIYLWYRDYNWVYFPDPKTKKVSATKQ
 IKTHGEPTTLYFNGNIRPKGYDIFTVGIGVNGDPGATPLEAEKFMQSISSKTENYTNVDD
 TNKIYDELNKYFKTIVEEKHSIVDGNVTDPMGEMIEFQLKNGQSFTHDDYVLVGNDSGQ
 KNGVALGGPNSDGGILKDVTVTYDKTSQTIKINHLNLGSGQKVVLTYDVRLLKDNYSNKF
 YNTNNRTTLPKSEKEPNTIRDFPIPKIRDVREFPVLTI SNQKKMGEVEFIKVNKDKHSE
 SLLGAKFQLQIEKDFSGYKQFVPEGSDVTTKNDGKIYFKALQDGNKYLYEISSPDGYIEV
 KTKPVVTFTIQNGEVTNLKADPNANKNQIGYLEGNGKHLITNTPKRPPGV

SEQ ID NO. 4115: SAG0649 FROM COH1 GBS TYPE III STRAIN
 GETQDTNQAALGKVI VVKKTGDNATPLGKATFVLKNDNDKSETSHETVEGSGEATFENIKPG

Table 41: Comparative Sequences relating to SAG0649

DYTLREETAPIGYKKTDKTWKVKVADNGATII EGMDADKAEKRKEVLNAQYPKSAIYEDT
KENYPLVNVESKVGQYKALNPINGKDGRRREIAEGWLSKKITGVNDLDKNKYKIELTVE
GKTTVETKELNQPLDVVLLDNSNSMNNRANNSQRALKAGEAVEKLIDKITSNKNRVA
LVITYASTIFDGTEATVSKGVADQNGKALNDSVSWDYHKTTFTATTNYSYLNLTNDANEV
NILKSRI PKEAEHINGDRITLYQFGATFTQKALMKANEILETQSSNARKKLI FHVTDGVPT
MSYAINFNPIYSTSYQNQFNSFLNKIPDRSGILQEDFI INGDDYQIVKGDGESFKLFSDR
KVPVTGGTTQAAAYRVPQNLQSVMSNEGAI NSGYIYLWRDYNWVYFPDPKTKKVSATKQ
IKTHGEPTTLYFNGNIRPKGYDIFTVGIGVNGDPGATPLEAEKFMQSISSKTENYTNVDD
TNKIYDELNKYFKTIVEEKHSIVDGNVTDPMGEMIEFQKNGQSFTHDDYVLVGNDSQSL
KNGVALGGPNSDGGILKDVTVTYDKTSQTIKINHLNLGSGQKVVLTYDVRKLDNYISNKF
YNTNNRTTLLSPKSEKEPNTIRDFPIPKIRDVREFFVLTISNQQKMGEVEFIKVNKDKHSE
SLLGAKFQLQIEKDFSGYKQFVPEGSVDTTKNDGKIYFKALQDGNKYLYEISSPDGYIEV
KTKPVVFTTIQNGEVTLNKAADPNANKNQIGYLEGNKGHLITNTPKRPPGV

SEQ ID NO. 4115: SAG0649 FROM M781 GBS TYPE III STRAIN
GKVIIVKKTGDTATPLGKATFVLKNDNDKSETSHETVEGSGKATFENIKPGDYTLREETAP
IGYKKTDKTWKVKVADNGATII EGMDADKAEKRKEVLNAQYPKSAIYEDTKENYPLVNV
GSKVGEQYKALNPINGKDGRRREIAEGWLSKKITGVNDLDKNKYKIELTVEGKTTVETKEL
NQPLDVVLLDNSNSMNNRANNSQRALKAGEAVEKLIDKITSNKNRVALVITYASTIFD
GTEATVSKGVADQNGKALNDSVSWDYHKTTFTATTNYSYLNLTNDANEVNILKSRI PKE
AEHINGDRITLYQFGATFTQKALMKANEILETQSSNARKKLI FHVTDGVPTMSYAINFNPI
YSTSYQNQFNSFLNKIPDRSGILQEDFI INGDDYQIVKGDGESFKLFSDRKVPVTGGTTQ
AAAYRVPQNLQSVMSNEGAI NSGYIYLWRDYNWVYFPDPKTKKVSATKQIKTHGEPTTLY
FNGNIRPKGYDIFTVGIGVNGDPGATPLEAEKFMQSISSKTENYTNVDDTNKIYDELNK
YFKTIVEEKHSIVDGNVTDPMGEMIEFQKNGQSFTHDDYVLVGNDSQSLKNGVALGGPN
SDGGILKDVTVTYDKTSQTIKINHLNLGSGQKVVLTYDVRKLDNYISNKFYNTNNRTTLL
PKSEKEPNTIRDFPIPKIRDVREFFVLTISNQQKMGEVEFIKVNKDKHSESLLGAKFQLQ
IEKDFSGYKQFVPEGSVDTTKNDGKIYFKALQDGNKYLYEISSPDGYIEVKTTPVVTFTI
QNGEVTLNKAADPNANKNQIGYLEGNKGHLITNTPKRPPGV

SEQ ID NO. 4117: SAG0649 FROM CJB110 GBS NONTYPEABLE STRAIN
GETQDTNQLGKVIIVKKTGDNATPLGKATFVLKNDNDKSETSHETVEGSGKATFENIKPG
DYTLREETAPIGYKKTDKTWKVKVADNGATII EGMDADKAEKRKEVLNAQYPKSAIYEDT
KENYPLVNVESKVGQYKALNPINGKDGRRREIAEGWLSKKITGVNDLDKNKYKIELTVE
GKTTVETKELNQPLDVVLLDNSNSMNNRANNSQRALKAGEAVEKLIDKITSNKNRVA
LVITYASTIFDGTEATVSKGVADQNGKALNDSVSWDYHKTTFTATTNYSYLNLTNDANEV
NILKSRI PKEAEHINGDRITLYQFGATFTQKALMKANEILETQSSNARKKLI FHVTDGVPT
MSYAINFNPIYSTSYQNQFNSFLNKIPDRSGILQEDFI INGDDYQIVKGDGESFKLFSDR
KVPVTGGTTQAAAYRVPQNLQSVMSNEGAI NSGYIYLWRDYNWVYFPDPKTKKVSATKQ
IKTHGEPTTLYFNGNIRPKGYDIFTVGIGVNGDPGATPLEAEKFMQSISSKTENYTNVDD
TNKIYDELNKYFKTIVEEKHSIVDGNVTDPMGEMIEFQKNGQSFTHDDYVLVGNDSQSL
KNGVALGGPNSDGGILKDVTVTYDKTSQTIKINHLNLGSGQKVVLTYDVRKLDNYISNKF
YNTNNRTTLLSPKSEKEPNTIRDFPIPKIRDVREFFVLTISNQQKMGEVEFIKVNKDKHSE
SLLGAKFQLQIEKDFSGYKQFVPEGSVDTTKNDGKIYFKALQDGNKYLYEISSPDGYIEV
KTKPVVFTTIQNGEVTLNKAADPNANKNQIGYLEGNKGHLITNTPKRPPGV

SEQ ID NO. 4118: SAG0649 FROM JM9130013 GBS TYPE VIII STRAIN
GETQDTNQLGKVIIVKKTGDNATPLGKATFVLKNDNDKSETSHETVEGSGKATFENIKPG
DYTLREETAPIGYKKTDKTWKVKVADNGATII EGMDADKAEKRKEVLNAQYPKSAIYEDT
KENYPLVNVESKVGQYKALNPINGKDGRRREIAEGWLSKKITGVNDLDKNKYKIELTVE
GKTTVETKELNQPLDVVLLDNSNSMNNRANNSQRALKAGEAVEKLIDKITSNKNRVA
LVITYASTIFDGTEATVSKGVADQNGKALNDSVSWDYHKTTFTATTNYSYLNLTNDANEV
NILKSRI PKEAEHINGDRITLYQFGATFTQKALMKANEILETQSSNARKKLI FHVTDGVPT
MSYAINFNPIYSTSYQNQFNSFLNKIPDRSGILQEDFI INGDDYQIVKGDGESFKLFSDR
KVPVTGGTTQAAAYRVPQNLQSVMSNEGAI NSGYIYLWRDYNWVYFPDPKTKKVSATKQ
IKTHGEPTTLYFNGNIRPKGYDIFTVGIGVNGDPGATPLEAEKFMQSISSKTENYTNVDD
TNKIYDELNKYFKTIVEEKHSIVDGNVTDPMGEMIEFQKNGQSFTHDDYVLVGNDSQSL
KNGVALGGPNSDGGILKDVTVTYDKTSQTIKINHLNLGSGQKVVLTYDVRKLDNYISNKF
YNTNNRTTLLSPKSEKEPNTIRDFPIPKIRDVREFFVLTISNQQKMGEVEFIKVNKDKHSE
SLLGAKFQLQIEKDFSGYKQFVPEGSVDTTKNDGKIYFKALQDGNKYLYEISSPDGYIEV
KTKPVVFTTIQNGEVTLNKAADPNANKNQIGYLEGNKGHLITNTPKRPPGV

Table 41: Comparative Sequences relating to SAG0649

PRETTY of: /biotmp/msa178371.2{*} May 12, 2003 09:25 ..

	1				50
msa178371.2{104_CJB110}	-----	-----	-----	-ge	tqdtngalGK VIVKKTGDnA
msa178371.2{104_M781}	-----	-----	-----	-----	-----GK VIVKKTGDnA
msa178371.2{104_COH1}	-----	-----	-----	-ge	tqdtngalGK VIVKKTGDnA
msa178371.2{104_M732}	-----	-----	-----	-ge	tqdtngalGK VIVKKTGDnA
msa178371.2{104_090}	-----	-----	-----	-ge	tqdtngalGK VIVKKTGDnA
msa178371.2{104_18RS21}	-----	-----	-----	-ge	tqdtngalGK VIVKKTGDnA
msa178371.2{104_2603}	mkkrqkiwrg	lsvtllilslq	ipfgilvgge	-----	tqdtngalGK VIVKKTGDnA
msa178371.2{104_A909}	-----	-----	-----	-ge	tqdtngalGK VIVKKTGDnA
msa178371.2{104_JM9130013}	-----	-----	-----	-ge	tqdtngalGK VIVKKTGDnA
Consensus	*****	*****	*****	-----	*****
	51				100
msa178371.2{104_CJB110}	TPLGKATFVL	KNDNDKSETS	HETVEGSGxA	TFENIKPGDY	TLREETAPIG
msa178371.2{104_M781}	TPLGKATFVL	KNDNDKSETS	HETVEGSGkA	TFENIKPGDY	TLREETAPIG
msa178371.2{104_COH1}	TPLGKATFVL	KNDNDKSETS	HETVEGSGxA	TFENIKPGDY	TLREETAPIG
msa178371.2{104_M732}	TPLGKATFVL	KNDNDKSETS	HETVEGSGeA	TFENIKPGDY	TLREETAPIG
msa178371.2{104_090}	TPLGKATFVL	KNDNDKSETS	HETVEGSGeA	TFENIKPGDY	TLREETAPIG
msa178371.2{104_18RS21}	TPLGKATFVL	KNDNDKSETS	HETVEGSGeA	TFENIKPGDY	TLREETAPIG
msa178371.2{104_2603}	TPLGKATFVL	KNDNDKSETS	HETVEGSGeA	TFENIKPGDY	TLREETAPIG
msa178371.2{104_A909}	TPLGKATFVL	KNDNDKSETS	HETVEGSGeA	TFENIKPGDY	TLREETAPIG
msa178371.2{104_JM9130013}	TPLGKATFVL	KNDNDKSETS	HETVEGSGeA	TFENIKPGDY	TLREETAPIG
Consensus	*****	*****	*****	*****	*****
	101				150
msa178371.2{104_CJB110}	YKKTDKTWKV	KVADNGAtII	EGMDADKAek	RKEVLNAQYP	KSaiYEDTKE
msa178371.2{104_M781}	YKKTDKTWKV	KVADNGAxII	EGMDADKAek	RKEVLNAQYP	KSaiYEDTKE
msa178371.2{104_COH1}	YKKTDKTWKV	KVADNGAtII	EGMDADKAek	RKEVLNAQYP	KSaiYEDTKE
msa178371.2{104_M732}	YKKTDKTWKV	KVADNGAtII	EGMDADKAek	RKEVLNAQYP	KSaiYEDTKE
msa178371.2{104_090}	YKKTDKTWKV	KVADNGAtII	EGMDADKAek	RKEVLNAQYP	KSaiYEDTKE
msa178371.2{104_18RS21}	YKKTDKTWKV	KVADNGAtII	EGMDADKAek	RKEVLNAQYP	KSaiYEDTKE
msa178371.2{104_2603}	YKKTDKTWKV	KVADNGAtII	EGMDADKAek	RKEVLNAQYP	KSaiYEDTKE
msa178371.2{104_A909}	YKKTDKTWKV	KVADNGAtII	EGMDADKAek	RKEVLNAQYP	KSaiYEDTKE
msa178371.2{104_JM9130013}	YKKTDKTWKV	KVADNGAtII	EGMDADKAek	RKEVLNAQYP	KSaiYEDTKE
Consensus	*****	*****	*****	*****	*****
	151				200
msa178371.2{104_CJB110}	NYPLVNVEGS	KVGEQYKALN	PINGKDGRRR	IAEGWLSKKi	TGVNDLDKNK
msa178371.2{104_M781}	NYPLVNVEGS	KVGEQYKALN	PINGKDGRRR	IAEGWLSKKi	TGVNDLDKNK
msa178371.2{104_COH1}	NYPLVNVEGS	KVGEQYKALN	PINGKDGRRR	IAEGWLSKKn	TGVNDLDKNK
msa178371.2{104_M732}	NYPLVNVEGS	KVGEQYKALN	PINGKDGRRR	IAEGWLSKKn	TGVNDLDKNK
msa178371.2{104_090}	NYPLVNVEGS	KVGEQYKALN	PINGKDGRRR	IAEGWLSKKi	TGVNDLDKNK
msa178371.2{104_18RS21}	NYPLVNVEGS	KVGEQYKALN	PINGKDGRRR	IAEGWLSKKi	TGVNDLDKNK
msa178371.2{104_2603}	NYPLVNVEGS	KVGEQYKALN	PINGKDGRRR	IAEGWLSKKi	TGVNDLDKNK
msa178371.2{104_A909}	NYPLVNVEGS	KVGEQYKALN	PINGKDGRRR	IAEGWLSKKi	TGVNDLDKNK
msa178371.2{104_JM9130013}	NYPLVNVEGS	KVGEQYKALN	PINGKDGRRR	IAEGWLSKKi	TGVNDLDKNK
Consensus	*****	*****	*****	*****	*****
	201				250
msa178371.2{104_CJB110}	YKIELTVEGK	TTVETKELNQ	PLDVVVLLDN	SNSMNNERAN	NSQRALKAGE
msa178371.2{104_M781}	YKIELTVEGK	TTVETKELNQ	PLDVVVLLDN	SNSMNNERAN	NSQRALKAGE
msa178371.2{104_COH1}	YKIELTVEGK	TTVETKELNQ	PLDVVVLLDN	SNSMNNERAN	NSQRALKAGE
msa178371.2{104_M732}	YKIELTVEGK	TTVETKELNQ	PLDVVVLLDN	SNSMNNERAN	NSQRALKAGE
msa178371.2{104_090}	YKIELTVEGK	TTVETKELNQ	PLDVVVLLDN	SNSMNNERAN	NSQRALKAGE
msa178371.2{104_18RS21}	YKIELTVEGK	TTVETKELNQ	PLDVVVLLDN	SNSMNNERAN	NSQRALKAGE
msa178371.2{104_2603}	YKIELTVEGK	TTVETKELNQ	PLDVVVLLDN	SNSMNNERAN	NSQRALKAGE
msa178371.2{104_A909}	YKIELTVEGK	TTVETKELNQ	PLDVVVLLDN	SNSMNNERAN	NSQRALKAGE
msa178371.2{104_JM9130013}	YKIELTVEGK	TTVETKELNQ	PLDVVVLLDN	SNSMNNERAN	NSQRALKAGE
Consensus	*****	*****	*****	*****	*****
	251				300
msa178371.2{104_CJB110}	AVEKLIDKIT	SNKDNRVALV	TYASTIFDGT	EATVSKGVAD	QNGKALNDSV
msa178371.2{104_M781}	AVEKLIDKIT	SNKDNRVALV	TYASTIFDGT	EATVSKGVAD	QNGKALNDSV
msa178371.2{104_COH1}	AVEKLIDKIT	SNKDNRVALV	TYASTIFDGT	EATVSKGVAD	QNGKALNDSV
msa178371.2{104_M732}	AVEKLIDKIT	SNKDNRVALV	TYASTIFDGT	EATVSKGVAD	QNGKALNDSV
msa178371.2{104_090}	AVEKLIDKIT	SNKDNRVALV	TYASTIFDGT	EATVSKGVAD	QNGKALNDSV
msa178371.2{104_18RS21}	AVEKLIDKIT	SNKDNRVALV	TYASTIFDGT	EATVSKGVAD	QNGKALNDSV
msa178371.2{104_2603}	AVEKLIDKIT	SNKDNRVALV	TYASTIFDGT	EATVSKGVAD	QNGKALNDSV
msa178371.2{104_A909}	AVEKLIDKIT	SNKDNRVALV	TYASTIFDGT	EATVSKGVAD	QNGKALNDSV
msa178371.2{104_JM9130013}	AVEKLIDKIT	SNKDNRVALV	TYASTIFDGT	EATVSKGVAD	QNGKALNDSV
Consensus	*****	*****	*****	*****	*****
	301				350
msa178371.2{104_CJB110}	SWDYHKTTFT	ATHNYSYLN	LTNDANEVNI	LKSRIPEBAE	HINGDRTLYQ
msa178371.2{104_M781}	SWDYHKTTFT	ATHNYSYLN	LTNDANEVNI	LKSRIPEBAE	HINGDRTLYQ
msa178371.2{104_COH1}	SWDYHKTTFT	ATHNYSYLN	LTNDANEVNI	LKSRIPEBAE	HINGDRTLYQ
msa178371.2{104_M732}	SWDYHKTTFT	ATHNYSYLN	LTNDANEVNI	LKSRIPEBAE	HINGDRTLYQ
msa178371.2{104_090}	SWDYHKTTFT	ATHNYSYLN	LTNDANEVNI	LKSRIPEBAE	HINGDRTLYQ
msa178371.2{104_18RS21}	SWDYHKTTFT	ATHNYSYLN	LTNDANEVNI	LKSRIPEBAE	HINGDRTLYQ
msa178371.2{104_2603}	SWDYHKTTFT	ATHNYSYLN	LTNDANEVNI	LKSRIPEBAE	HINGDRTLYQ
msa178371.2{104_A909}	SWDYHKTTFT	ATHNYSYLN	LTNDANEVNI	LKSRIPEBAE	HINGDRTLYQ

Table 41: Comparative Sequences relating to SAG0649

msa178371.2{104_JM9130013}	SWDYHKITFT	ATTHNYSYLN	LTDANEVNI	LKSRIPEAE	HINGDRITLYQ
Consensus	*****	*****	*****	*****	*****
	351				400
msa178371.2{104_CJB110}	FGATFTQKAL	MKANEILETO	SSNARKKLIF	HVTIDGVPTMS	YAINFNPIYS
msa178371.2{104_M781}	FGATFTQKAL	MKANEILETO	SSNARKKLIF	HVTIDGVPTMS	YAINFNPIYS
msa178371.2{104_COH1}	FGATFTQKAL	MKANEILETO	SSNARKKLIF	HVTIDGVPTMS	YAINFNPIYS
msa178371.2{104_M732}	FGATFTQKAL	MKANEILETO	SSNARKKLIF	HVTIDGVPTMS	YAINFNPIYS
msa178371.2{104_090}	FGATFTQKAL	MKANEILETO	SSNARKKLIF	HVTIDGVPTMS	YAINFNPIYS
msa178371.2{104_18RS21}	FGATFTQKAL	MKANEILETO	SSNARKKLIF	HVTIDGVPTMS	YAINFNPIYS
msa178371.2{104_2603}	FGATFTQKAL	MKANEILETO	SSNARKKLIF	HVTIDGVPTMS	YAINFNPIYS
msa178371.2{104_A909}	FGATFTQKAL	MKANEILETO	SSNARKKLIF	HVTIDGVPTMS	YAINFNPIYS
msa178371.2{104_JM9130013}	FGATFTQKAL	MKANEILETO	SSNARKKLIF	HVTIDGVPTMS	YAINFNPIYS
Consensus	*****	*****	*****	*****	*****
	401				450
msa178371.2{104_CJB110}	TSYQNQFNSF	LNKIPDRSGI	LQEDFIINGD	DYQIVKGDGE	SFKLFSDRKV
msa178371.2{104_M781}	TSYQNQFNSF	LNKIPDRSGI	LQEDFIINGD	DYQIVKGDGE	SFKLFSDRKV
msa178371.2{104_COH1}	TSYQNQFNSF	LNKIPDRSGI	LQEDFIINGD	DYQIVKGDGE	SFKLFSDRKV
msa178371.2{104_M732}	TSYQNQFNSF	LNKIPDRSGI	LQEDFIINGD	DYQIVKGDGE	SFKLFSDRKV
msa178371.2{104_090}	TSYQNQFNSF	LNKIPDRSGI	LQEDFIINGD	DYQIVKGDGE	SFKLFSDRKV
msa178371.2{104_18RS21}	TSYQNQFNSF	LNKIPDRSGI	LQEDFIINGD	DYQIVKGDGE	SFKLFSDRKV
msa178371.2{104_2603}	TSYQNQFNSF	LNKIPDRSGI	LQEDFIINGD	DYQIVKGDGE	SFKLFSDRKV
msa178371.2{104_A909}	TSYQNQFNSF	LNKIPDRSGI	LQEDFIINGD	DYQIVKGDGE	SFKLFSDRKV
msa178371.2{104_JM9130013}	TSYQNQFNSF	LNKIPDRSGI	LQEDFIINGD	DYQIVKGDGE	SFKLFSDRKV
Consensus	*****	*****	*****	*****	*****
	451				500
msa178371.2{104_CJB110}	PVTGGTTQAA	YRVPQNQLSV	MSNEGYAINS	GYIYLYWRDY	NWVYFPDPKT
msa178371.2{104_M781}	PVTGGTTQAA	YRVPQNQLSV	MSNEGYAINS	GYIYLYWRDY	NWVYFPDPKT
msa178371.2{104_COH1}	PVTGGTTQAA	YRVPQNQLSV	MSNEGYAINS	GYIYLYWRDY	NWVYFPDPKT
msa178371.2{104_M732}	PVTGGTTQAA	YRVPQNQLSV	MSNEGYAINS	GYIYLYWRDY	NWVYFPDPKT
msa178371.2{104_090}	PVTGGTTQAA	YRVPQNQLSV	MSNEGYAINS	GYIYLYWRDY	NWVYFPDPKT
msa178371.2{104_18RS21}	PVTGGTTQAA	YRVPQNQLSV	MSNEGYAINS	GYIYLYWRDY	NWVYFPDPKT
msa178371.2{104_2603}	PVTGGTTQAA	YRVPQNQLSV	MSNEGYAINS	GYIYLYWRDY	NWVYFPDPKT
msa178371.2{104_A909}	PVTGGTTQAA	YRVPQNQLSV	MSNEGYAINS	GYIYLYWRDY	NWVYFPDPKT
msa178371.2{104_JM9130013}	PVTGGTTQAA	YRVPQNQLSV	MSNEGYAINS	GYIYLYWRDY	NWVYFPDPKT
Consensus	*****	*****	*****	*****	*****
	501				550
msa178371.2{104_CJB110}	KKVSATKQIK	THGEPTTLFY	NGNIRPKGYD	IFTVGIGVNG	DPGATPLEAE
msa178371.2{104_M781}	KKVSATKQIK	THGEPTTLFY	NGNIRPKGYD	IFTVGIGVNG	DPGATPLEAE
msa178371.2{104_COH1}	KKVSATKQIK	THGEPTTLFY	NGNIRPKGYD	IFTVGIGVNG	DPGATPLEAE
msa178371.2{104_M732}	KKVSATKQIK	THGEPTTLFY	NGNIRPKGYD	IFTVGIGVNG	DPGATPLEAE
msa178371.2{104_090}	KKVSATKQIK	THGEPTTLFY	NGNIRPKGYD	IFTVGIGVNG	DPGATPLEAE
msa178371.2{104_18RS21}	KKVSATKQIK	THGEPTTLFY	NGNIRPKGYD	IFTVGIGVNG	DPGATPLEAE
msa178371.2{104_2603}	KKVSATKQIK	THGEPTTLFY	NGNIRPKGYD	IFTVGIGVNG	DPGATPLEAE
msa178371.2{104_A909}	KKVSATKQIK	THGEPTTLFY	NGNIRPKGYD	IFTVGIGVNG	DPGATPLEAE
msa178371.2{104_JM9130013}	KKVSATKQIK	THGEPTTLFY	NGNIRPKGYD	IFTVGIGVNG	DPGATPLEAE
Consensus	*****	*****	*****	*****	*****
	551				600
msa178371.2{104_CJB110}	KFMQSISSKT	ENYTNVDDTN	KIYDELNKYF	KTIIVEEKHSI	VDGNVTDPMG
msa178371.2{104_M781}	KFMQSISSKT	ENYTNVDDTN	KIYDELNKYF	KTIIVEEKHSI	VDGNVTDPMG
msa178371.2{104_COH1}	KFMQSISSKT	ENYTNVDDTN	KIYDELNKYF	KTIIVEEKHSI	VDGNVTDPMG
msa178371.2{104_M732}	KFMQSISSKT	ENYTNVDDTN	KIYDELNKYF	KTIIVEEKHSI	VDGNVTDPMG
msa178371.2{104_090}	KFMQSISSKT	ENYTNVDDTN	KIYDELNKYF	KTIIVEEKHSI	VDGNVTDPMG
msa178371.2{104_18RS21}	KFMQSISSKT	ENYTNVDDTN	KIYDELNKYF	KTIIVEEKHSI	VDGNVTDPMG
msa178371.2{104_2603}	KFMQSISSKT	ENYTNVDDTN	KIYDELNKYF	KTIIVEEKHSI	VDGNVTDPMG
msa178371.2{104_A909}	KFMQSISSKT	ENYTNVDDTN	KIYDELNKYF	KTIIVEEKHSI	VDGNVTDPMG
msa178371.2{104_JM9130013}	KFMQSISSKT	ENYTNVDDTN	KIYDELNKYF	KTIIVEEKHSI	VDGNVTDPMG
Consensus	*****	*****	*****	*****	*****
	601				650
msa178371.2{104_CJB110}	EMIEFQLKNG	QSFTHDDYVL	VGNDGSQKLN	GVALGGPNSD	GGILKDVTVT
msa178371.2{104_M781}	EMIEFQLKNG	QSFTHDDYVL	VGNDGSQKLN	GVALGGPNSD	GGILKDVTVT
msa178371.2{104_COH1}	EMIEFQLKNG	QSFTHDDYVL	VGNDGSQKLN	GVALGGPNSD	GGILKDVTVT
msa178371.2{104_M732}	EMIEFQLKNG	QSFTHDDYVL	VGNDGSQKLN	GVALGGPNSD	GGILKDVTVT
msa178371.2{104_090}	EMIEFQLKNG	QSFTHDDYVL	VGNDGSQKLN	GVALGGPNSD	GGILKDVTVT
msa178371.2{104_18RS21}	EMIEFQLKNG	QSFTHDDYVL	VGNDGSQKLN	GVALGGPNSD	GGILKDVTVT
msa178371.2{104_2603}	EMIEFQLKNG	QSFTHDDYVL	VGNDGSQKLN	GVALGGPNSD	GGILKDVTVT
msa178371.2{104_A909}	EMIEFQLKNG	QSFTHDDYVL	VGNDGSQKLN	GVALGGPNSD	GGILKDVTVT
msa178371.2{104_JM9130013}	EMIEFQLKNG	QSFTHDDYVL	VGNDGSQKLN	GVALGGPNSD	GGILKDVTVT
Consensus	*****	*****	*****	*****	*****
	651				700
msa178371.2{104_CJB110}	YDKTSQTIKI	NHLNLGSGQK	VVLTVDVRLK	DNYISNKFYN	TNNRTTLPSPK
msa178371.2{104_M781}	YDKTSQTIKI	NHLNLGSGQK	VVLTVDVRLK	DNYISNKFYN	TNNRTTLPSPK
msa178371.2{104_COH1}	YDKTSQTIKI	NHLNLGSGQK	VVLTVDVRLK	DNYISNKFYN	TNNRTTLPSPK
msa178371.2{104_M732}	YDKTSQTIKI	NHLNLGSGQK	VVLTVDVRLK	DNYISNKFYN	TNNRTTLPSPK
msa178371.2{104_090}	YDKTSQTIKI	NHLNLGSGQK	VVLTVDVRLK	DNYISNKFYN	TNNRTTLPSPK
msa178371.2{104_18RS21}	YDKTSQTIKI	NHLNLGSGQK	VVLTVDVRLK	DNYISNKFYN	TNNRTTLPSPK
msa178371.2{104_2603}	YDKTSQTIKI	NHLNLGSGQK	VVLTVDVRLK	DNYISNKFYN	TNNRTTLPSPK

Table 41: Comparative Sequences relating to SAG0649

msa178371.2{104_A909}	YDKTSQTIKI	NHLNLGSGQK	VVLTYDVRLK	DNYISNKFYN	TNNRTTTLSPK
msa178371.2{104_JM9130013}	YDKTSQTIKI	NHLNLGSGQK	VVLTYDVRLK	DNYISNKFYN	TNNRTTTLSPK
Consensus	*****	*****	*****	*****	*****
	701				750
msa178371.2{104_CJB110}	SEKEPNTIRD	FPIPKIRDVR	EFFVLTISNQ	KKMGEVEFIK	VNKDKHSESL
msa178371.2{104_M781}	SEKEPNTIRD	FPIPKIRDVR	EFFVLTISNQ	KKMGEVEFIK	VNKDKHSESL
msa178371.2{104_COH1}	SEKEPNTIRD	FPIPKIRDVR	EFFVLTISNQ	KKMGEVEFIK	VNKDKHSESL
msa178371.2{104_M732}	SEKEPNTIRD	FPIPKIRDVR	EFFVLTISNQ	KKMGEVEFIK	VNKDKHSESL
msa178371.2{104_090}	SEKEPNTIRD	FPIPKIRDVR	EFFVLTISNQ	KKMGEVEFIK	VNKDKHSESL
msa178371.2{104_18RS21}	SEKEPNTIRD	FPIPKIRDVR	EFFVLTISNQ	KKMGEVEFIK	VNKDKHSESL
msa178371.2{104_2603}	SEKEPNTIRD	FPIPKIRDVR	EFFVLTISNQ	KKMGEVEFIK	VNKDKHSESL
msa178371.2{104_A909}	SEKEPNTIRD	FPIPKIRDVR	EFFVLTISNQ	KKMGEVEFIK	VNKDKHSESL
msa178371.2{104_JM9130013}	SEKEPNTIRD	FPIPKIRDVR	EFFVLTISNQ	KKMGEVEFIK	VNKDKHSESL
Consensus	*****	*****	*****	*****	*****
	751				800
msa178371.2{104_CJB110}	LGAKFQLQIe	KDFSGYKQFV	PEGSDVTTKN	DGKIYFKALQ	DGNYKLYEIS
msa178371.2{104_M781}	LGAKFQLQIe	KDFSGYKQFV	PEGSDVTTKN	DGKIYFKALQ	DGNYKLYEIS
msa178371.2{104_COH1}	LGAKFQLQIe	KDFSGYKQFV	PEGSDVTTKN	DGKIYFKALQ	DGNYKLYEIS
msa178371.2{104_M732}	LGAKFQLQIe	KDFSGYKQFV	PEGSDVTTKN	DGKIYFKALQ	DGNYKLYEIS
msa178371.2{104_090}	LGAKFQLQIe	KDFSGYKQFV	PEGSDVTTKN	DGKIYFKALQ	DGNYKLYEIS
msa178371.2{104_18RS21}	LGAKFQLQIe	KDFSGYKQFV	PEGSDVTTKN	DGKIYFKALQ	DGNYKLYEIS
msa178371.2{104_2603}	LGAKFQLQIe	KDFSGYKQFV	PEGSDVTTKN	DGKIYFKALQ	DGNYKLYEIS
msa178371.2{104_A909}	LGAKFQLQIe	KDFSGYKQFV	PEGSDVTTKN	DGKIYFKALQ	DGNYKLYEIS
msa178371.2{104_JM9130013}	LGAKFQLQIe	KDFSGYKQFV	PEGSDVTTKN	DGKIYFKALQ	DGNYKLYEIS
Consensus	*****	*****	*****	*****	*****
	801				850
msa178371.2{104_CJB110}	SPDGYIEVKT	KPVVTFITQN	GEVTNLKADP	NANKNQIGYL	Egngkhlitn
msa178371.2{104_M781}	SPDGYIEVKT	KPVVTFITQN	GEVTNLKADP	NANKNQIGYL	Egngkhlitn
msa178371.2{104_COH1}	SPDGYIEVKT	KPVVTFITQN	GEVTNLKADP	NANKNQIGYL	Egngkhlitn
msa178371.2{104_M732}	SPDGYIEVKT	KPVVTFITQN	GEVTNLKADP	NANKNQIGYL	Egngkhlitn
msa178371.2{104_090}	SPDGYIEVKT	KPVVTFITQN	GEVTNLKADP	NANKNQIGYL	Egngkhlitn
msa178371.2{104_18RS21}	SPDGYIEVKT	KPVVTFITQN	GEVTNLKADP	NANKNQIGYL	Egngkhlitn
msa178371.2{104_2603}	SPDGYIEVKT	KPVVTFITQN	GEVTNLKADP	NANKNQIGYL	Egngkhlitn
msa178371.2{104_A909}	SPDGYIEVKT	KPVVTFITQN	GEVTNLKADP	NANKNQIGYL	Egngkhlitn
msa178371.2{104_JM9130013}	SPDGYIEVKT	KPVVTFITQN	GEVTNLKADP	NANKNQIGYL	E-----
Consensus	*****	*****	*****	*****	E-----
	851				890
msa178371.2{104_CJB110}	tpkrppgv--	-----	-----	-----	-----
msa178371.2{104_M781}	tpkrppgv--	-----	-----	-----	-----
msa178371.2{104_COH1}	tpkrppgv--	-----	-----	-----	-----
msa178371.2{104_M732}	tpkrppgv--	-----	-----	-----	-----
msa178371.2{104_090}	tpkrppgv--	-----	-----	-----	-----
msa178371.2{104_18RS21}	tpkrppgv--	-----	-----	-----	-----
msa178371.2{104_2603}	tpkrppgvfp	ktggigtivy	ilvgstfmil	ticsfrkql	-----
msa178371.2{104_A909}	tpkrppgv--	-----	-----	-----	-----
msa178371.2{104_JM9130013}	-----	-----	-----	-----	-----
Consensus	-----*	*****	*****	*****	*****